



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 10:39 AM UTC

PDB ID : 5Z58 / pdb_00005z58
EMDB ID : EMD-6891
Title : Cryo-EM structure of a human activated spliceosome (early Bact) at 4.9 angstrom.
Authors : Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on : 2018-01-17
Resolution : 4.90 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

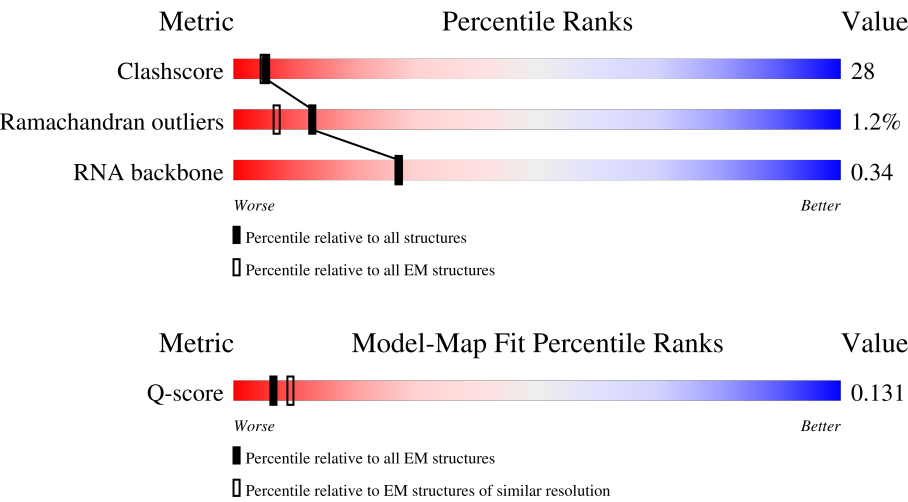
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	1274 (4.40 - 5.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2335	
2	B	117	
3	C	972	
4	D	2136	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	357	
6	a	126	
6	h	126	
7	b	231	
7	i	231	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	107	
14	G	274	
15	H	188	
16	o	255	
17	p	225	
18	w	501	
19	u	793	
20	v	464	
21	1	1304	
22	2	895	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
23	3	1217	
24	4	424	
25	5	125	
26	6	110	
27	7	86	
28	J	848	
29	L	802	
30	M	343	
31	P	229	
32	R	540	
33	T	514	
34	V	908	
35	X	396	
36	Y	322	
37	Z	619	
38	z	472	
39	x	1041	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
41	GTP	C	1500	-	-	X	-

2 Entry composition [i](#)

There are 43 unique types of molecules in this entry. The entry contains 94673 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2211	Total	C	N	O	S	0	0
			18165	11706	3163	3220	76		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	P	0	0
			1768	792	295	597	84		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	860	Total	C	N	O	S	0	0
			6716	4294	1120	1270	32		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1722	Total	C	N	O		0	0
			8528	5084	1722	1722			

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	299	Total	C	N	O	S	0	0
			2338	1470	410	445	13		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	81	Total	C	N	O		0	0
			399	237	81	81			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
6	h	80	Total	C	N	O	0	0
			393	233	80	80		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	b	82	Total	C	N	O	0	0
			405	241	82	82		
7	i	86	Total	C	N	O	0	0
			422	250	86	86		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	c	82	Total	C	N	O	0	0
			406	242	82	82		
8	j	82	Total	C	N	O	0	0
			406	242	82	82		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	d	97	Total	C	N	O	0	0
			480	286	97	97		
9	k	85	Total	C	N	O	0	0
			422	252	85	85		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	f	74	Total	C	N	O	0	0
			361	213	74	74		
10	m	74	Total	C	N	O	0	0
			361	213	74	74		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	e	79	Total	C	N	O	0	0
			391	233	79	79		
11	l	79	Total	C	N	O	0	0
			391	233	79	79		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total	C	N	O	0	0
			363	215	74	74		
12	n	68	Total	C	N	O	0	0
			334	198	68	68		

- Molecule 13 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	93	Total	C	N	O	P	0	0
			1988	889	363	643	93		

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	77	Total	C	N	O	P	0	0
			1545	689	240	539	77		

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	136	Total	C	N	O	P	0	0
			2886	1289	499	962	136		

- Molecule 16 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	o	162	Total	C	N	O	0	0
			804	480	162	162		

- Molecule 17 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	p	165	Total	C	N	O	0	0
			813	483	165	165		

- Molecule 18 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	437	Total	C	N	O	S	0	0
			2369	1448	460	458	3		

- Molecule 19 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	u	105	Total	C	N	O	0	0
			525	315	105	105		

- Molecule 20 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	v	98	Total	C	N	O	0	0
			486	290	98	98		

- Molecule 21 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1	1038	Total	C	N	O	S	0	0
			7702	4900	1347	1415	40		

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	183	Total	C	N	O	S	0	0
			1252	809	213	226	4		

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1177	Total	C	N	O	S	0	0
			9220	5854	1566	1755	45		

- Molecule 24 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	4	78	Total	C	N	O	0	0
			527	345	83	99		

- Molecule 25 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	5	108	Total	C	N	O	S	0	0
			807	512	142	150	3		

- Molecule 26 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	89	Total	C	N	O	S	0	0
			670	410	119	128	13		

- Molecule 27 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	66	Total	C	N	O	S	0	0
			540	343	94	98	5		

- Molecule 28 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	J	522	Total	C	N	O	S	0	0
			3463	2156	653	648	6		

- Molecule 29 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	132	Total	C	N	O	S	0	0
			1077	691	188	194	4		

- Molecule 30 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	36	Total	C	N	O	S	0	0
			267	167	45	52	3		

- Molecule 31 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	P	96	Total	C	N	O	S	0	0
			829	508	162	157	2		

- Molecule 32 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R	309	Total	C	N	O	S	0	0
			2314	1454	413	435	12		

- Molecule 33 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	313	Total	C	N	O	S	0	0
			2457	1552	447	450	8		

- Molecule 34 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	V	451	Total	C	N	O		0	0
			2238	1336	451	451			

- Molecule 35 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	X	158	Total	C	N	O	S	0	0
			1012	645	172	194	1		

- Molecule 36 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	104	Total	C	N	O	S	0	0
			737	466	126	143	2		

- Molecule 37 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Z	113	Total	C	N	O		0	0
			755	474	147	134			

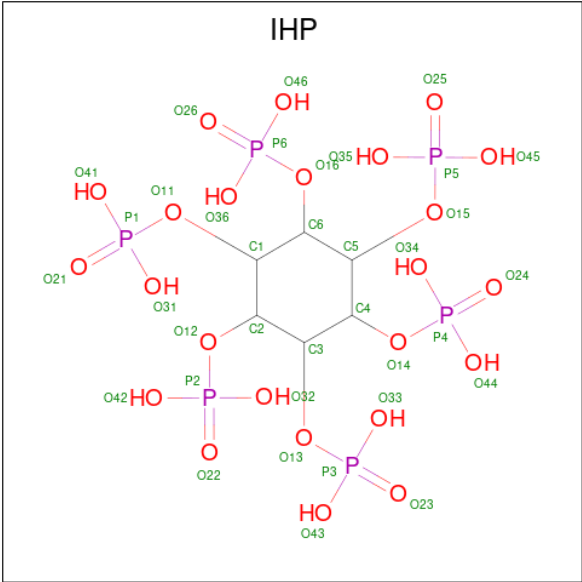
- Molecule 38 is a protein called Peptidyl-prolyl cis-trans isomerase CWC27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	z	177	Total	C	N	O	S	1	0
			1381	869	241	266	5		

- Molecule 39 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

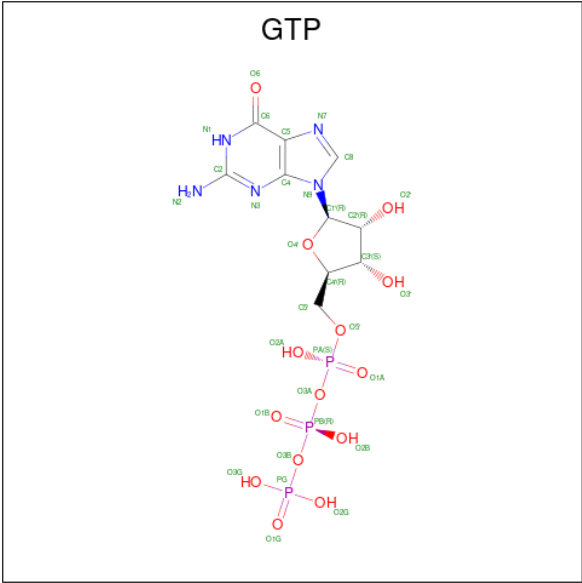
Mol	Chain	Residues	Atoms					AltConf	Trace
39	x	583	Total	C	N	O		0	0
			2882	1715	583	584			

- Molecule 40 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆).



Mol	Chain	Residues	Atoms				AltConf
40	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 41 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
41	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 42 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
42	C	1	Total 1	Mg 1	0
42	F	5	Total 5	Mg 5	0

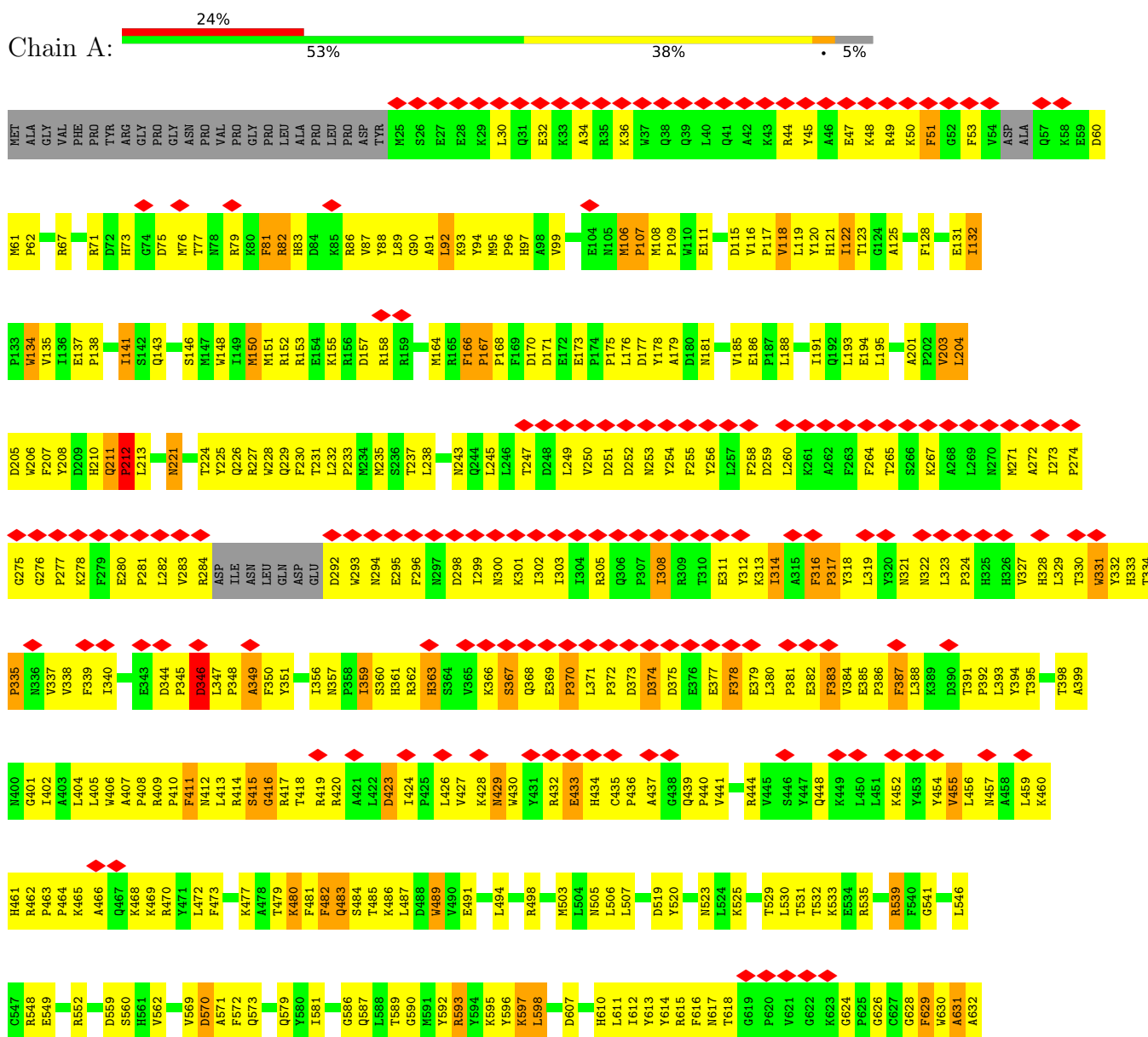
- Molecule 43 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
43	6	3	Total 3	Zn 3	0
43	M	1	Total 1	Zn 1	0

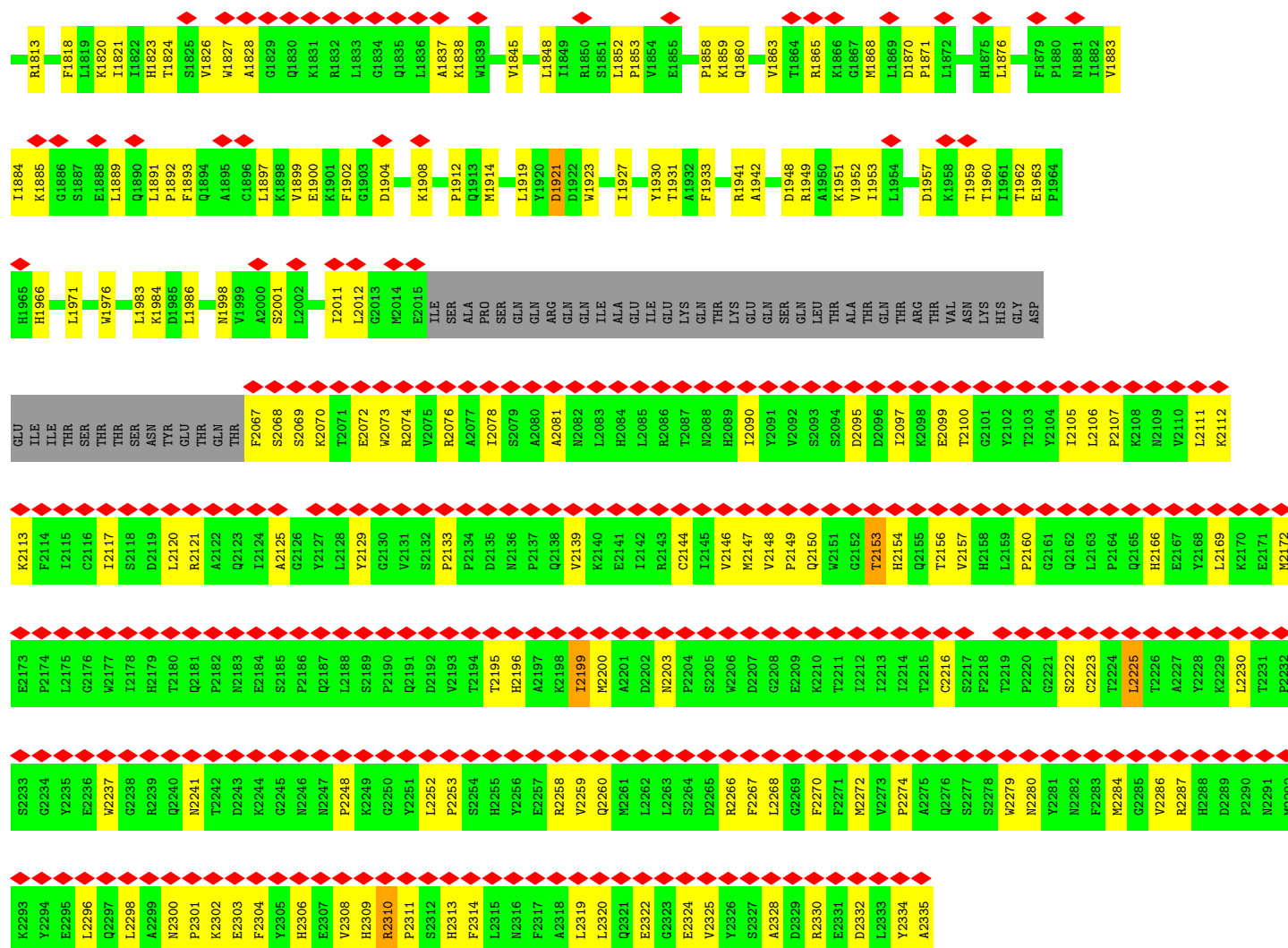
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

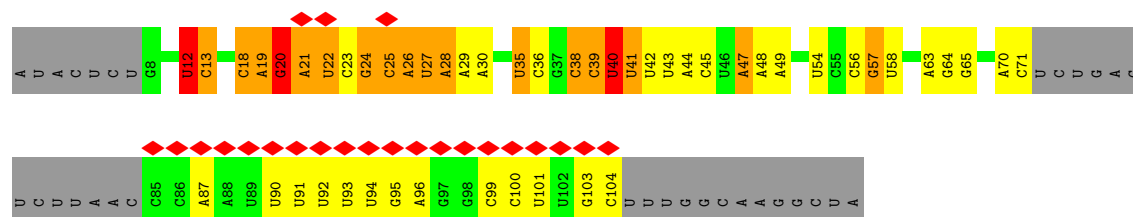
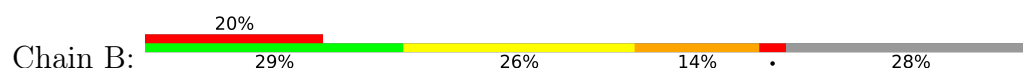
• Molecule 1: Pre-mRNA-processing-splicing factor 8



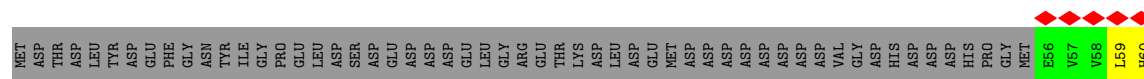
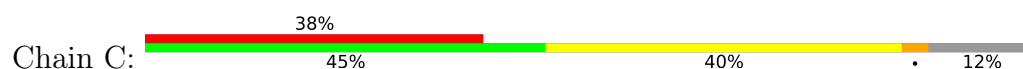




• Molecule 2: U5 snRNA

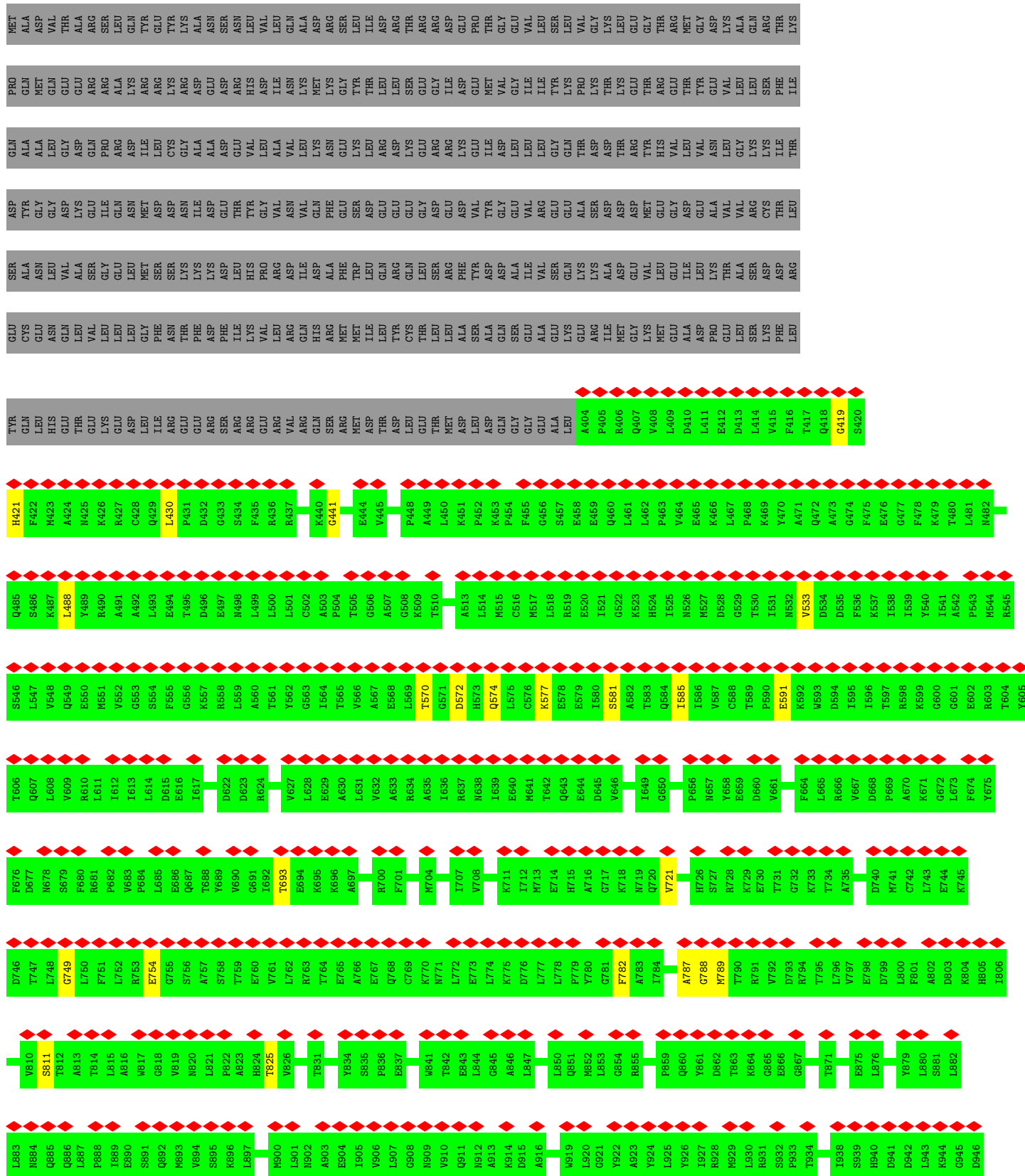


• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component



SER	E61	M123	P185	N258	G332	I401	P473	S533	P594	E668	A729	K790	S880
ILE	D62	D124	V186	K289	D333	L408	L474	V534	V595	E669	R730	I791	F881
LYS	K63	N125	T187	D261	I334	K409	K475	A535	N596	T669	S731	L792	G882
PHE	K64	S126	V188	R262	N335	L410	C476	R536	P597	S670	I732	D793	F883
ASP	Y65	E127	V189	L263	Y336	R411	H477	E537	S598	S671	W733	A794	E884
PRO	Y66	L128	L190	L264	F339	I412	T478	E540	E599	L672	A794	W795	T885
LEU	P67	L129	L191	L265	G344	P414	K480	E541	L600	K673	F735	W796	L886
MET	T68	R130	P191	E266	W345	R417	S483	Y541	P601	C674	G736	A797	R888
GLU	A69	N131	T193	P270	L343	L416	K482	Y542	K602	A676	D738	Q798	Q892
LEU	E70	G136	G195	Y275	W444	L418	S484	R543	M603	E677	A739	E799	Q893
LEU	E71	G137	L199	R279	F349	V419	D485	P544	G606	T678	T740	F800	Q894
ALA	W72	G138	L200	H280	N350	C420	D486	P545	L607	P679	G741	L801	A895
LYS	W73	L139	F200	H281	P351	F423	G487	A546	R608	N680	P742	H802	F896
GLN	I80	H140	T202	L281	K352	F424	V488	G547	K609	K681	W743	R803	S897
ASP	G141	H140	M203	V282	T353	G425	Q489	Y549	K612	N683	L744	G804	L898
VAL	Q82	K142	D204	E284	R354	E426	Q489	W550	W614	T685	L745	G805	S899
LEU	Q83	T143	H208	G287	K355	T428	A492	E553	S613	T686	W746	G806	H902
ASN	E84	C144	W208	L288	F356	C434	F493	G554	Y614	G687	D747	Q807	H903
THR	D85	F145	T215	I289	K357	G494	G493	V555	S616	L617	T749	I808	V907
MET	T86	G148	V216	S290	K358	H437	R495	W556	T618	L618	L750	I809	P908
	Q87	L149	A217	M291	K359	I438	G496	P558	T619	E690	F751	P810	Q909
	P88	L150	G218	Y292	P361	P439	V496	P568	K620	E691	S752	T811	G909
L89	E151	Q152	G218	S293	T362	S440	L497	P569	W621	E692	E753	W815	D910
E91	T90	G152	R220	S294	S363	K442	S498	W560	E622	E693	W754	Y817	P911
P92	E91	P155	I221	D295	S364	V443	T500	K561	E623	E694	D755	S818	L912
I93	I94	E156	G224	E296	Q366	G444	H502	A563	S624	K694	K756	M822	D913
K95	K96	I156	G224	E297	K367	A445	A503	T564	E626	G695	L757	A823	K914
ARG	P96	ILE	V225	L298	S368	K446	G504	T565	H627	L758	A757	T824	S915
LYS	V97	ARG	V226	L300	E296	P447	G505	E567	E628	L759	W760	P825	I916
LYS	K98	LYS	L227	L306	E371	K448	P506	P568	L629	W761	S761	R826	V917
ASP	T99	ASP	F228	N302	F372	I449	V507	W569	L630	W762	W762	E829	R919
LYS	LYS	GLN	T229	L303	E372	E450	K508	G570	G631	W763	W763	P830	P920
LYS	PHE	LEU	D230	L304	E373	H451	V509	N571	T632	W764	W764	W843	E922
THR	THR	CYS	A231	G305	P376	T452	L510	E572	L635	Q706	Q706	W846	P923
LEU	LEU	THR	A232	G306	L377	Y453	G511	E573	W636	Q707	Q707	R852	Q924
MET	GLU	THR	E233	N306	Y378	G456	L514	A574	L637	W708	W708	R853	P925
ASP	ASP	THR	G234	V307	K379	D458	T515	Q575	D638	W709	W709	R854	A926
LEU	LEU	ILE	V235	C308	K379	S459	T516	F577	M641	W710	W710	G855	P927
THR	THR	PHE	M236	F309	I380	D460	L517	E578	K646	R711	R711	H856	P928
LEU	LEU	VAL	T239	S310	L380	D461	D518	R578	E649	K712	K712	I863	A930
PRO	PRO	VAL	E240	S311	Q383	L461	E519	P579	S649	L714	L714	P864	R931
VAL	VAL	ILE	R241	S312	V384	G462	E520	L580	E650	G715	G715	G865	E932
T112	T112	E174	L242	G317	G385	G463	D521	K581	T651	E716	F717	S866	F933
V113	V113	Q175	I243	F318	G386	E464	S522	F582	D652	F718	W718	P867	M934
V114	V114	K244	K243	T319	D387	D465	Q523	W583	D653	F719	Q719	I871	R939
Y114	Y114	E176	H245	F323	D389	D466	C525	T584	K654	T720	T720	T875	R940
E115	E115	R177	A246	Y327	T390	M465	T526	T585	V655	K721	K721	A877	G942
M116	M116	G178	R250	I326	S391	S466	G528	T586	E656	W722	W722	I878	L943
D117	D117	V179	G180	Y327	L392	D467	W529	S586	D657	D723	D723	S878	SER
F118	F118	G181	V253	T330	P293	C468	L530	W587	P657	W724	W724	D879	GLU
L119	L119	K182	T254	F331	L399	D469	W531	T588	E658	L726	L726		ASP
		S183	V255		G400	P470		W589	W659				VAL
L122	L122	T184	C256	I257		G472		A591	V660				

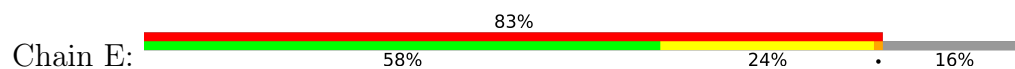
Chain D:



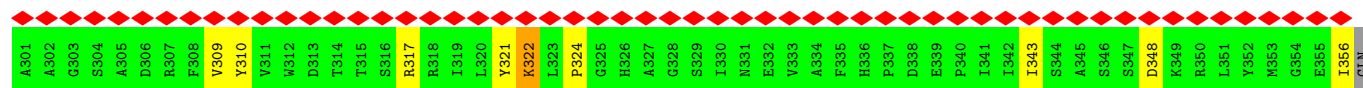
M1687	E1688	G1689	H1690	A1691	N1692	R1693	P1694	L1695	Q1696	D1697	D1698	E1699	G1700	R1701	C1702	V1703	I1704	M1705	C1706	Q1707	R1708	S1709	K1710	K1711	D1712	F1713	F1714	K1715	K1716	A1717	L1718	H1719	E1720	P1721	L1722	P1723	V1724	E1725	S1726	H1727	L1728	D1729	H1730	C1731	M1732	H1733	D1734	H1735	F1736	N1737	A1738	E1739	L1740	V1741	T1742	K1743	T1744	I1745	
M1627	E1628	R1629	R1630	L1631	V1632	E1633	Q1634	L1635	F1636	S1637	S1638	G1639	A1640	I1641	Q1642	V1643	V1644	V1645	A1646	S1647	R1648	S1649	L1650	C1651	W1652	G1653	F1654	M1655	V1656	A1657	A1658	H1659	L1660	V1661	I1662	L1663	M1664	D1665	T1666	Q1667	Y1668	Y1669	L1670	G1671	K1672	I1673	H1674	A1675	V1676	V1677	L1678	Y1679	P1680	I1681	L1682	D1683	V1684	L1685	Q1686
K1567	Q1568	T1569	R1570	L1571	L1572	A1573	L1574	D1575	V1576	L1577	T1578	T1579	C1580	A1581	D1582	D1583	I1584	Q1585	R1586	L1587	R1588	F1589	L1590	H1591	C1592	T1593	E1594	M1595	K1596	D1596	L1597	T1598	P1599	Y1600	L1601	E1602	L1603	L1604	S1605	D1606	S1607	T1608	L1609	K1610	E1611	T1612	L1613	L1614	N1615	G1616	V1617	G1618	Y1619	L1620	H1621	E1622	G1623	L1624	S1625
S1507	A1508	T1509	S1510	F1511	F1512	M1513	F1514	H1515	P1516	M1517	V1518	R1519	A1520	V1521	P1522	L1523	E1524	L1525	H1526	I1527	Q1528	G1529	F1530	M1531	I1532	S1533	H1534	T1535	Q1536	T1537	R1538	L1539	L1540	S1541	M1542	K1543	A1544	P1545	V1546	Y1547	H1548	A1549	I1550	L1551	K1552	H1553	S1554	P1555	K1556	L1557	P1558	V1559	L1560	V1561	F1562	P1563	P1564	S1565	
E1387	Q1388	V1389	Y1390	M1391	D1392	W1393	Y1394	E1395	K1396	F1397	Q1398	D1399	R1400	L1401	N1402	K1403	K1404	V1405	V1406	L1407	L1408	T1409	G1410	E1411	T1412	S1413	T1414	D1415	L1416	K1417	L1418	L1419	G1420	K1421	G1422	M1423	I1424	I1425	I1426	S1427	T1428	P1429	E1430	K1431	V1432	D1433	I1434	L1435	S1436	R1437	R1438	Y1439	K1440	Q1441	L1442	K1443	N1444	V1445	
M1447	I1448	N1449	L1450	F1451	V1452	V1453	D1454	E1455	V1456	H1457	L1458	T1459	G1460	G1461	E1462	N1463	G1464	P1465	V1466	L1467	E1468	V1469	I1470	C1471	S1472	R1473	M1474	R1475	Y1476	I1477	S1478	S1479	Q1480	I1481	E1482	R1483	P1484	L1485	R1486	I1487	V1488	A1489	L1490	S1491	S1492	L1493	L1494	S1495	N1496	A1497	L1498	D1499	V1500	A1501	H1502	W1503	L1504	G1505	
F1327	F1328	M1329	P1330	I1331	Q1332	T1333	Q1334	V1335	F1336	M1337	T1338	V1339	Y1340	M1341	S1342	D1343	D1344	M1345	V1346	F1347	V1348	C1349	A1350	P1351	T1352	G1353	S1354	G1355	K1356	T1357	I1358	C1359	A1360	E1361	F1362	A1363	I1364	L1365	R1366	M1367	L1368	L1369	Q1370	S1371	S1372	E1373	G1374	R1375	C1376	V1377	Y1378	I1379	T1380	P1381	M1382	E1383	A1384	L1385	
T1205	P1206	D1207	F1208	Q1209	W1210	D1211	E1212	K1213	W1214	H1215	G1216	S1217	S1218	E1219	A1220	F1221	W1222	I1223	L1224	V1225	E1226	D1227	V1228	D1229	S1230	E1231	V1232	I1233	L1234	H1235	H1236	E1237	Y1238	F1239	L1240	L1241	K1242	A1243	L1244	Y1245	A1246	Q1247	D1248	E1249	H1250	L1251	I1252	T1253	F1254	F1255	V1256	T1257	L1258	F1259	E1260	P1261	L1262	P1263	P1264
Q1265	Y1266	F1267	I1268	R1269	D1273	R1274	W1275	L1276	S1277	C1278	E1279	T1280	Q1281	L1282	P1283	V1284	S1285	F1286	R1287	H1288	L1289	I1290	L1291	P1292	E1293	K1294	Y1295	P1296	P1297	P1298	T1299	E1300	L1301	L1302	D1303	L1304	Q1305	P1306	L1307	P1308	V1309	S1310	A1311	L1312	R1313	N1314	S1315	A1316	F1317	E1318	S1319	L1320	Y1321	Q1322	D1323	K1324	F1325	P1326	
E1144	K1145	K1146	M1147	F1150	E1151	R1152	L1153	Y1154	D1155	L1156	N1157	H1158	N1159	E1160	I1161	G1162	E1163	L1164	I1165	R1166	M1167	P1168	K1169	M1170	G1171	K1172	T1173	I1174	H1175	K1176	Y1177	V1178	H1179	L1180	F1181	P1182	K1183	L1184	E1185	L1186	S1187	V1188	H1189	L1190	Q1191	P1192	I1193	T1194	R1195	S1196	T1197	L1198	V1200	E1201	L1202	T1203	I1204		
M1081	V1082	Y1083	V1084	T1085	Q1086	S1087	G1088	R1089	L1090	L1091	M1092	R1093	A1094	I1095	F1096	E1097	I1098	V1099	L1100	N1101	R1102	G1103	W1104	A1105	Q1106	L1107	T1108	D1109	K1110	T1111	L1112	K1116	M1117	I1118	D1119	K1120	R1121	M1122	W1123	Q1124	S1125	M1126	C1127	P1128	L1129	R1130	Q1131	F1132	T1133	R1134	L1135	P1136	E1137	L1138	V1139	W1140	K1141		
E1011	I1012	E1013	L1014	F1015	R1016	V1017	F1018	S1019	L1020	S1021	S1022	E1023	F1024	K1025	N1026	I1027	T1028	V1029	R1030	E1031	E1032	E1033	K1034	L1035	E1036	L1037	Q1038	L1039	L1040	L1041	E1042	R1043	V1044	P1045	I1046	P1047	V1048	K1049	E1050	S1051	I1052	E1053	E1054	K1058	I1059	I1067	S1068	Q1069	L1070	K1071	L1072	E1073	G1074	F1075	K1006	P1007	T1008	L1009	S1010
P947	L948	L949	D950	Q951	R952	D955	L956	V957	H958	T959	A960	A961	L962	H963	L964	D965	K966	H967	V970	K971	Y972	D973	K974	K975	T976	G977	H978	F979	Q980	V981	T982	E983	L984	G985	R986	H990	Y991	Y992	E993	T994	D995	T997	V998	Q999	T1000	Y1001	N1002	Q1003	L1004	L1005	K1006	P1007	T1008	L1009	S1010				

M1747	M1807	L1867	V1927	E1987	V2047	Y2107
K1748	M1808	L1868	D1928	M1988	T2048	F2108
Q1749	D1809	R1869	V1929	E1989	G2049	M2109
D1750	V1810	Q1870	L1930	D1990	P2050	S2110
A1751	D1811	L1871	S1931	E1991	V2051	D2111
V1752	P1812	A1872	S1932	E1992	T2052	A2112
D1753	L1813	Q1873	N1933	R1993	A2053	Y2113
Y1754	N1814	K1874	G1934	N1994	P2054	M2114
L1755	L1815	V1875	W1935	A1995	T2055	G2115
T1756	G1816	P1876	L1936	L1996	L2056	C2116
W1757	M1817	H1877	S1937	L1997	P2057	D2117
T1758	I1818	K1878	P1938	Q1998	Q2058	Q2118
F1759	A1819	L1879	A1939	L1999	R2059	Y2119
L1760	A1820	N1880	L1940	T2000	R2060	Y2120
Y1761	Y1821	M1881	A1941	D2001	E2061	K2121
R1762	Y1822	P1882	A1942	S2002	E2062	F2122
R1763	Y1823	K1883	M1943	Q2003	G2063	S2123
M1764	Y1824	F1884	E1944	T2004	W2064	V2124
T1765	N1825	M1885	L1945	A2005	W2065	D2125
Q1766	Y1826	D1886	A1946	D2006	V2066	VAL
L1767	T1827	P1887	Q1947	V2007	V2067	LYS
P1768	T1828	H1888	M1948	A2008	T2068	GLU
M1769	I1829	V1889	V1949	R2009	G2069	ALA
Y1770	E1830	K1890	T1950	F2010	D2070	GLY
Y1771	L1831	T1891	Q1951	C2011	A2071	THR
M1772	F1832	N1892	A1952	N2012	K2072	ASP
L1773	S1833	L1893	M1953	R2013	S2073	ALA
Q1774	M1834	L1894	W1954	T2014	N2074	GLY
G1775	S1835	L1895	S1955	P2015	S2075	GLN
T1776	L1836	Q1896	L1956	N2016	T2076	GLN
S1777	N1837	A1897	D1957	T2017	T2077	THR
H1778	A1838	H1898	S1958	E2018	S2078	PRO
R1779	K1839	L1899	Y1959	L2019	T2079	GLY
H1780	T1840	S1900	L1960	S2020	K2080	ALA
L1781	K1841	R1901	K1961	Y2021	R2081	LEU
S1782	V1842	M1902	Q1962	E2022	T2082	LEU
D1783	R1843	Q1903	L1963	V2023	T2083	GLN
H1784	G1844	L1904	P1964	V2024	L2084	GLY
L1785	L1845	S1905	H1965	D2025	Q2085	PRO
S1786	I1846	A1906	F1966	K2026	Q2086	ARG
E1787	E1847	L1907	T1967	D2027	K2087	CYS
L1788	I1848	L1908	S1968	S2028	A2088	SER
V1789	I1849	Q1909	E1969	L2029	K2089	LEU
E1790	S1850	S1910	H1970	R2030	V2090	GLN
Q1791	N1851	D1911	I1971	S2031	K2091	ALA
T1792	A1852	T1912	K1972	G2032	L2092	P58
L1793	A1853	E1913	R1973	G2033	D2093	I59
S1794	E1854	E1914	G1974	P2034	F2094	M60
D1795	Y1855	L1915	T1975	V2035	V2095	
L1796	E1856	L1916	T1976	V2036	A2096	
E1797	N1857	S1917	K1977	V2037	P2097	
Q1798	I1858	K1918	G1978	L2038	A2098	
S1799	P1859	A1919	V1979	V2039	T2099	
K1800	I1860	I1920	E1980	Q2040	G2100	
C1801	R1861	R1921	S1981	L2041	A2101	
T1802	H1862	L1922	V1982	E2042	H2102	
S1803	H1863	I1923	F1983	R2043	N2103	
E1804	E1864	Q1924	I1984	E2044	V2104	
L1805	D1865	A1925	I1985	E2045	T2105	
D1806	N1866	C1926	M1986	E2046	L2106	

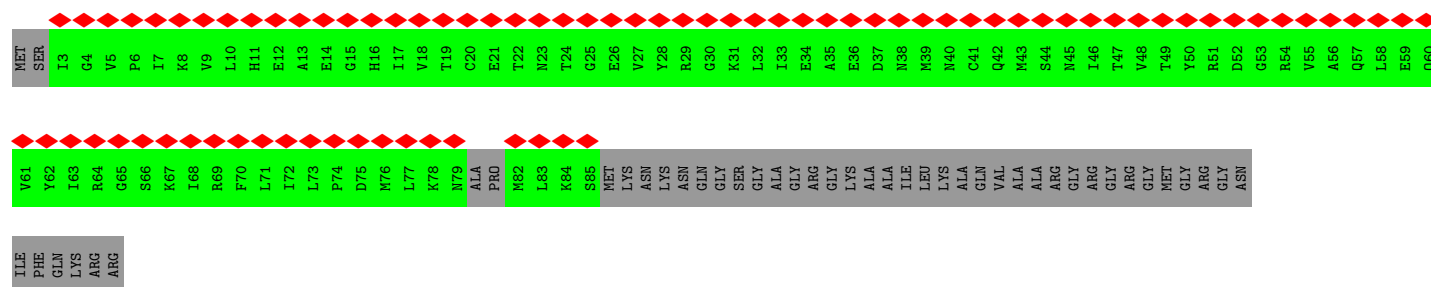
• Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



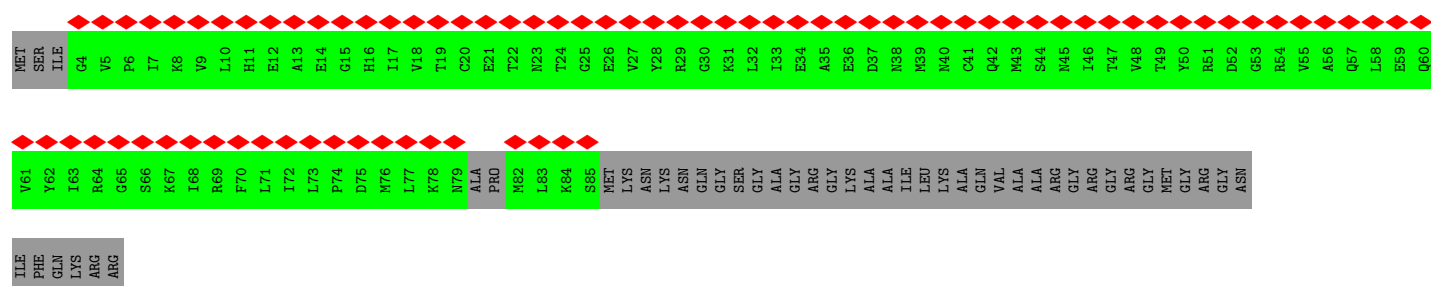
MET	L61	G121	I181	L241
ILE	L62	S122	R182	S242
GLU	S63	M123	K183	L243
GLN	G64	L124	K184	S244
LYS	H65	F125	A185	S245
ARG	E66	S126	A186	E246
GLY	G67	A127	L187	G247
PRO	E68	S128	Q188	S248
LEU	V69	T129	T189	Y249
LEU	Y70	D130	F190	L250
LEU	C71	K131	Q191	L251
VAL	C72	T132	N192	S252
PRO	K73	V133	L193	M253
VAL	F74	A134	Y194	A254
LYS	H75	V135	Q195	M255
ARG	P76	W136	V196	D256
GLN	N77	D137	L197	N257
ARG	G78	S138	A198	T258
HIS	S79	E139	V199	V259
GLU	T80	T140	T200	R260
LEU	L81	G141	F201	V261
LEU	Y82	E142	N202	W262
GLY	S83	R143	D203	D263
ALA	A84	V144	T204	V264
GLY	G85	K145	S205	R265
ASP	F86	R146	D206	P266
SER	D87	L147	Q207	F267
SER	R88	K148	T208	A268
ASP	L89	G149	T209	P269
	I90	H150	S210	K270
	L91	T151	G211	E271
	L92	S152	G212	R272
	W93	F153	T213	C273
	N94	V154	D214	V274
	V95	N155	N215	K275
	Y96	S156	D216	T276
	G97	C157	T217	F277
	D98	Y158	K218	Q278
	C99	P159	V219	G279
	D100	A160	W220	N280
	N101	R161	D221	V281
	I102	R162	L222	H282
	A103	G163	R223	M283
	T104	P164	Q224	F284
	Q165	Q165	N225	E285
	L105	L166	K226	K286
	K106	V167	L227	N287
	G107	C168	T228	L288
	S109	T169	Y229	L289
	G110	G170	T230	R290
	A111	S171	N231	C291
	V112	D172	R232	S292
	M113	D173	G233	W293
	E114	G174	H234	S294
	L115	T175	A235	P295
	H116	V176	D236	D296
	Y117	K177	S237	G297
	N118	L178	V238	S298
	T119	W179	T239	K299
	D120	D180	G240	I300



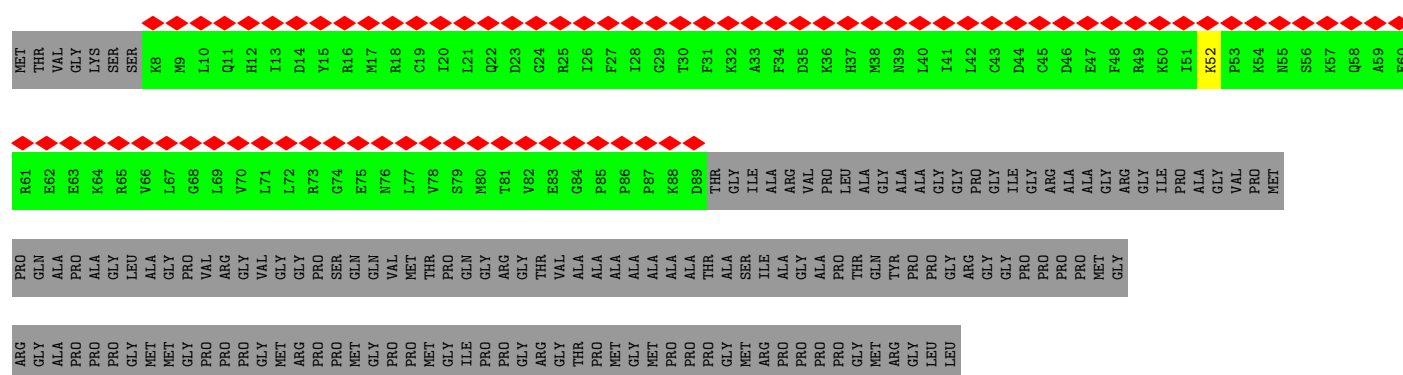
• Molecule 6: Small nuclear ribonucleoprotein Sm D3



• Molecule 6: Small nuclear ribonucleoprotein Sm D3

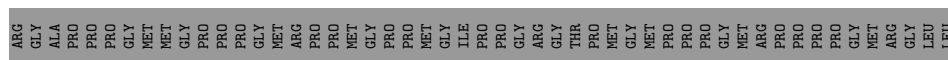


• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

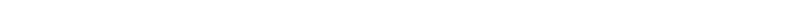


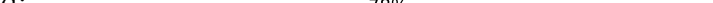
• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

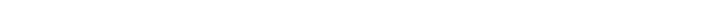




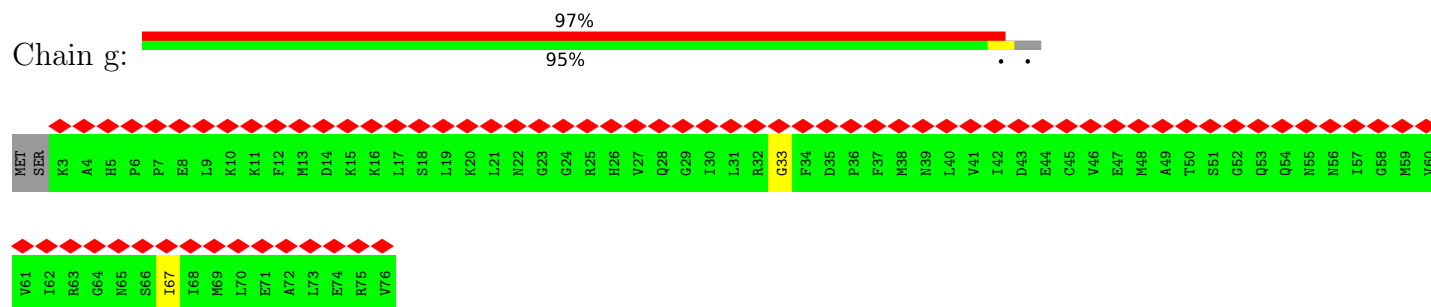
Chain c:  68% 69% 31%

Chain j:  69% 31%

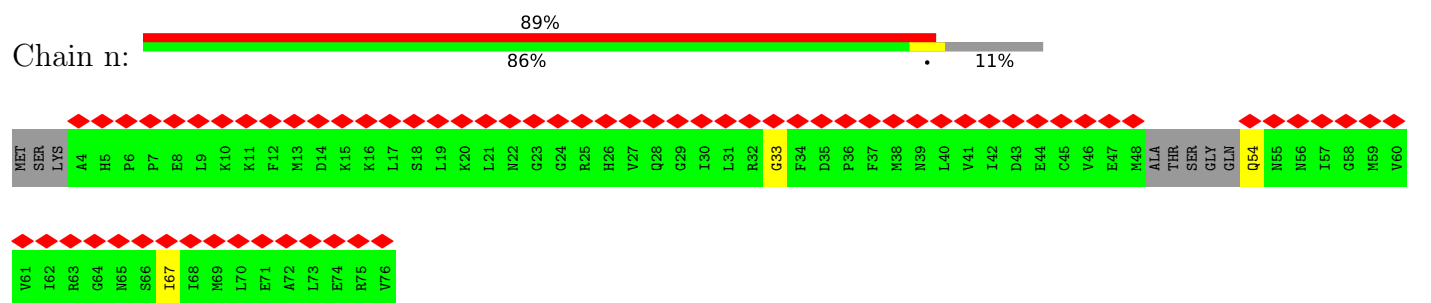
Chain d:  77% 78% 18%

Chain k:  72% 67% 5% 28%

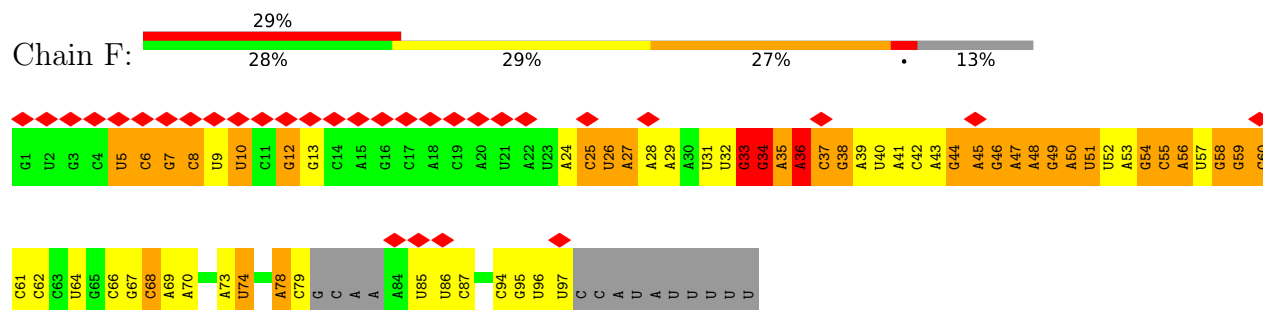
Chain g:



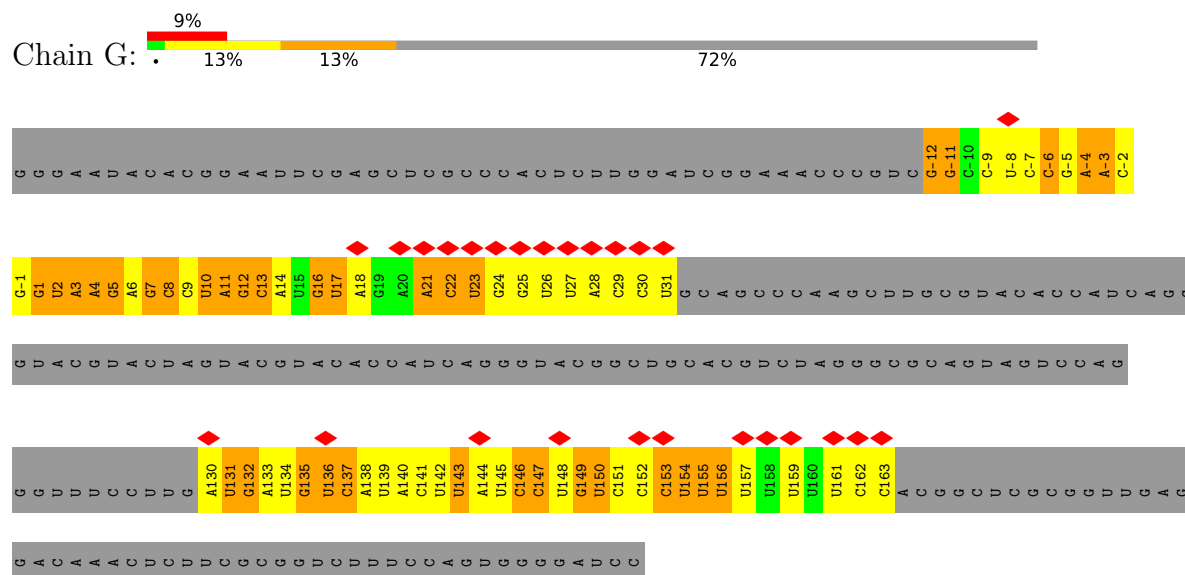
Chain n:

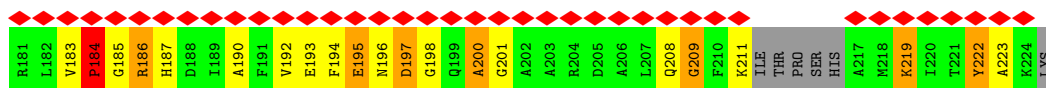


Chain F:

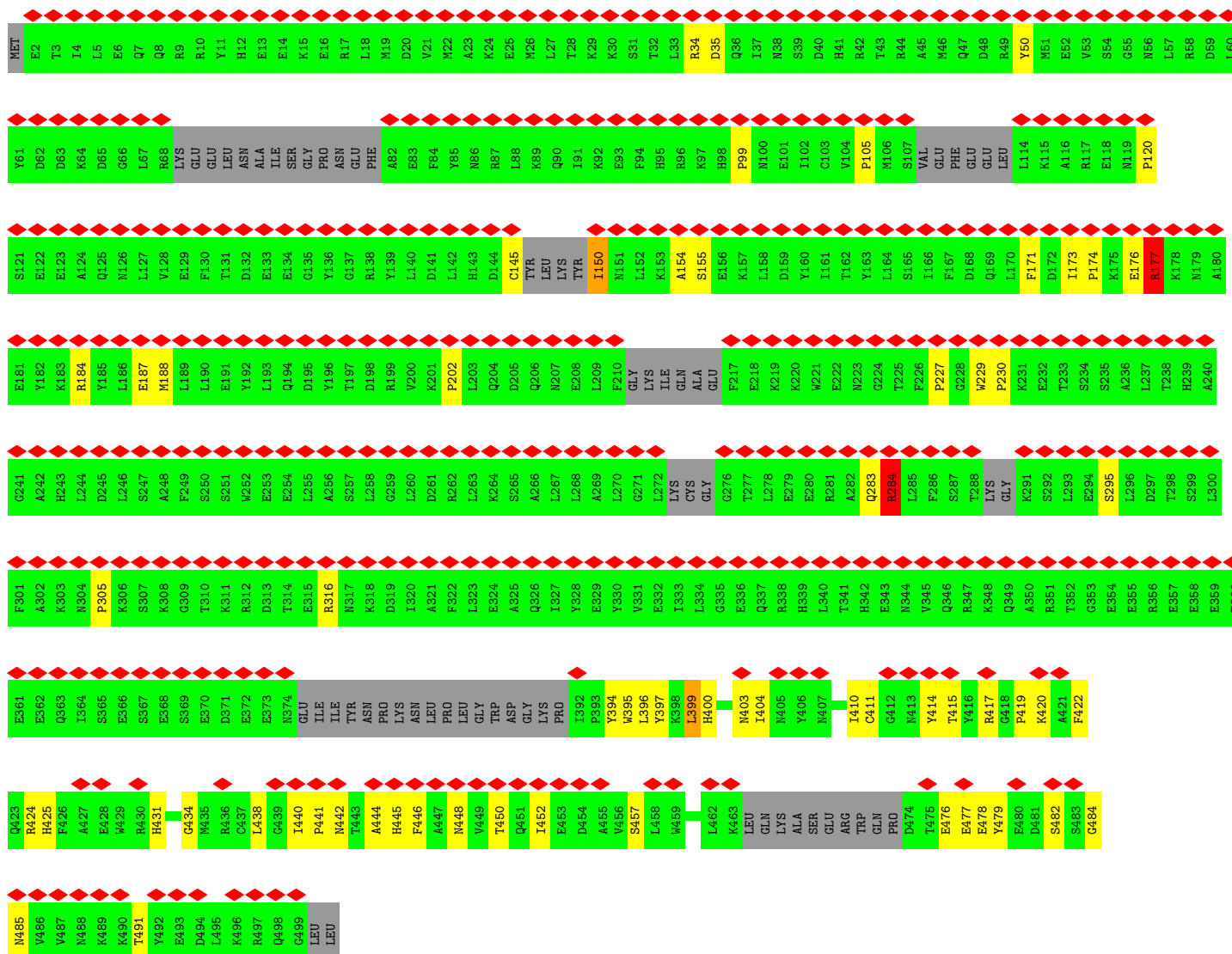
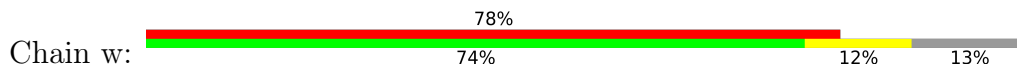


Chain G:

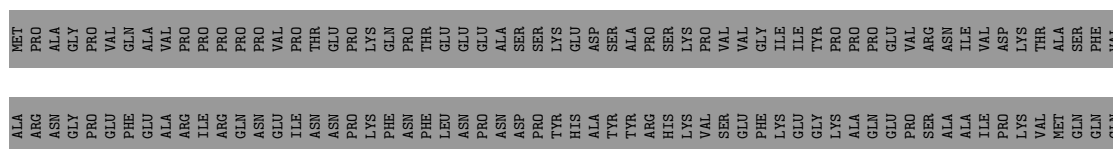




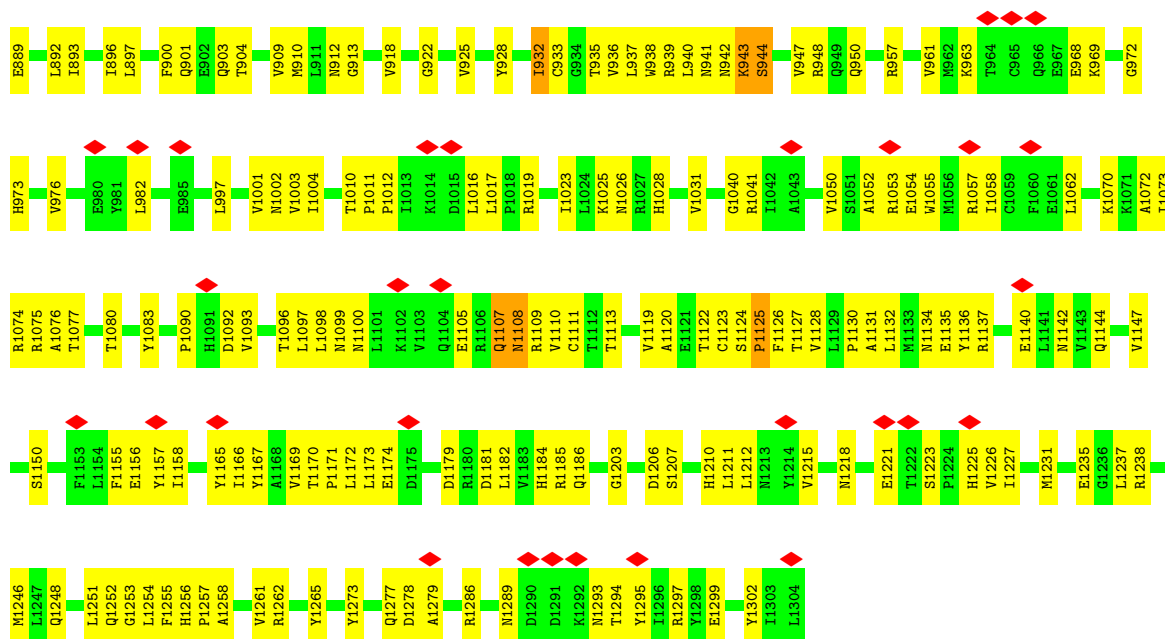
• Molecule 18: Splicing factor 3A subunit 3



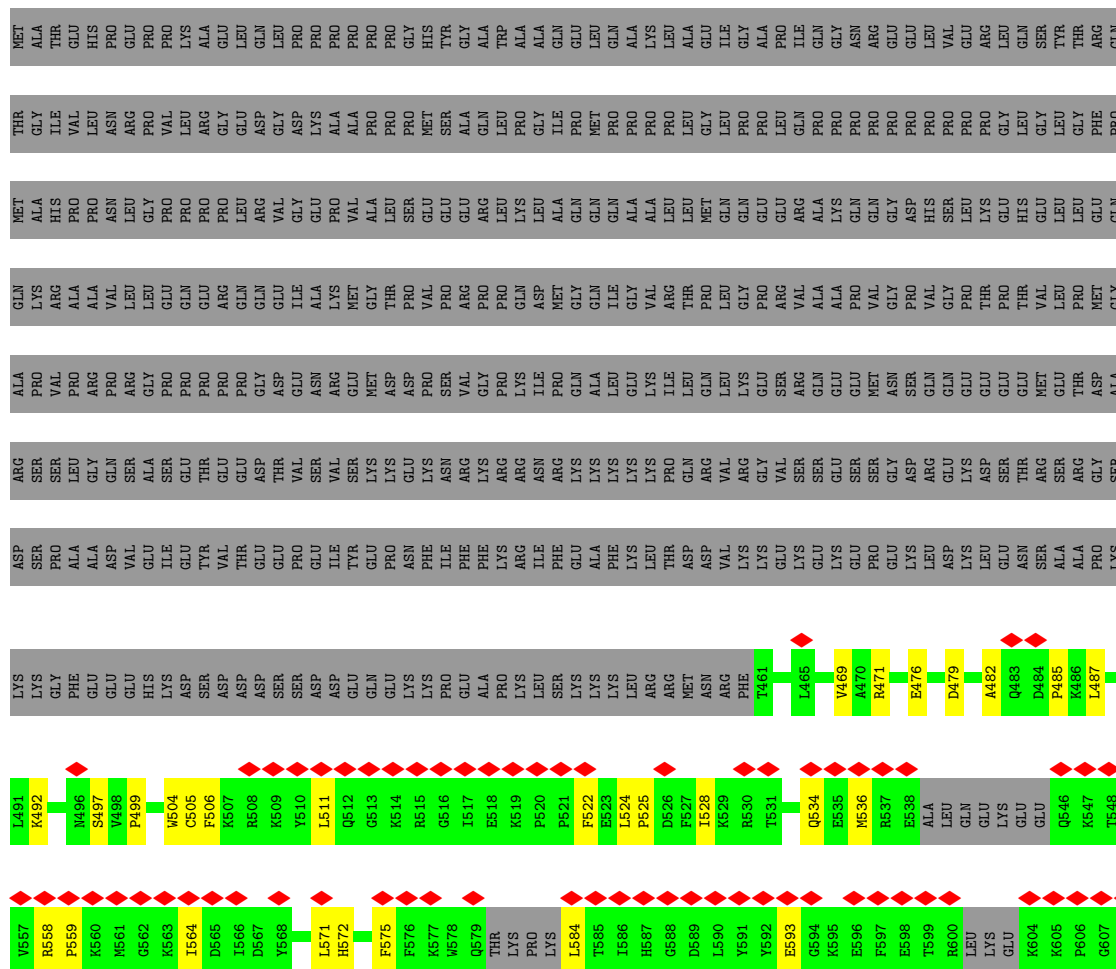
• Molecule 19: Splicing factor 3A subunit 1

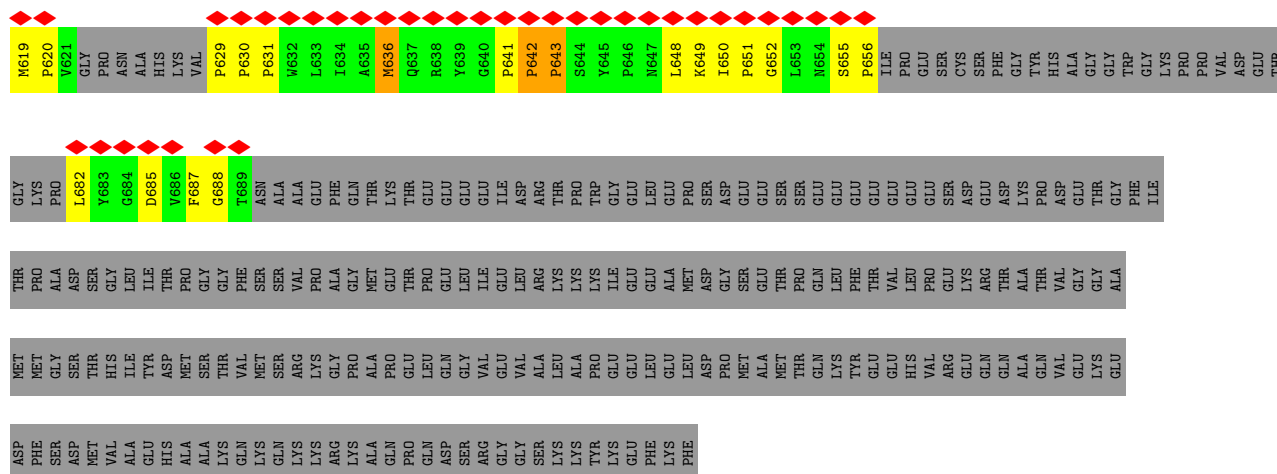




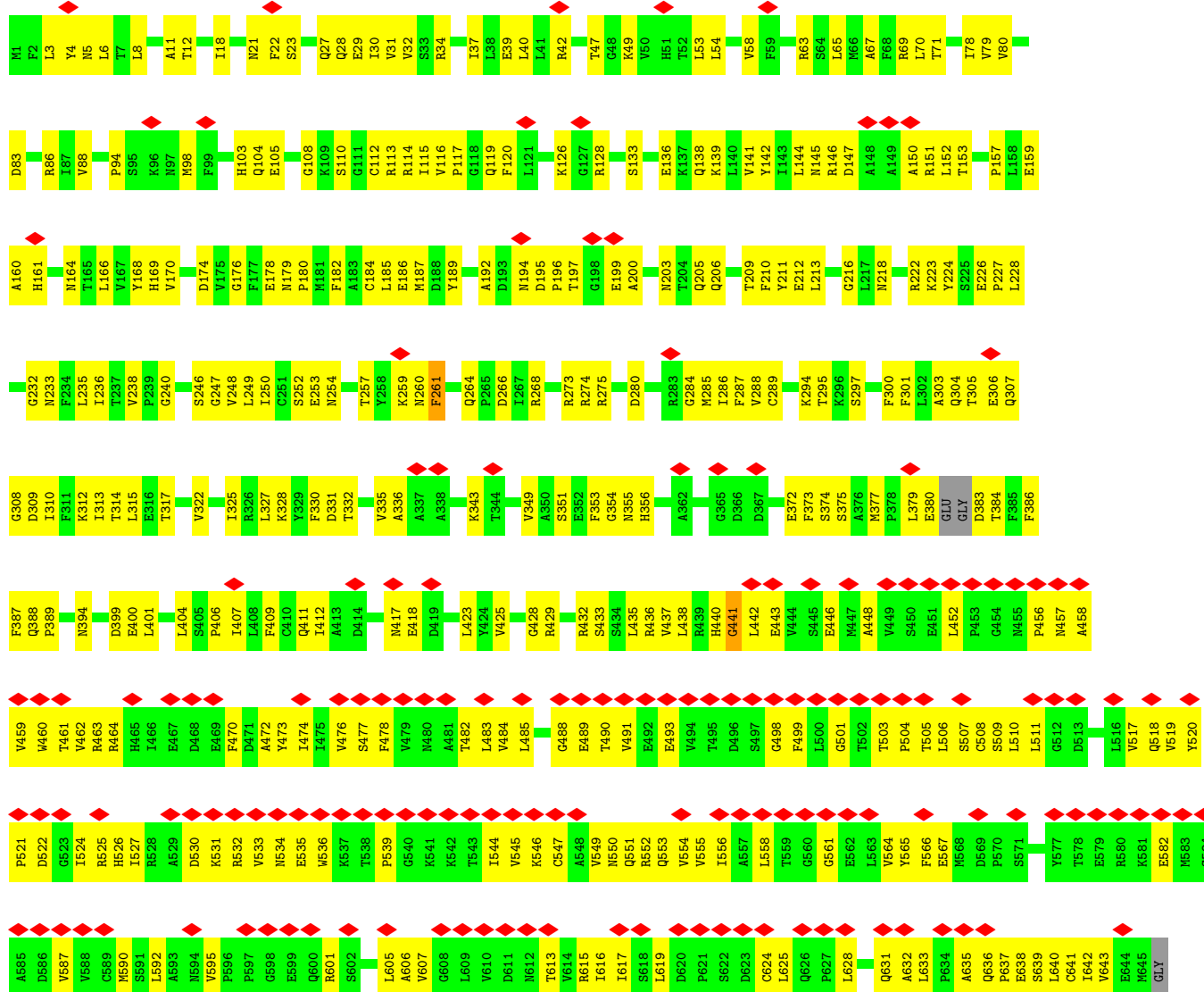


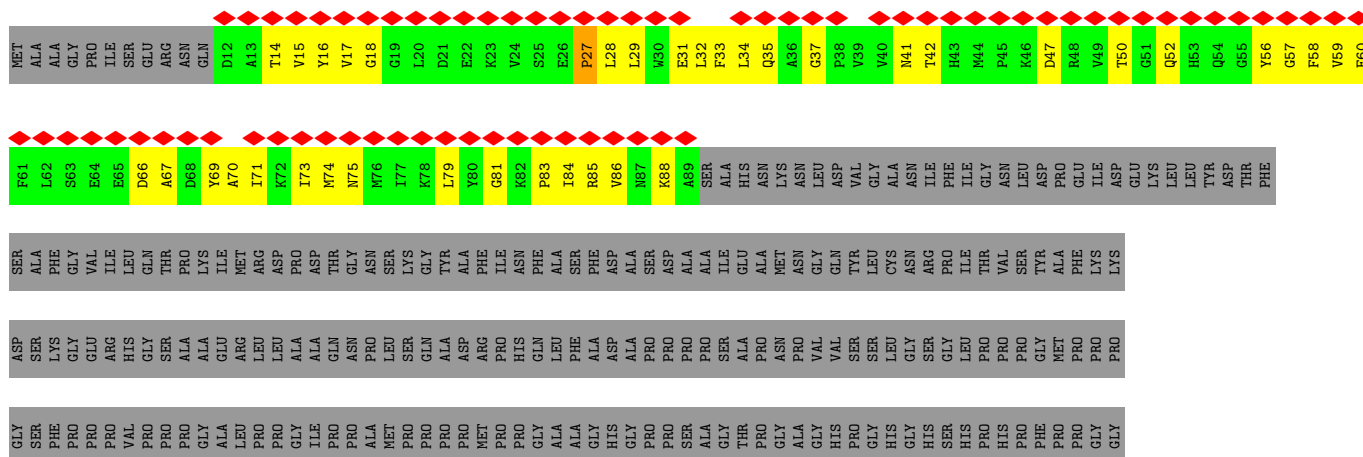
• Molecule 22: Splicing factor 3B subunit 2



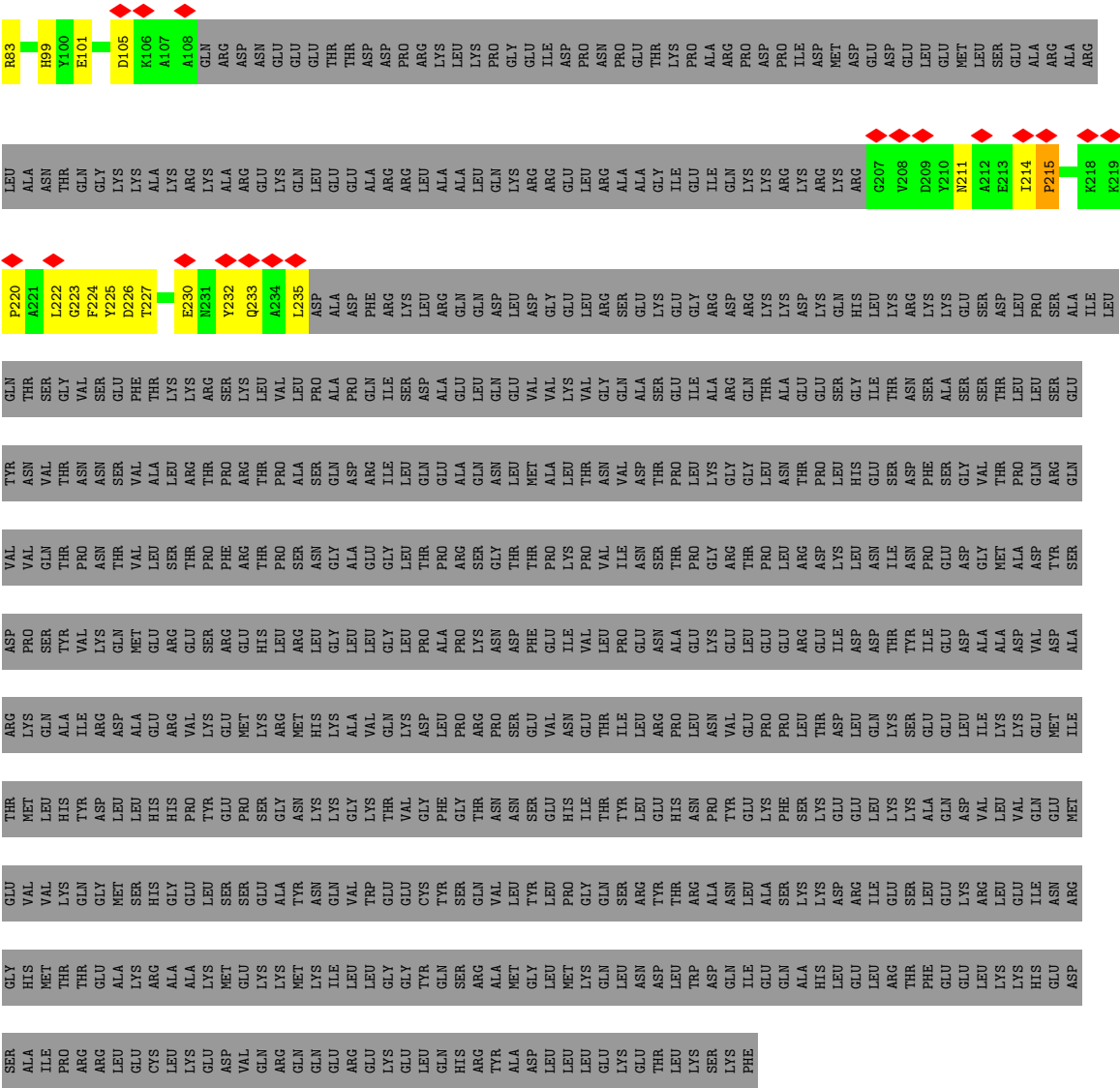


• Molecule 23: Splicing factor 3B subunit 3





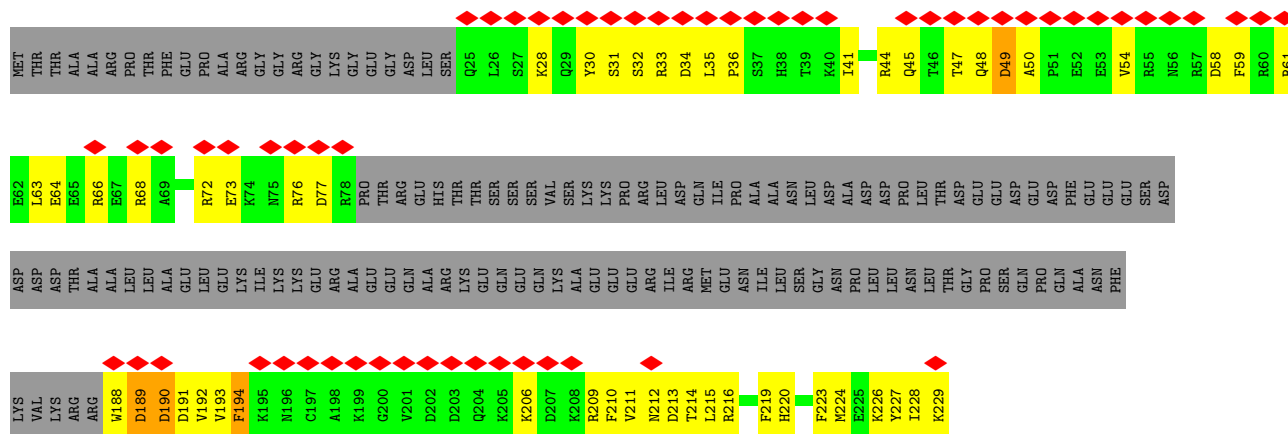




ILE
ALA
LYS
LEU
GLU
LYS
HIS
ARG
ALA
THR
GLY
GLU
GLY
GLY
ALA
SER
ASP
LEU
PRO
GLU
ASP
PRO
ASP
ASP
GLU
ALA
ILE
ILE
THR

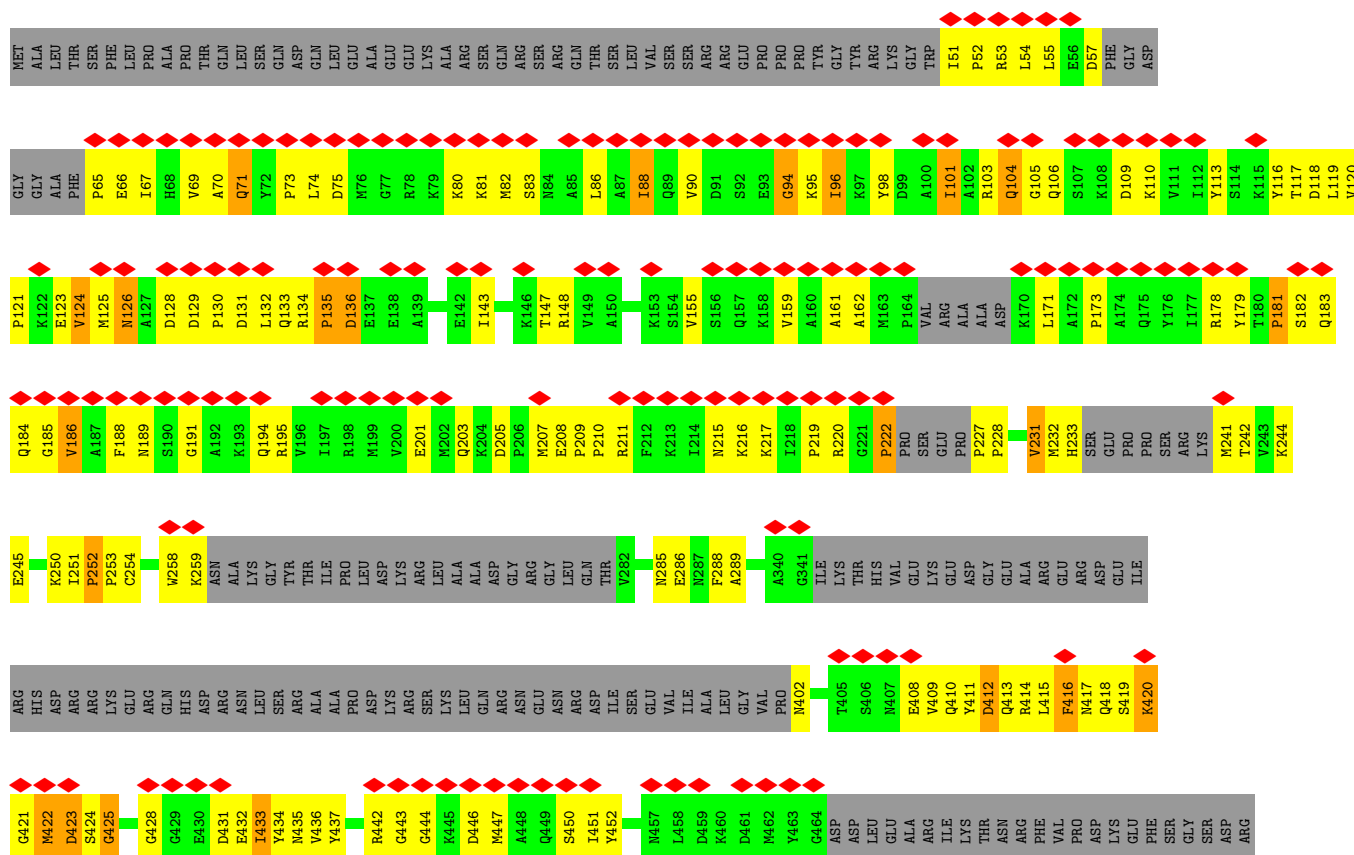
• Molecule 31: Spliceosome-associated protein CWC15 homolog

Chain P: 26% 20% 21% 58%

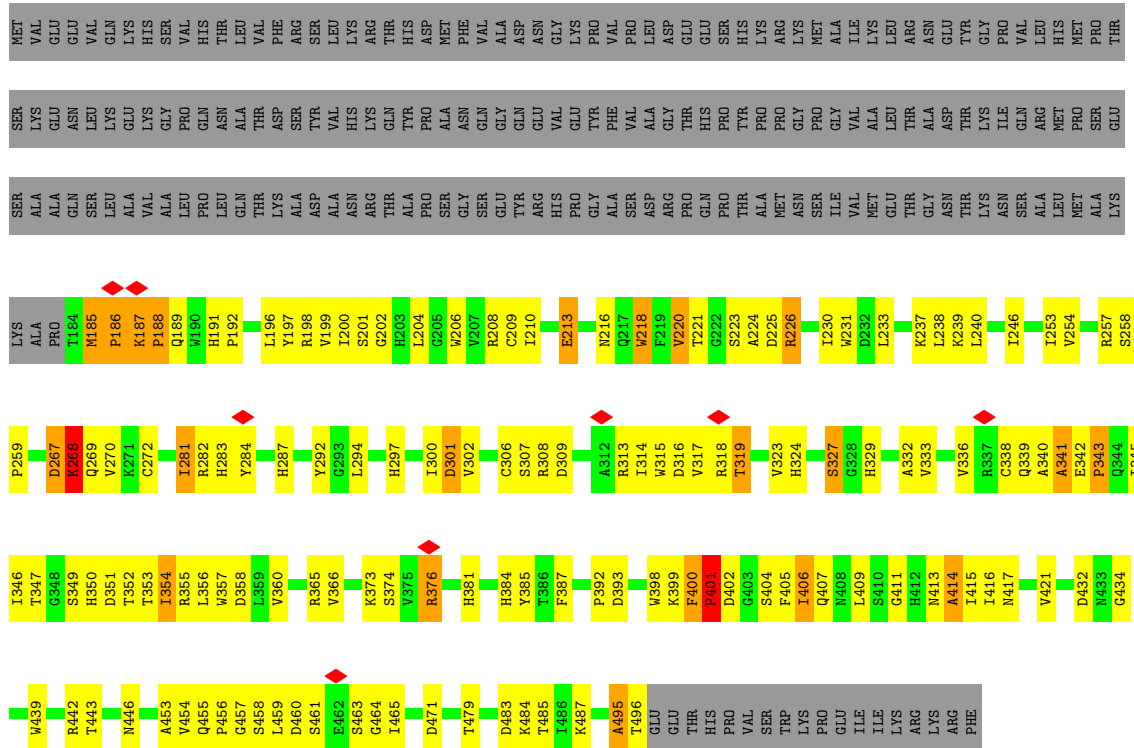


• Molecule 32: Skip

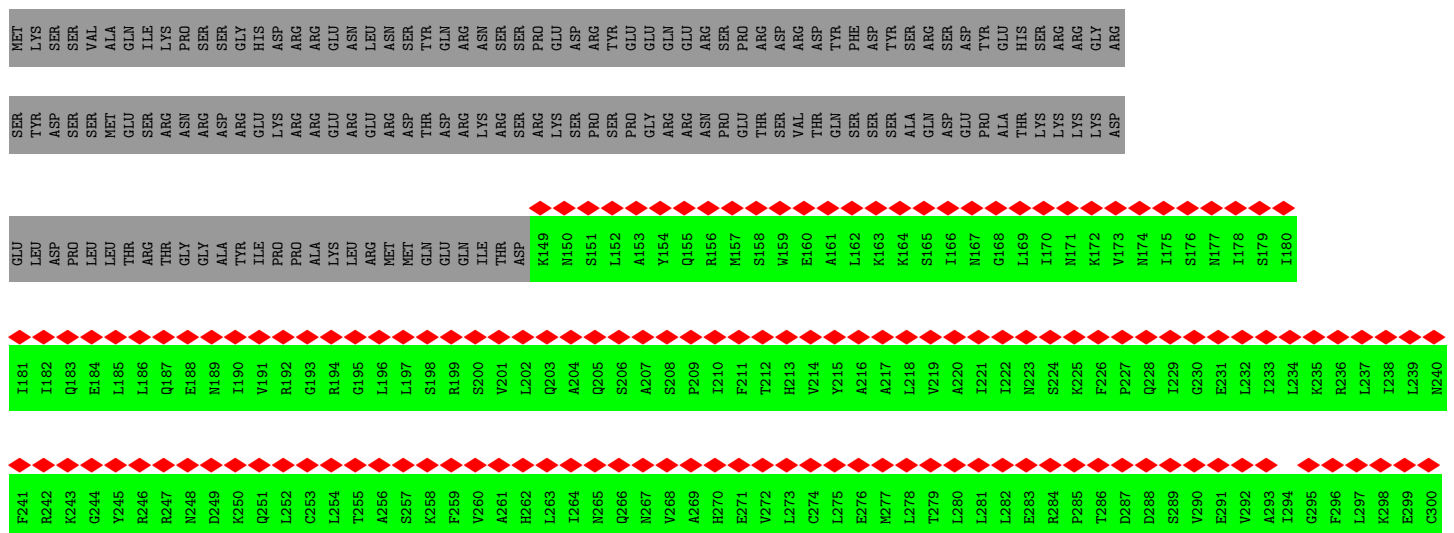
Chain R: 29% 31% 23% 43%

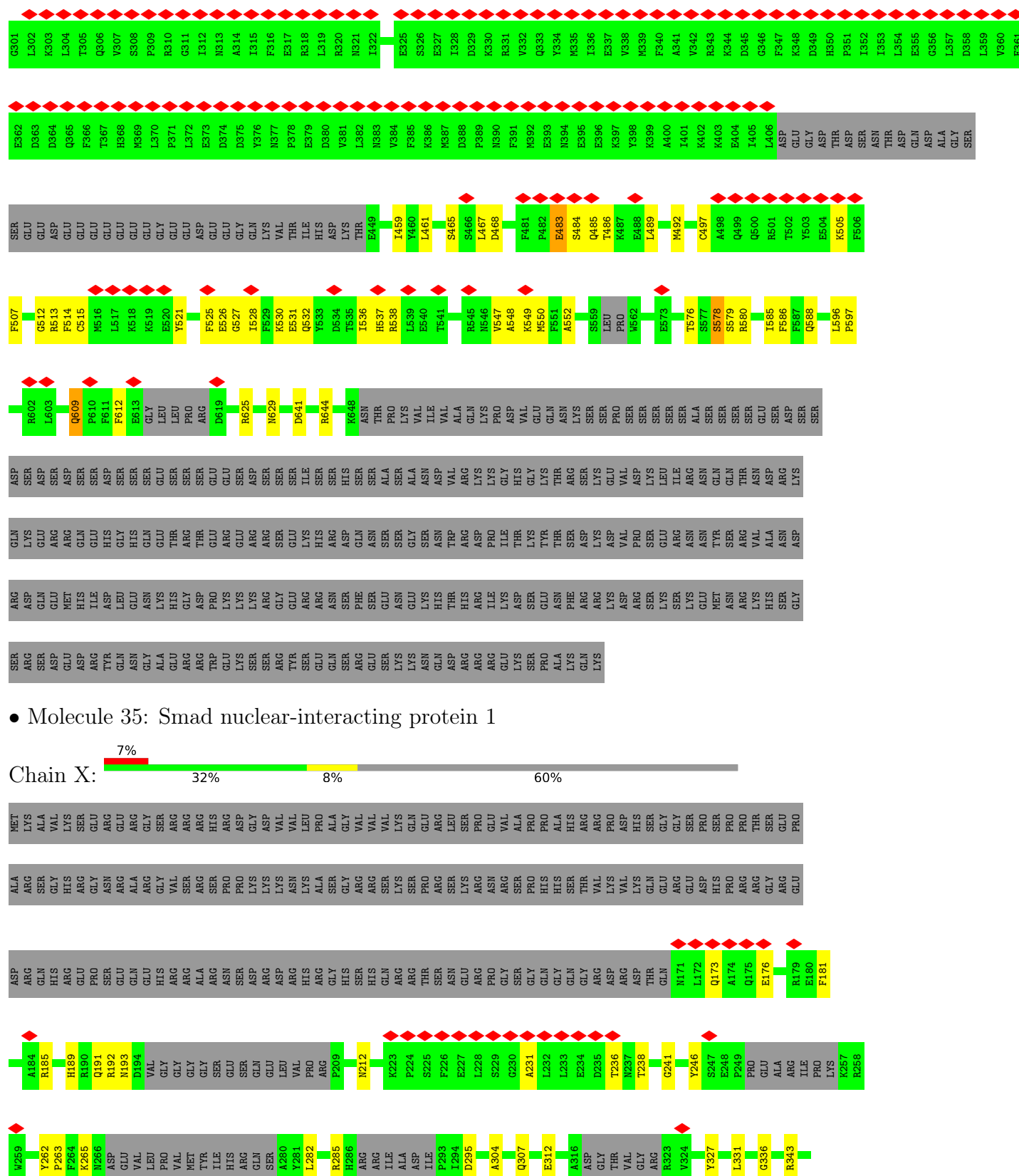


Chain T: 32% 25% 0% 39%



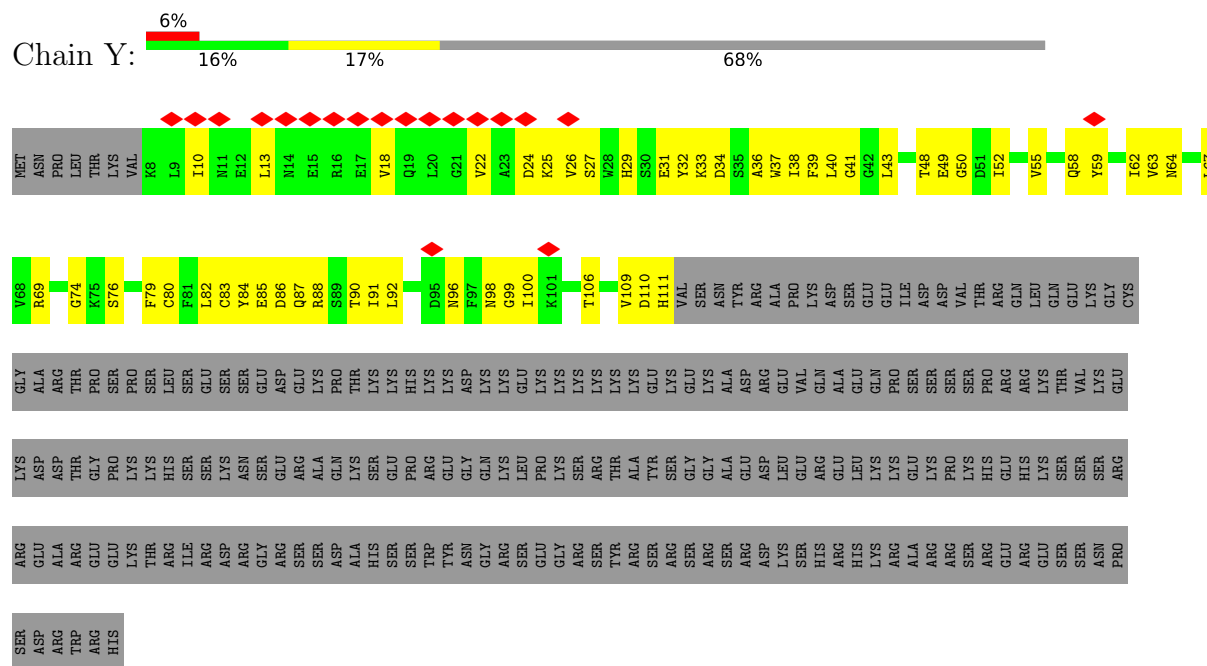
Chain V:



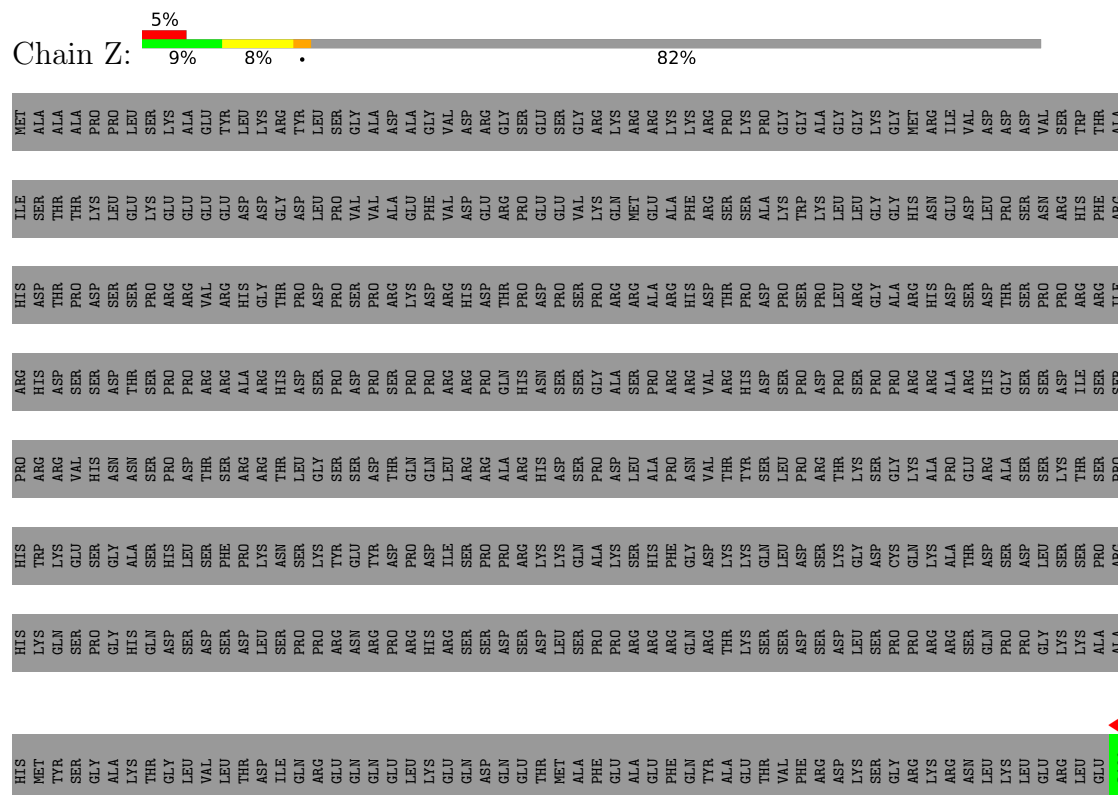


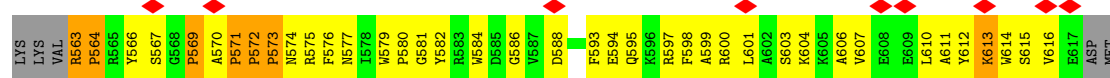
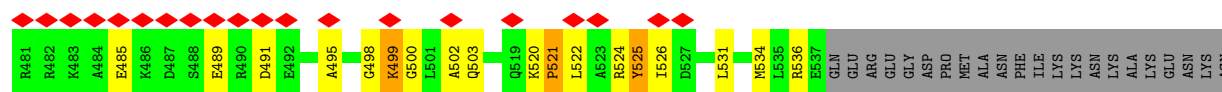


- Molecule 36: RNA-binding motif protein, X-linked 2

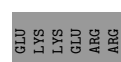
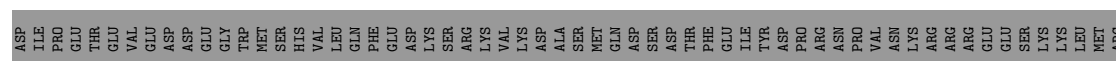
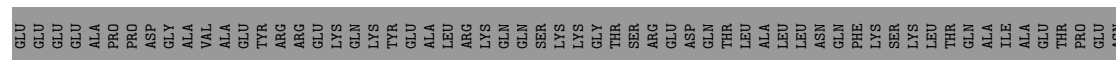
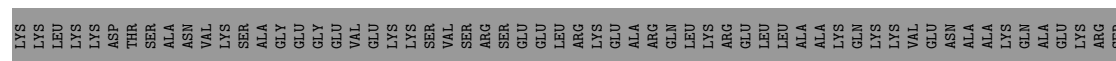
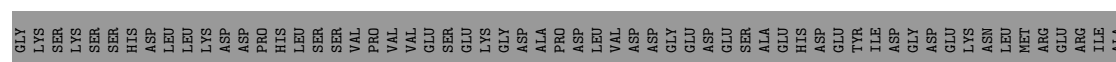
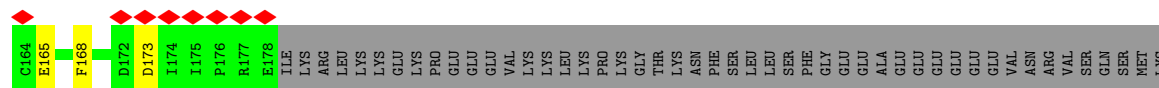
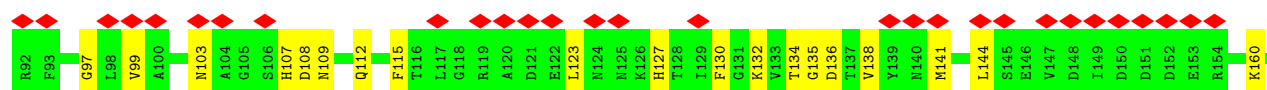
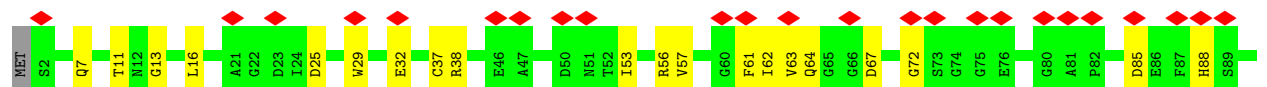


- Molecule 37: BUD13 homolog

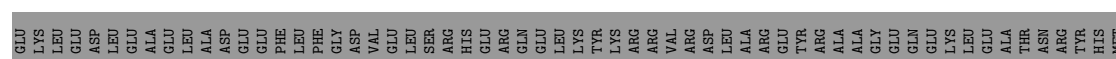
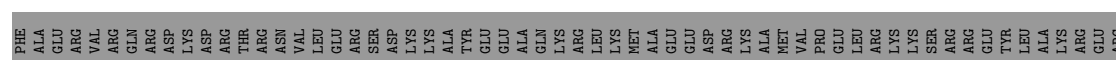
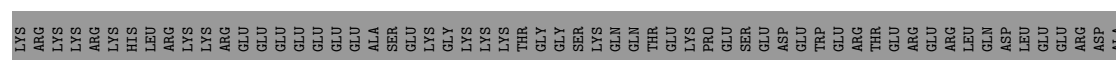
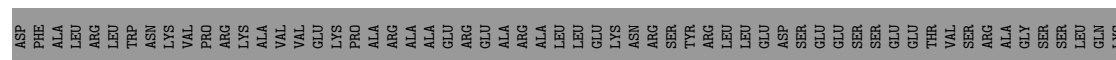
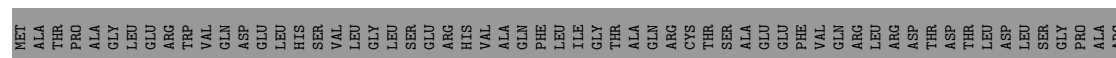




• Molecule 38: Peptidyl-prolyl cis-trans isomerase CWC27 homolog



• Molecule 39: Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16



GLU	ASP	PRO	HIS	ALA	LYS	LYS	THR	V968	F969	F970	H971	H972	H973	S974	SER	ARG	THR	LEU	GLU	PHE	GLU	GLY	Q979	Q980	P981	R982	W983	L984	L985	Y986	H987	E988	L989	V990	L991	T992	T993	K994	E995	F996	N997	R998	Q999	V1000	L1001	E1002	I1003	E1004	S1005	S1006	V1007	L1008	L1009	E1010	V1011	A1012	P1013	H1014	Y1015	Y1016	K1017	ALA	LYS	GLU	LEU
PRO	LYS	GLU	THR	ARG	GLY	GLN	PRO	GLN	VAL	ARG	ALA	ALA	THR	ALA	GLN	ASP	LEU	VAL	GLU	GLU	PRO	SER	GLY	PRO	THR	THR	THR	GLN	A396	Q397	K398	K399	E390	S391	L392	Q393	A394	V395	C450	T451	Q452	P453	L399	P400	V401	F402	P403	F404	R405	E406	E407	L408	L409	A410	A411	I412	A413	N414	H415	Q416	V417	L418	L419	I420	
E421	G422	E423	T424	G425	S426	G427	K428	L429	T430	Q431	L432	P433	Q434	Y435	L436	F437	E438	E439	G440	T441	T442	M443	K444	G445	M446	K447	L448	A449	C450	T451	Q452	P453	L454	R455	V456	A457	A458	M459	S460	V461	A462	A463	R464	V465	A466	I467	E468	M469	Q470	V471	K472	L473	G474	M475	E476	V477	Y479	S480							
I481	R482	F483	E484	D485	C486	T487	SER	ARG	T491	V492	L493	R494	Y495	M496	T497	D498	G499	M500	L501	L502	R503	E504	F505	L506	S507	E508	P509	D510	L511	A512	S513	Y514	S515	V516	V517	M518	V519	D520	E521	A522	H523	E524	R525	T526	L527	H528	T529	D530	I531	L532	F533	G534	L535	K537	D538	V539	A540								
R541	F542	R543	P544	E545	L546	K547	V548	L549	V550	A551	S552	A553	T554	M555	D556	T557	A558	R559	F560	S561	T562	F563	F564	D565	D566	A567	P568	V569	F570	R571	I572	P573	R574	G575	R576	F577	P578	V579	D580	I581	F582	Y583	T584	K585	A586	P587	E588	A589	D590	Y591	L592	E593	A594	C595	V596	V597	S598	V599	L600						
Q601	T602	H603	V604	T605	D606	PRO	PRO	G609	D610	I611	L612	V613	F614	L615	T616	G617	Q618	E619	E620	I621	E622	A623	H604	C625	E626	M627	L628	Q629	D630	R631	C632	R633	R634	L635	G636	SER	LYS	I639	R640	E641	L642	L643	V644	L645	P646	I647	Y648	A649	N650	L651	P652	S653	D654	M655	G656	A657	L659	F660							
Q661	P662	T663	P664	PRO	GLY	A667	R668	R669	V670	V671	V672	T674	M675	L676	A677	E678	T679	S680	L681	T682	L683	E684	G685	I686	I687	Y688	V689	T690	L690	D691	P692	G693	F694	C695	K696	Q697	K698	S699	Y700	H701	P702	R703	T704	G705	M706	E707	S708	L709	T710	W711	T712	P713	C714	S715	K716	A717	S718	A719	M720						
Q721	R722	A723	G724	R725	A726	G727	R728	V729	A730	A731	G732	K733	G734	F735	R736	L737	A740	W741	A742	Y743	Q744	H745	E746	L747	E748	E749	T750	V751	V752	F753	E754	I755	Q756	R757	T758	S759	L760	G761	M762	V763	L764	V765	L766	L767	K768	S769	L770	G771	I772	H773	D774	L775	M776	H777	F778	D779	F780	L781							
D782	P783	F784	P785	Y786	E787	T788	L789	L790	L791	A792	L793	E794	Q795	L796	Y797	A798	L799	G800	A801	N803	H804	L805	G806	L808	T809	L810	S811	G812	R813	K814	M815	A816	E817	L818	P819	V820	D821	P822	M823	L824	S825	K826	M827	I828	L829	A830	S831	GLU	LYS	TYR	SER	C836	S837	E838	E839	I840	L841								
T842	V843	A844	A845	M846	L847	S848	VAL	ASN	ASN	GLN	ILE	PHE	TYR	ARG	PRO	LYS	ASP	LYS	VAL	HIS	ALA	D865	N866	A867	R868	V869	N870	F871	F872	L873	P874	G875	G876	D877	H878	L879	V880	L881	L882	N883	V884	Y885	T886	Q887	W888	A889	E890	SER	GLY	TYR	SER	GLN	TRP	C898	Y899	E900	N901								
F902	V903	Q904	F905	R906	S907	M908	R909	R910	A911	R912	D913	V914	R915	E916	Q917	L918	E919	G920	L921	L922	E923	R924	V925	E926	V927	G928	L929	S930	S931	C932	Q933	G934	D935	Y936	I937	R938	V939	R940	K941	A942	I943	T944	A945	G946	F947	F948	Y949	H950	T951	A952	R953	LEU	THR	ARG	SER	G958	Y959	R960	T961						
V962	LYS	GLN	GLN	LYS	LYS	V968	F969	L970	H971	P972	H973	S974	SER	LEU	PHE	GLU	Q979	Q980	P981	R982	W983	L984	L985	Y986	H987	E988	L989	V990	L991	T992	T993	K994	E995	F996	N997	R998	Q999	V1000	L1001	E1002	I1003	E1004	S1005	S1006	V1007	L1008	L1009	E1010	V1011	A1012	P1013	H1014	Y1015	Y1016	K1017	ALA	LYS	GLU	LEU						

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96523	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.184	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0346	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: IHP, ZN, GTP, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.84	40/18665 (0.2%)	0.96	56/25340 (0.2%)
2	B	0.66	1/1970 (0.1%)	0.93	6/3060 (0.2%)
3	C	1.08	13/6864 (0.2%)	1.27	40/9334 (0.4%)
4	D	0.55	0/8527	1.11	27/11887 (0.2%)
5	E	0.87	0/2392	1.00	6/3242 (0.2%)
6	a	0.77	0/397	0.99	0/549
6	h	0.77	0/391	0.99	0/540
7	b	0.83	0/404	1.12	2/561 (0.4%)
7	i	0.84	0/421	1.15	3/583 (0.5%)
8	c	0.88	0/405	1.11	0/563
8	j	0.87	0/405	1.11	0/563
9	d	1.12	0/479	1.25	1/666 (0.2%)
9	k	1.14	0/420	1.23	1/583 (0.2%)
10	f	1.20	0/360	1.25	0/497
10	m	1.21	1/360 (0.3%)	1.25	0/497
11	e	1.03	0/390	1.24	1/542 (0.2%)
11	l	1.02	0/390	1.23	0/542
12	g	0.86	0/362	1.08	1/501 (0.2%)
12	n	0.85	0/332	1.08	1/458 (0.2%)
13	F	0.35	0/2224	0.66	5/3462 (0.1%)
14	G	0.25	0/1717	0.54	0/2664
15	H	0.51	7/3217 (0.2%)	0.77	8/4997 (0.2%)
16	o	0.93	0/803	2.15	35/1119 (3.1%)
17	p	1.60	3/810 (0.4%)	2.10	25/1122 (2.2%)
18	w	0.62	6/2376 (0.3%)	0.99	14/3269 (0.4%)
19	u	0.36	0/519	0.95	3/717 (0.4%)
20	v	0.50	2/482 (0.4%)	1.16	8/666 (1.2%)
21	1	0.27	0/7826	0.61	3/10617 (0.0%)
22	2	0.59	4/1277 (0.3%)	0.92	9/1724 (0.5%)
23	3	0.23	0/9408	0.57	6/12767 (0.0%)
24	4	1.08	2/535 (0.4%)	1.28	5/724 (0.7%)
25	5	0.20	0/823	0.53	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	6	0.20	0/678	0.59	0/909
27	7	0.22	0/556	0.49	0/751
28	J	0.80	1/3500 (0.0%)	1.13	3/4750 (0.1%)
29	L	0.47	0/1103	0.71	0/1487
30	M	0.20	0/272	0.57	0/363
31	P	0.98	0/841	1.27	4/1117 (0.4%)
32	R	0.85	7/2351 (0.3%)	1.14	10/3163 (0.3%)
33	T	1.44	13/2522 (0.5%)	1.42	26/3438 (0.8%)
34	V	0.89	1/2234 (0.0%)	1.17	2/3111 (0.1%)
35	X	0.21	0/1011	0.57	0/1348
36	Y	0.24	0/747	0.58	0/1006
37	Z	0.65	6/772 (0.8%)	1.11	9/1056 (0.9%)
38	z	0.21	0/1414	0.54	0/1916
39	x	0.59	1/2871 (0.0%)	0.82	11/3981 (0.3%)
All	All	0.74	108/96823 (0.1%)	0.99	331/133875 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1
23	3	0	4
27	7	0	1
30	M	0	1
32	R	0	1
33	T	0	2
35	X	0	1
All	All	0	33

All (108) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	387	ASP	CA-C	-8.61	1.48	1.52
17	p	156	ASN	C-N	-8.31	1.22	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	316	PHE	C-N	-8.15	1.25	1.34
1	A	483	GLN	CA-C	-7.71	1.43	1.52
33	T	353	THR	CA-C	-7.66	1.43	1.52
15	H	142	C	C1'-N1	7.55	1.59	1.48
1	A	212	PRO	N-CA	-7.28	1.38	1.47
2	B	103	G	C1'-N9	-7.22	1.37	1.48
24	4	50	THR	CB-OG1	7.12	1.55	1.43
3	C	319	THR	CA-C	-7.07	1.44	1.52
24	4	42	THR	CB-OG1	7.00	1.54	1.43
15	H	150	U	C1'-N1	6.96	1.58	1.48
17	p	155	LEU	C-N	-6.93	1.24	1.33
1	A	416	GLY	C-O	6.78	1.31	1.23
15	H	97	G	C1'-N9	-6.78	1.37	1.48
18	w	284	ARG	CA-CB	-6.71	1.42	1.53
1	A	472	LEU	CA-C	-6.71	1.45	1.52
1	A	607	ASP	CA-C	-6.66	1.44	1.52
15	H	151	C	C1'-N1	6.64	1.58	1.48
15	H	184	C	C1'-N1	6.57	1.58	1.48
15	H	141	C	C1'-N1	6.51	1.58	1.48
3	C	637	LEU	CA-C	-6.45	1.44	1.52
3	C	876	PRO	N-CA	-6.42	1.39	1.47
22	2	619	MET	C-N	6.37	1.41	1.33
1	A	321	ASN	N-CA	-6.34	1.38	1.46
1	A	141	ILE	CA-CB	-6.31	1.46	1.54
1	A	581	ILE	CA-CB	-6.27	1.47	1.54
1	A	533	LYS	N-CA	-6.21	1.38	1.46
1	A	125	ALA	C-O	-6.20	1.16	1.24
18	w	415	THR	CB-OG1	6.19	1.53	1.43
3	C	317	CYS	CA-C	-6.19	1.46	1.52
37	Z	570	ALA	C-N	6.17	1.40	1.33
33	T	208	ARG	CA-C	-6.07	1.44	1.52
33	T	333	VAL	N-CA	-6.07	1.39	1.46
1	A	593	ARG	CA-C	-6.04	1.44	1.52
3	C	446	LYS	C-N	5.95	1.41	1.34
33	T	332	ALA	CA-C	-5.80	1.45	1.52
1	A	135	VAL	CA-C	-5.77	1.45	1.52
18	w	491	THR	CB-OG1	5.76	1.52	1.43
18	w	177	ARG	CA-CB	-5.73	1.43	1.53
1	A	221	ASN	CA-C	-5.72	1.45	1.52
1	A	272	ALA	CA-C	-5.71	1.45	1.52
32	R	252	PRO	C-N	5.70	1.41	1.33
39	x	926	GLU	CA-CB	-5.66	1.45	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	T	270	VAL	CA-C	-5.66	1.45	1.52
37	Z	563	ARG	C-N	5.66	1.41	1.33
1	A	482	PHE	N-CA	-5.62	1.39	1.46
18	w	448	ASN	CA-CB	-5.62	1.44	1.53
1	A	150	MET	CA-C	-5.60	1.45	1.52
3	C	875	ILE	C-O	-5.57	1.17	1.24
1	A	415	SER	C-O	-5.55	1.17	1.23
1	A	106	MET	C-N	-5.55	1.28	1.34
33	T	376	ARG	CA-C	-5.53	1.45	1.52
15	H	110	A	C1'-N9	-5.52	1.39	1.48
20	v	165	ARG	CA-CB	-5.52	1.44	1.53
1	A	221	ASN	N-CA	-5.50	1.39	1.46
37	Z	569	PRO	N-CD	5.50	1.55	1.47
1	A	317	PRO	N-CA	-5.48	1.40	1.47
22	2	620	PRO	N-CD	5.48	1.55	1.47
34	V	505	LYS	C-O	-5.45	1.17	1.24
32	R	231	VAL	CA-C	-5.43	1.45	1.52
18	w	457	SER	CB-OG	5.39	1.52	1.42
33	T	218	TRP	CA-C	-5.38	1.46	1.52
3	C	369	PHE	C-O	-5.38	1.17	1.24
33	T	319	THR	CA-C	-5.36	1.45	1.52
1	A	505	ASN	CA-C	-5.32	1.46	1.52
22	2	643	PRO	N-CD	5.31	1.55	1.47
1	A	598	LEU	CA-C	-5.30	1.45	1.52
3	C	899	SER	N-CA	-5.30	1.39	1.46
3	C	659	VAL	C-O	-5.30	1.18	1.23
1	A	1120	PRO	N-CD	5.29	1.55	1.47
17	p	187	HIS	N-CA	5.29	1.53	1.46
1	A	107	PRO	N-CA	-5.28	1.40	1.47
1	A	489	TRP	CA-C	-5.26	1.45	1.52
32	R	130	PRO	N-CD	5.25	1.55	1.47
37	Z	521	PRO	N-CD	5.22	1.55	1.47
1	A	203	VAL	C-O	-5.22	1.17	1.24
1	A	134	TRP	CA-C	-5.21	1.46	1.52
32	R	222	PRO	N-CD	5.20	1.55	1.47
1	A	610	HIS	CA-C	-5.19	1.46	1.52
10	m	14	LEU	CA-C	5.18	1.59	1.52
1	A	597	LYS	CA-C	5.18	1.59	1.52
3	C	258	ASN	N-CA	-5.17	1.39	1.45
1	A	411	PHE	CA-C	-5.15	1.45	1.52
3	C	311	SER	CA-C	-5.13	1.48	1.53
32	R	253	PRO	N-CD	5.13	1.54	1.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	v	154	ALA	CA-CB	-5.12	1.44	1.53
1	A	116	VAL	CA-C	-5.12	1.47	1.52
32	R	252	PRO	N-CD	5.11	1.54	1.47
33	T	216	ASN	CA-C	-5.11	1.46	1.53
33	T	267	ASP	C-O	-5.10	1.18	1.24
1	A	335	PRO	N-CA	-5.10	1.40	1.47
32	R	227	PRO	N-CD	5.10	1.54	1.47
1	A	455	VAL	CA-C	-5.10	1.46	1.52
1	A	170	ASP	CA-C	5.08	1.59	1.52
1	A	531	THR	CA-C	-5.07	1.46	1.53
1	A	407	ALA	N-CA	-5.07	1.39	1.45
33	T	268	LYS	CA-C	-5.07	1.46	1.52
22	2	642	PRO	C-N	5.06	1.40	1.34
3	C	447	PRO	N-CD	5.06	1.54	1.47
37	Z	564	PRO	N-CD	5.06	1.54	1.47
1	A	617	ASN	CA-C	-5.05	1.48	1.53
28	J	340	GLN	C-O	-5.05	1.21	1.23
33	T	465	ILE	N-CA	-5.05	1.40	1.46
37	Z	572	PRO	N-CD	5.04	1.54	1.47
1	A	1118	PRO	N-CD	5.02	1.54	1.47
33	T	346	ILE	CA-C	-5.01	1.46	1.52
1	A	654	ASN	CA-C	-5.00	1.46	1.52

All (331) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	T	187	LYS	CA-C-N	13.13	132.89	119.76
33	T	187	LYS	C-N-CA	13.13	132.89	119.76
24	4	83	PRO	CA-CB-CG	10.35	124.17	104.50
2	B	104	C	C2'-C3'-O3'	-9.92	94.61	109.50
31	P	189	ASP	N-CA-C	-9.51	100.67	112.47
33	T	191	HIS	CA-C-N	9.46	126.47	119.66
33	T	191	HIS	C-N-CA	9.46	126.47	119.66
18	w	442	ASN	CA-CB-CG	-9.32	103.28	112.60
18	w	441	PRO	N-CA-CB	9.20	111.89	103.33
37	Z	569	PRO	CA-N-CD	-8.91	99.52	112.00
1	A	1119	ASP	C-N-CD	8.87	140.12	120.60
37	Z	573	PRO	CA-N-CD	-8.80	99.67	112.00
1	A	696	MET	CA-C-N	8.76	130.49	120.06
1	A	696	MET	C-N-CA	8.76	130.49	120.06
18	w	227	PRO	N-CA-CB	8.75	111.06	103.36
13	F	36	A	C2'-C3'-O3'	-8.69	100.67	113.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	1	1108	ASN	N-CA-C	8.69	124.00	109.76
3	C	144	CYS	N-CA-CB	8.66	123.56	110.22
3	C	776	GLU	N-CA-C	8.63	125.02	113.97
15	H	141	C	O3'-P-O5'	-8.57	91.14	104.00
15	H	150	U	O3'-P-O5'	-8.57	91.14	104.00
15	H	113	G	O3'-P-O5'	-8.53	91.21	104.00
15	H	114	A	O3'-P-O5'	-8.51	91.23	104.00
1	A	211	GLN	CA-C-N	8.44	130.39	119.84
1	A	211	GLN	C-N-CA	8.44	130.39	119.84
33	T	213	GLU	CA-C-N	8.11	129.97	119.84
33	T	213	GLU	C-N-CA	8.11	129.97	119.84
19	u	222	PRO	N-CA-CB	8.06	111.87	103.00
16	o	16	THR	CA-C-O	-8.06	111.74	120.36
39	x	1004	GLU	N-CA-C	8.01	120.01	111.28
32	R	101	ILE	CB-CA-C	-7.95	101.53	111.70
16	o	99	SER	N-CA-C	7.94	122.75	112.26
22	2	641	PRO	N-CA-CB	7.92	110.76	103.08
18	w	120	PRO	N-CA-CB	7.86	111.06	103.51
19	u	221	PRO	N-CA-CB	7.86	110.70	103.08
1	A	677	VAL	CB-CA-C	-7.81	101.78	112.24
22	2	656	PRO	N-CA-CB	7.78	111.56	103.00
3	C	919	ARG	CA-C-N	7.77	127.48	119.56
3	C	919	ARG	C-N-CA	7.77	127.48	119.56
2	B	12	U	C2'-C3'-O3'	-7.74	102.09	113.70
19	u	200	PRO	N-CA-CB	7.74	110.87	103.52
16	o	117	TYR	CA-C-O	7.68	128.47	120.40
22	2	651	PRO	N-CA-CB	7.67	109.77	103.32
20	v	115	PRO	N-CA-CB	7.65	111.28	103.25
17	p	187	HIS	N-CA-C	-7.61	103.95	113.23
23	3	916	ASN	CA-C-N	7.57	129.30	119.84
23	3	916	ASN	C-N-CA	7.57	129.30	119.84
32	R	433	ILE	N-CA-C	7.53	118.30	110.62
17	p	219	LYS	O-C-N	7.53	132.07	123.27
20	v	139	PRO	N-CA-CB	7.52	111.15	103.25
18	w	230	PRO	N-CA-CB	7.52	110.33	103.19
39	x	785	PRO	N-CA-CB	7.49	109.97	103.31
24	4	27	PRO	N-CA-CB	7.48	111.10	103.25
3	C	823	ALA	N-CA-C	7.47	120.75	110.06
20	v	220	PRO	N-CA-CB	7.47	110.33	103.08
20	v	217	PRO	N-CA-CB	7.45	110.31	103.08
39	x	933	GLN	N-CA-C	7.40	119.43	111.36
1	A	81	PHE	N-CA-C	7.37	119.39	111.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	PRO	CA-C-N	7.33	127.00	119.82
1	A	167	PRO	C-N-CA	7.33	127.00	119.82
17	p	192	VAL	CA-C-O	7.31	128.52	120.48
1	A	276	GLY	CA-C-N	7.29	127.87	120.14
1	A	276	GLY	C-N-CA	7.29	127.87	120.14
4	D	1044	VAL	CA-C-N	7.25	126.75	118.85
4	D	1044	VAL	C-N-CA	7.25	126.75	118.85
18	w	305	PRO	N-CA-CB	7.24	110.77	102.88
20	v	218	PRO	N-CA-CB	7.22	110.83	103.25
16	o	71	VAL	CA-C-N	7.21	131.63	120.75
16	o	71	VAL	C-N-CA	7.21	131.63	120.75
1	A	423	ASP	N-CA-C	-7.20	104.52	112.72
32	R	252	PRO	CA-C-N	-7.19	112.36	119.76
32	R	252	PRO	C-N-CA	-7.19	112.36	119.76
4	D	1666	THR	N-CA-C	7.16	121.46	112.87
18	w	174	PRO	N-CA-CB	7.14	110.75	103.25
3	C	215	VAL	CB-CA-C	-7.13	102.52	112.14
23	3	915	LEU	CA-C-N	-7.08	115.06	122.28
23	3	915	LEU	C-N-CA	-7.08	115.06	122.28
18	w	105	PRO	N-CA-CB	7.06	110.79	103.23
39	x	509	PRO	N-CA-CB	7.06	110.66	103.25
17	p	155	LEU	N-CA-CB	7.03	122.37	110.49
17	p	184	PRO	N-CA-CB	7.02	110.62	103.25
33	T	220	VAL	CB-CA-C	-7.02	99.65	110.95
37	Z	570	ALA	CA-C-N	-7.00	113.17	120.38
37	Z	570	ALA	C-N-CA	-7.00	113.17	120.38
4	D	533	VAL	N-CA-C	6.99	118.86	112.29
24	4	50	THR	CA-CB-OG1	6.95	120.02	109.60
20	v	221	PRO	N-CA-CB	6.95	110.55	103.25
1	A	1303	LEU	CA-C-N	-6.94	112.33	123.23
1	A	1303	LEU	C-N-CA	-6.94	112.33	123.23
23	3	441	GLY	N-CA-C	6.92	121.22	110.91
1	A	667	GLY	N-CA-C	-6.89	103.41	113.48
33	T	405	PHE	N-CA-C	6.84	119.75	111.82
16	o	121	LEU	CA-C-O	6.80	128.79	121.44
18	w	399	LEU	CD1-CG-CD2	6.80	125.76	110.80
20	v	162	PRO	N-CA-CB	6.78	110.45	103.00
37	Z	563	ARG	CA-C-N	-6.76	113.00	119.76
37	Z	563	ARG	C-N-CA	-6.76	113.00	119.76
17	p	53	PHE	CA-C-O	-6.75	112.90	120.32
18	w	419	PRO	N-CA-CB	6.73	110.32	103.25
16	o	58	ASP	N-CA-CB	-6.69	100.66	111.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	x	403	PRO	N-CA-CB	6.68	110.92	103.44
3	C	799	GLU	CA-C-N	6.68	126.37	119.56
3	C	799	GLU	C-N-CA	6.68	126.37	119.56
13	F	33	G	C2'-C3'-O3'	-6.65	103.73	113.70
18	w	202	PRO	N-CA-CB	6.63	110.55	103.52
39	x	821	ASP	CA-C-N	6.63	126.41	119.05
39	x	821	ASP	C-N-CA	6.63	126.41	119.05
17	p	185	GLY	N-CA-C	-6.63	104.56	113.24
1	A	455	VAL	CB-CA-C	-6.62	103.09	112.22
3	C	148	CYS	CB-CA-C	6.58	122.04	110.85
22	2	629	PRO	N-CA-CB	6.57	110.22	103.00
1	A	1921	ASP	CB-CA-C	-6.50	109.06	116.54
22	2	619	MET	CA-C-N	-6.49	113.60	120.03
22	2	619	MET	C-N-CA	-6.49	113.60	120.03
18	w	99	PRO	N-CA-CB	6.47	110.45	103.33
1	A	617	ASN	CB-CA-C	-6.45	102.10	111.91
16	o	87	LEU	CA-C-N	6.45	126.21	119.05
16	o	87	LEU	C-N-CA	6.45	126.21	119.05
22	2	636	MET	CG-SD-CE	6.43	115.05	100.90
17	p	148	PRO	N-CA-CB	6.41	109.30	103.08
1	A	581	ILE	CB-CA-C	-6.38	103.80	111.97
33	T	323	VAL	CB-CA-C	-6.36	103.82	111.97
1	A	170	ASP	N-CA-C	6.36	119.00	110.35
17	p	149	PRO	N-CA-CB	6.35	109.58	102.60
2	B	20	G	N9-C1'-C2'	6.31	123.46	114.00
33	T	192	PRO	O-C-N	6.29	124.11	121.15
16	o	40	THR	CA-C-N	6.27	131.49	122.40
16	o	40	THR	C-N-CA	6.27	131.49	122.40
33	T	354	ILE	CB-CA-C	-6.23	103.18	110.91
17	p	198	GLY	N-CA-C	-6.23	104.80	112.77
3	C	89	LEU	N-CA-C	6.19	118.82	111.33
39	x	1003	ILE	N-CA-C	6.18	119.15	108.95
33	T	381	HIS	CA-C-N	6.15	127.52	119.84
33	T	381	HIS	C-N-CA	6.15	127.52	119.84
13	F	34	G	C2'-C3'-O3'	-6.12	104.52	113.70
1	A	204	LEU	N-CA-C	6.12	118.92	111.82
3	C	843	VAL	CB-CA-C	-6.11	103.89	112.14
32	R	181	PRO	N-CA-C	6.11	125.06	112.47
16	o	73	ASN	N-CA-C	6.10	119.77	111.17
4	D	1006	LYS	CA-C-N	6.06	126.22	119.32
4	D	1006	LYS	C-N-CA	6.06	126.22	119.32
28	J	412	ASP	N-CA-C	6.05	117.44	108.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	T	327	SER	N-CA-C	-6.03	102.75	110.53
3	C	264	ILE	CB-CA-C	-6.03	105.71	111.44
39	x	821	ASP	O-C-N	5.98	127.26	121.28
16	o	79	ILE	CA-C-N	5.98	125.78	120.10
16	o	79	ILE	C-N-CA	5.98	125.78	120.10
16	o	75	ARG	N-CA-CB	-5.98	102.66	111.51
17	p	200	ALA	N-CA-C	-5.97	104.85	111.36
1	A	132	ILE	CA-C-O	5.97	123.21	119.51
17	p	46	MET	N-CA-C	-5.96	104.69	111.07
12	g	67	ILE	CB-CA-C	-5.96	104.80	111.23
3	C	707	ILE	N-CA-C	5.94	118.52	111.09
12	n	67	ILE	CB-CA-C	-5.94	104.82	111.23
37	Z	525	TYR	N-CA-C	5.92	118.55	108.67
2	B	40	U	N1-C1'-C2'	5.91	120.86	112.00
16	o	50	SER	CA-C-O	5.89	127.80	121.55
1	A	487	LEU	N-CA-C	5.88	119.14	109.85
33	T	254	VAL	CB-CA-C	-5.87	102.39	110.96
3	C	922	GLU	CA-C-N	5.87	125.80	119.76
3	C	922	GLU	C-N-CA	5.87	125.80	119.76
1	A	167	PRO	N-CA-C	5.87	117.86	110.70
17	p	161	GLU	N-CA-C	-5.85	106.09	113.23
3	C	358	LYS	N-CA-C	-5.84	101.77	110.23
1	A	387	PHE	N-CA-C	5.83	118.11	111.11
16	o	113	LYS	N-CA-C	5.80	118.36	111.33
24	4	27	PRO	CA-CB-CG	5.79	115.51	104.50
1	A	2199	ILE	CB-CA-C	-5.77	104.46	112.02
33	T	188	PRO	N-CA-C	5.76	120.24	111.19
1	A	1119	ASP	CA-C-N	-5.76	113.18	127.00
1	A	1119	ASP	C-N-CA	-5.76	113.18	127.00
3	C	536	ARG	N-CA-C	-5.75	100.92	109.83
1	A	698	PRO	CA-C-N	5.72	132.47	121.54
1	A	698	PRO	C-N-CA	5.72	132.47	121.54
33	T	187	LYS	CB-CA-C	5.71	115.25	111.20
4	D	1135	LEU	CA-C-N	5.71	125.64	119.76
4	D	1135	LEU	C-N-CA	5.71	125.64	119.76
4	D	782	PHE	N-CA-C	5.70	118.08	109.41
5	E	309	VAL	CB-CA-C	-5.70	104.06	110.96
4	D	1291	LEU	CA-C-N	5.68	126.00	119.92
4	D	1291	LEU	C-N-CA	5.68	126.00	119.92
2	B	25	C	C1'-C2'-O2'	5.68	120.32	111.80
16	o	149	LYS	CB-CA-C	-5.67	101.99	110.16
13	F	33	G	C4'-C3'-O3'	5.67	121.50	113.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2153	THR	N-CA-C	-5.67	101.79	109.95
1	A	243	ASN	N-CA-C	5.66	118.22	111.71
3	C	747	ASP	N-CA-C	5.64	117.98	107.99
3	C	544	VAL	CA-C-N	5.64	125.84	120.31
3	C	544	VAL	C-N-CA	5.64	125.84	120.31
39	x	981	PRO	N-CA-CB	5.62	109.16	103.25
16	o	71	VAL	O-C-N	-5.62	115.55	122.57
3	C	446	LYS	CA-C-N	-5.62	112.73	118.85
3	C	446	LYS	C-N-CA	-5.62	112.73	118.85
7	i	52	LYS	CA-C-N	-5.61	114.15	119.76
7	i	52	LYS	C-N-CA	-5.61	114.15	119.76
1	A	118	VAL	CB-CA-C	-5.61	101.01	110.71
4	D	1048	VAL	N-CA-C	-5.58	106.36	113.22
1	A	314	ILE	CA-CB-CG1	-5.56	100.95	110.40
23	3	917	PRO	N-CA-C	-5.55	101.04	112.47
1	A	2225	LEU	N-CA-C	5.55	117.83	109.23
32	R	96	ILE	N-CA-C	-5.54	102.38	109.30
7	b	52	LYS	CA-C-N	-5.53	114.23	119.76
7	b	52	LYS	C-N-CA	-5.53	114.23	119.76
5	E	322	LYS	N-CA-C	-5.53	98.18	108.02
31	P	50	ALA	CA-C-N	5.52	125.36	119.28
31	P	50	ALA	C-N-CA	5.52	125.36	119.28
39	x	443	ASN	N-CA-C	5.52	117.29	111.28
16	o	32	PRO	CA-C-N	5.51	130.65	122.99
16	o	32	PRO	C-N-CA	5.51	130.65	122.99
16	o	34	ILE	CA-C-O	-5.50	114.25	120.74
3	C	281	ILE	CB-CA-C	-5.50	104.94	111.97
33	T	307	SER	N-CA-C	5.48	117.52	109.24
37	Z	520	LYS	CA-C-N	-5.48	112.99	119.84
37	Z	520	LYS	C-N-CA	-5.48	112.99	119.84
15	H	157	G	P-O5'-C5'	-5.48	112.69	120.90
1	A	2203	ASN	N-CA-C	5.47	120.77	109.11
1	A	2241	ASN	N-CA-C	5.47	118.25	110.10
16	o	16	THR	O-C-N	5.47	129.46	123.22
5	E	281	VAL	N-CA-C	5.46	116.17	108.36
5	E	284	PHE	N-CA-C	5.46	119.44	112.34
1	A	157	ASP	N-CA-C	5.46	120.05	112.90
16	o	159	GLU	N-CA-C	-5.46	104.98	111.69
3	C	469	ASP	CA-C-N	-5.45	113.66	119.98
3	C	469	ASP	C-N-CA	-5.45	113.66	119.98
7	i	5	LYS	N-CA-C	5.44	118.13	111.82
24	4	81	GLY	N-CA-C	-5.44	108.34	115.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	T	421	VAL	N-CA-C	5.44	116.11	108.17
22	2	642	PRO	CA-C-N	-5.44	113.02	119.05
22	2	642	PRO	C-N-CA	-5.44	113.02	119.05
5	E	237	SER	N-CA-C	5.42	117.94	110.35
4	D	1228	VAL	CB-CA-C	-5.42	104.94	112.04
3	C	907	VAL	CB-CA-C	-5.42	105.04	110.89
1	A	487	LEU	N-CA-CB	-5.41	102.44	111.20
3	C	744	ILE	CB-CA-C	-5.40	102.58	110.62
33	T	317	VAL	CB-CA-C	-5.38	104.99	112.04
1	A	427	VAL	CB-CA-C	-5.38	105.02	111.85
1	A	2100	THR	N-CA-C	-5.37	106.73	113.28
16	o	125	VAL	CA-C-N	5.37	128.01	120.28
16	o	125	VAL	C-N-CA	5.37	128.01	120.28
17	p	158	LEU	CA-C-N	5.37	126.55	119.84
17	p	158	LEU	C-N-CA	5.37	126.55	119.84
3	C	420	CYS	CA-CB-SG	-5.36	102.07	114.40
5	E	156	SER	N-CA-C	5.36	116.67	108.42
4	D	749	GLY	N-CA-C	-5.35	108.32	114.69
16	o	40	THR	N-CA-C	-5.34	106.26	112.89
31	P	194	PHE	N-CA-C	5.34	117.78	108.76
32	R	231	VAL	CB-CA-C	-5.34	105.08	112.24
3	C	815	VAL	CB-CA-C	-5.34	105.14	111.97
16	o	33	VAL	N-CA-CB	-5.33	103.73	111.52
33	T	281	ILE	CB-CA-C	-5.33	106.37	111.06
28	J	356	TYR	N-CA-C	-5.33	102.31	110.14
4	D	1228	VAL	N-CA-C	5.32	116.69	110.62
4	D	811	SER	N-CA-C	5.32	115.15	108.45
4	D	2096	ALA	CA-C-N	5.32	125.52	120.31
4	D	2096	ALA	C-N-CA	5.32	125.52	120.31
1	A	1125	ILE	N-CA-C	5.32	116.09	110.72
21	1	1125	PRO	CA-C-N	5.31	128.13	120.38
21	1	1125	PRO	C-N-CA	5.31	128.13	120.38
20	v	199	TRP	N-CA-C	5.30	117.28	107.73
18	w	50	TYR	N-CA-CB	-5.29	103.10	110.29
1	A	1126	VAL	N-CA-C	5.29	116.01	110.62
17	p	20	LYS	N-CA-C	5.27	117.43	111.11
4	D	1693	ARG	CA-C-N	5.27	125.07	119.28
4	D	1693	ARG	C-N-CA	5.27	125.07	119.28
2	B	12	U	C4'-C3'-O3'	5.26	120.90	113.00
1	A	132	ILE	CA-C-N	5.26	126.42	119.84
1	A	132	ILE	C-N-CA	5.26	126.42	119.84
4	D	1127	CYS	CA-C-N	5.26	125.57	119.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1127	CYS	C-N-CA	5.26	125.57	119.47
16	o	146	ASP	CA-C-N	5.26	130.03	122.40
16	o	146	ASP	C-N-CA	5.26	130.03	122.40
1	A	166	PHE	N-CA-C	5.25	117.28	110.40
17	p	170	LEU	N-CA-C	-5.25	105.64	111.36
17	p	190	ALA	O-C-N	5.25	129.46	123.27
16	o	88	PRO	CB-CA-C	-5.24	103.98	112.62
1	A	1117	HIS	CA-C-N	-5.22	113.31	119.84
1	A	1117	HIS	C-N-CA	-5.22	113.31	119.84
32	R	143	ILE	CB-CA-C	-5.22	105.29	111.97
32	R	411	TYR	N-CA-C	5.21	118.22	110.14
1	A	429	ASN	N-CA-C	5.21	119.39	113.19
17	p	48	MET	N-CA-C	5.21	119.63	113.28
3	C	809	ILE	O-C-N	5.20	123.75	120.42
17	p	51	GLN	N-CA-C	5.20	117.59	109.52
33	T	346	ILE	CB-CA-C	-5.20	103.36	110.96
34	V	483	GLU	N-CA-C	5.20	117.02	111.36
15	H	171	U	C2'-C3'-O3'	-5.19	105.91	113.70
4	D	488	LEU	N-CA-C	5.19	119.71	113.17
3	C	863	ILE	CA-C-O	5.18	122.21	119.15
3	C	97	VAL	N-CA-C	5.17	116.06	110.21
33	T	414	ALA	N-CA-C	-5.16	100.29	108.14
17	p	83	TYR	CA-C-O	-5.16	115.17	121.05
1	A	1134	TRP	CA-C-N	5.15	125.15	119.89
1	A	1134	TRP	C-N-CA	5.15	125.15	119.89
4	D	572	ASP	N-CA-C	-5.14	103.36	110.35
3	C	308	CYS	CB-CA-C	-5.13	100.73	109.51
1	A	99	VAL	CB-CA-C	-5.13	105.21	112.14
3	C	307	VAL	N-CA-C	5.13	115.43	107.78
3	C	552	ILE	CB-CA-C	-5.13	104.32	110.99
3	C	866	SER	CA-C-N	5.13	126.25	119.84
3	C	866	SER	C-N-CA	5.13	126.25	119.84
28	J	275	ASN	N-CA-C	5.12	116.61	108.67
9	k	99	MET	N-CA-C	5.12	116.86	108.76
17	p	38	VAL	O-C-N	5.12	127.11	121.83
9	d	99	MET	N-CA-C	5.12	116.84	108.76
16	o	90	LEU	CA-C-O	-5.12	113.19	120.51
18	w	150	ILE	N-CA-CB	-5.11	102.81	111.50
17	p	168	SER	N-CA-C	-5.11	105.90	111.82
16	o	90	LEU	O-C-N	5.10	129.37	122.59
33	T	401	PRO	N-CA-C	5.09	122.96	112.47
15	H	155	C	P-O3'-C3'	5.09	127.84	120.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	125	ASN	N-CA-C	5.09	116.51	111.07
1	A	424	ILE	CA-C-N	5.09	126.20	119.84
1	A	424	ILE	C-N-CA	5.09	126.20	119.84
11	e	85	THR	N-CA-C	-5.09	105.92	112.68
15	H	156	U	C4'-C3'-C2'	5.08	107.68	102.60
4	D	1875	VAL	CA-C-N	5.08	124.52	119.24
4	D	1875	VAL	C-N-CA	5.08	124.52	119.24
16	o	83	LEU	N-CA-C	5.08	117.47	111.33
32	R	88	ILE	N-CA-C	-5.08	102.54	109.55
17	p	197	ASP	O-C-N	-5.08	115.79	122.39
1	A	539	ARG	CB-CA-C	-5.07	101.30	109.72
17	p	201	GLY	N-CA-C	-5.07	106.28	112.77
1	A	2310	ARG	CG-CD-NE	5.07	123.16	112.00
3	C	243	ILE	CB-CA-C	-5.06	105.50	111.97
4	D	574	GLN	N-CA-C	5.05	117.90	111.69
3	C	310	SER	N-CA-C	5.05	116.66	109.14
33	T	479	THR	N-CA-C	5.05	117.62	109.40
34	V	459	ILE	CB-CA-C	-5.04	105.51	111.97
13	F	34	G	C4'-C3'-O3'	5.03	120.55	113.00
33	T	253	ILE	CB-CA-C	-5.03	102.76	110.50
16	o	99	SER	N-CA-CB	-5.00	102.96	111.17

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	1	1028	HIS	Peptide
21	1	1105	GLU	Peptide
21	1	1107	GLN	Peptide
21	1	220	GLN	Peptide
21	1	415	LEU	Peptide
21	1	418	PRO	Peptide
21	1	460	PRO	Peptide
21	1	717	THR	Peptide
21	1	943	LYS	Peptide
22	2	558	ARG	Peptide
23	3	261	PHE	Peptide
23	3	530	ASP	Peptide
23	3	552	ARG	Peptide
23	3	916	ASN	Peptide
27	7	74	GLN	Peptide
1	A	1119	ASP	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	697	MET	Peptide
1	A	941	LYS	Peptide
3	C	622	GLU	Peptide
3	C	736	GLY	Peptide
3	C	823	ALA	Peptide
4	D	430	LEU	Peptide
30	M	196	ASP	Peptide
32	R	94	GLY	Peptide
33	T	400	PHE	Mainchain,Peptide
35	X	193	ASN	Peptide
9	d	112	ASN	Peptide
9	k	112	ASN	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	18165	0	17930	1570	0
2	B	1768	0	897	124	0
3	C	6716	0	6691	991	0
4	D	8528	0	3745	72	0
5	E	2338	0	2272	138	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	10	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	2	0
9	k	422	0	175	2	0
10	f	361	0	158	1	0
10	m	361	0	158	0	0
11	e	391	0	163	3	0
11	l	391	0	163	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	g	363	0	160	1	0
12	n	334	0	143	3	0
13	F	1988	0	1005	132	0
14	G	1545	0	786	130	0
15	H	2886	0	1463	261	0
16	o	804	0	350	9	0
17	p	813	0	366	14	0
18	w	2369	0	1298	97	0
19	u	525	0	216	0	0
20	v	486	0	206	3	0
21	1	7702	0	7389	304	0
22	2	1252	0	1040	59	0
23	3	9220	0	9139	520	0
24	4	527	0	438	41	0
25	5	807	0	729	28	0
26	6	670	0	654	21	0
27	7	540	0	509	24	0
28	J	3463	0	2544	115	0
29	L	1077	0	1067	57	0
30	M	267	0	225	24	0
31	P	829	0	814	195	0
32	R	2314	0	2189	412	0
33	T	2457	0	2416	253	0
34	V	2238	0	969	51	0
35	X	1012	0	731	18	0
36	Y	737	0	608	67	0
37	Z	755	0	591	156	0
38	z	1381	0	1298	29	0
39	x	2882	0	1308	23	0
40	A	36	0	6	0	0
41	C	32	0	12	11	0
42	C	1	0	0	0	0
42	F	5	0	0	0	0
43	6	3	0	0	0	0
43	M	1	0	0	0	0
All	All	94673	0	74251	4761	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 28.

All (4761) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Y:37:TRP:CH2	37:Z:498:GLY:HA2	1.23	1.65
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.57
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54
3:C:77:VAL:HG11	33:T:196:LEU:CG	1.39	1.52
36:Y:37:TRP:CH2	37:Z:498:GLY:CA	1.93	1.51
1:A:2270:PHE:CB	4:D:1264:PRO:CB	1.86	1.50
32:R:442:ARG:HH11	32:R:443:GLY:C	1.17	1.50
37:Z:564:PRO:HB2	37:Z:582:TYR:CG	1.45	1.49
18:w:485:ASN:CA	23:3:978:LEU:HD21	1.42	1.47
31:P:193:VAL:HG23	31:P:194:PHE:CD2	1.46	1.47
1:A:844:GLU:CB	32:R:422:MET:CE	1.94	1.45
31:P:193:VAL:CG2	31:P:194:PHE:HD2	1.28	1.45
23:3:440:HIS:CE1	23:3:733:PRO:HD3	1.50	1.43
32:R:414:ARG:NH1	37:Z:598:PHE:CZ	1.86	1.43
1:A:73:HIS:HD2	1:A:81:PHE:CE2	1.37	1.42
1:A:530:LEU:H	30:M:198:GLN:NE2	1.18	1.42
1:A:2270:PHE:CD1	4:D:1264:PRO:CB	2.03	1.41
3:C:705:VAL:HG23	3:C:717:PHE:CD2	1.55	1.41
3:C:77:VAL:HG12	33:T:196:LEU:C	1.46	1.41
3:C:79:THR:CG2	33:T:199:VAL:HB	1.51	1.40
28:J:293:ASN:CB	29:L:225:TYR:CB	1.98	1.39
1:A:312:TYR:CE2	3:C:882:GLY:HA3	1.58	1.39
3:C:77:VAL:CG1	33:T:196:LEU:C	1.94	1.39
3:C:79:THR:HG23	33:T:199:VAL:CB	1.49	1.39
5:E:260:ARG:NH1	5:E:273:CYS:SG	1.95	1.39
1:A:530:LEU:HB2	30:M:198:GLN:NE2	1.38	1.38
28:J:339:TRP:HA	32:R:116:TYR:CE2	1.58	1.38
3:C:387:ASP:O	3:C:388:VAL:HG12	1.20	1.37
32:R:442:ARG:CD	32:R:443:GLY:H	1.37	1.37
1:A:393:LEU:HA	3:C:379:LYS:CG	1.52	1.36
1:A:762:ARG:HH22	31:P:226:LYS:NZ	1.19	1.35
28:J:339:TRP:HA	32:R:116:TYR:CD2	1.60	1.35
32:R:414:ARG:NH1	37:Z:598:PHE:CE2	1.93	1.35
1:A:844:GLU:CB	32:R:422:MET:HE3	1.51	1.35
1:A:393:LEU:N	3:C:379:LYS:HE2	1.42	1.34
3:C:149:LEU:CD1	3:C:427:PHE:CD2	2.08	1.34
32:R:442:ARG:HD3	32:R:443:GLY:N	1.05	1.34
1:A:121:HIS:NE2	1:A:481:PHE:HB3	1.42	1.34
32:R:414:ARG:NE	37:Z:598:PHE:CZ	1.95	1.34
3:C:452:THR:CG2	3:C:577:PHE:HD2	1.40	1.34
1:A:312:TYR:CZ	3:C:882:GLY:HA3	1.61	1.34

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:45:C:N4	18:w:395:TRP:CD1	1.95	1.34
1:A:1962:THR:CG2	37:Z:524:ARG:HB2	1.57	1.33
1:A:384:VAL:HG12	3:C:331:PHE:CB	1.58	1.32
1:A:388:LEU:CD1	3:C:399:LEU:HD21	1.58	1.32
3:C:145:PHE:CA	3:C:312:SER:HB2	1.57	1.31
32:R:414:ARG:CZ	37:Z:598:PHE:CZ	2.14	1.31
3:C:670:SER:HA	3:C:823:ALA:CB	1.60	1.31
1:A:392:PRO:C	3:C:379:LYS:HE2	1.54	1.30
31:P:212:ASN:O	33:T:458:SER:HA	1.30	1.30
1:A:73:HIS:CD2	1:A:81:PHE:CE2	2.20	1.30
1:A:384:VAL:HA	3:C:331:PHE:CD2	1.67	1.30
1:A:305:ARG:HB3	3:C:879:ASP:OD1	1.28	1.29
1:A:73:HIS:CD2	1:A:81:PHE:CZ	2.20	1.29
31:P:211:VAL:HG13	33:T:457:GLY:CA	1.62	1.29
3:C:77:VAL:CG1	33:T:196:LEU:HG	1.63	1.28
3:C:705:VAL:CG2	3:C:717:PHE:CE2	2.15	1.28
1:A:264:PHE:CZ	1:A:459:LEU:HD13	1.66	1.27
23:3:440:HIS:CE1	23:3:733:PRO:CD	2.14	1.27
1:A:384:VAL:CG1	3:C:331:PHE:HB3	1.64	1.27
1:A:2268:LEU:HD23	4:D:1261:PRO:O	1.21	1.27
1:A:388:LEU:HD11	3:C:399:LEU:CD2	1.63	1.27
1:A:2268:LEU:HD22	4:D:1261:PRO:CB	1.65	1.26
1:A:666:LYS:CB	1:A:668:VAL:HG22	1.64	1.26
3:C:78:GLU:O	33:T:198:ARG:HA	1.35	1.26
1:A:530:LEU:CA	30:M:198:GLN:HE22	1.49	1.26
3:C:145:PHE:HA	3:C:312:SER:CB	1.65	1.26
31:P:211:VAL:CG1	33:T:457:GLY:HA3	1.65	1.26
1:A:406:TRP:HZ3	3:C:265:LEU:O	1.14	1.26
31:P:193:VAL:CG2	31:P:194:PHE:CD2	2.09	1.26
5:E:146:ARG:NH1	5:E:148:LYS:CE	1.98	1.25
32:R:414:ARG:CZ	37:Z:598:PHE:HZ	1.47	1.25
1:A:2113:LYS:HE3	4:D:1229:ASP:O	1.33	1.25
1:A:530:LEU:CB	30:M:198:GLN:HE22	1.47	1.24
14:G:131:U:OP1	18:w:396:LEU:HD13	1.31	1.24
24:4:14:THR:HA	24:4:59:VAL:O	1.32	1.24
32:R:442:ARG:HD2	32:R:444:GLY:N	1.50	1.24
3:C:679:PRO:HB2	3:C:807:GLN:OE1	1.25	1.24
3:C:84:GLU:O	33:T:238:LEU:HD23	1.34	1.24
1:A:530:LEU:N	30:M:198:GLN:NE2	1.84	1.23
36:Y:37:TRP:CZ3	37:Z:498:GLY:CA	2.20	1.23
36:Y:37:TRP:CZ3	37:Z:498:GLY:HA2	1.73	1.23

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:140:HIS:CG	3:C:230:ASP:HB2	1.74	1.22
1:A:121:HIS:CE1	1:A:481:PHE:HB3	1.73	1.22
23:3:440:HIS:NE2	23:3:733:PRO:CD	2.03	1.22
2:B:42:U:N3	14:G:-3:A:C2	2.07	1.22
18:w:485:ASN:CB	23:3:978:LEU:HD21	1.68	1.22
1:A:762:ARG:HH22	31:P:226:LYS:CE	1.51	1.22
3:C:78:GLU:HG2	3:C:80:ILE:CD1	1.69	1.22
3:C:145:PHE:CA	3:C:312:SER:CB	2.18	1.22
18:w:284:ARG:CB	18:w:295:SER:O	1.87	1.22
28:J:256:LYS:O	29:L:232:TYR:CD2	1.93	1.22
1:A:530:LEU:CB	30:M:198:GLN:NE2	2.02	1.21
3:C:77:VAL:HG13	33:T:196:LEU:O	1.40	1.21
3:C:497:LEU:HD13	3:C:577:PHE:CZ	1.76	1.21
36:Y:18:VAL:CB	37:Z:600:ARG:HH21	1.53	1.21
1:A:2325:VAL:HG13	4:D:788:GLY:O	1.40	1.21
1:A:1320:LYS:HE2	32:R:434:TYR:CE1	1.76	1.21
3:C:137:HIS:CD2	3:C:236:MET:HB2	1.75	1.21
32:R:442:ARG:CD	32:R:443:GLY:N	1.95	1.20
1:A:2298:LEU:HB3	4:D:1283:PRO:CB	1.71	1.20
23:3:699:VAL:HA	23:3:715:MET:O	1.40	1.20
1:A:91:ALA:CB	32:R:207:MET:HE3	1.71	1.20
15:H:45:C:C4	18:w:395:TRP:CD1	2.29	1.20
1:A:384:VAL:CG2	3:C:334:ILE:HG21	1.72	1.19
1:A:755:HIS:ND1	31:P:223:PHE:CG	2.10	1.19
3:C:705:VAL:HG23	3:C:717:PHE:CE2	1.75	1.19
1:A:227:ARG:HA	1:A:416:GLY:O	1.39	1.19
1:A:401:GLY:HA3	3:C:386:GLY:HA2	1.20	1.19
5:E:146:ARG:NH1	5:E:148:LYS:HE3	1.53	1.19
13:F:68:C:N4	31:P:33:ARG:HB3	1.55	1.18
1:A:695:ASP:HB3	33:T:374:SER:OG	1.40	1.18
32:R:442:ARG:NH1	32:R:443:GLY:C	2.00	1.18
1:A:2268:LEU:CD2	4:D:1261:PRO:O	1.91	1.17
3:C:149:LEU:HD13	3:C:427:PHE:CG	1.79	1.17
1:A:232:LEU:CD1	1:A:404:LEU:HD12	1.75	1.17
1:A:705:LYS:CB	32:R:251:ILE:HD12	1.72	1.17
3:C:140:HIS:CG	3:C:230:ASP:CB	2.27	1.17
1:A:406:TRP:CZ3	3:C:265:LEU:O	1.98	1.17
1:A:696:MET:CB	33:T:415:ILE:CD1	2.22	1.17
3:C:77:VAL:CG1	33:T:196:LEU:O	1.89	1.16
1:A:393:LEU:HA	3:C:379:LYS:HG3	1.28	1.16
3:C:78:GLU:CG	3:C:80:ILE:HD11	1.72	1.16

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:221:ILE:HD11	3:C:479:THR:OG1	1.46	1.16
1:A:758:ARG:HB3	31:P:227:TYR:CE2	1.79	1.16
1:A:384:VAL:HG21	3:C:334:ILE:CG2	1.76	1.15
3:C:679:PRO:CB	3:C:807:GLN:OE1	1.95	1.15
1:A:1900:GLU:OE1	37:Z:522:LEU:HB2	1.47	1.15
1:A:755:HIS:CE1	31:P:223:PHE:CG	2.35	1.14
1:A:1262:LYS:HG2	32:R:431:ASP:CB	1.77	1.14
3:C:670:SER:HA	3:C:823:ALA:HB1	1.27	1.14
5:E:74:PHE:CE1	5:E:81:LEU:HD21	1.82	1.14
24:4:28:LEU:O	24:4:32:LEU:HB2	1.48	1.14
32:R:101:ILE:O	32:R:104:GLN:HG3	1.48	1.14
39:x:664:PRO:O	39:x:667:ALA:HB3	1.46	1.14
1:A:1405:LEU:HB3	32:R:415:LEU:HD23	1.29	1.14
15:H:156:U:H6	15:H:156:U:H5"	1.10	1.14
36:Y:18:VAL:CB	37:Z:600:ARG:NH2	2.10	1.14
1:A:1405:LEU:HB3	32:R:415:LEU:CD2	1.78	1.14
1:A:2298:LEU:O	4:D:1283:PRO:CB	1.95	1.14
3:C:77:VAL:HG12	33:T:197:TYR:N	1.61	1.14
1:A:1757:GLU:OE1	32:R:451:ILE:HG12	1.49	1.13
14:G:11:A:C2	14:G:12:G:C8	2.36	1.13
3:C:452:THR:CG2	3:C:577:PHE:CD2	2.31	1.13
3:C:679:PRO:HD2	3:C:807:GLN:HB3	1.16	1.13
1:A:252:ASP:CB	1:A:334:THR:HG21	1.79	1.13
1:A:705:LYS:HB2	32:R:251:ILE:HD12	1.28	1.13
1:A:762:ARG:NH2	31:P:226:LYS:NZ	1.95	1.13
1:A:91:ALA:CA	32:R:207:MET:HE3	1.79	1.12
3:C:216:THR:HG22	3:C:245:HIS:HE1	0.97	1.12
23:3:440:HIS:ND1	23:3:733:PRO:HG3	1.63	1.12
1:A:299:ILE:CD1	3:C:921:LEU:HB2	1.79	1.12
3:C:81:VAL:HG13	33:T:201:SER:CB	1.77	1.12
3:C:140:HIS:CB	3:C:230:ASP:HB2	1.79	1.12
3:C:507:VAL:HG11	3:C:565:ILE:HG23	1.30	1.12
3:C:216:THR:HG22	3:C:245:HIS:CE1	1.85	1.12
13:F:68:C:C4	31:P:33:ARG:HB3	1.85	1.12
1:A:696:MET:CB	33:T:415:ILE:HD11	1.80	1.11
1:A:758:ARG:HB3	31:P:227:TYR:HE2	0.96	1.11
1:A:1548:TYR:CD2	1:A:1549:VAL:HG22	1.83	1.11
1:A:439:GLN:NE2	1:A:614:TYR:CZ	2.18	1.11
3:C:77:VAL:HG11	33:T:196:LEU:CB	1.79	1.11
1:A:762:ARG:NH2	31:P:226:LYS:CE	2.14	1.11
1:A:1548:TYR:HD2	1:A:1549:VAL:HG22	1.14	1.11

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:45:C:N4	18:w:395:TRP:NE1	1.98	1.11
32:R:420:LYS:HE3	32:R:420:LYS:HA	1.18	1.11
3:C:465:MET:HE1	3:C:475:MET:HG3	1.14	1.11
37:Z:566:TYR:CE2	37:Z:584:TRP:CZ3	2.39	1.11
1:A:692:ASP:HA	33:T:376:ARG:NH2	1.65	1.10
18:w:485:ASN:HD22	23:3:976:LYS:HG2	1.01	1.10
23:3:440:HIS:HE1	23:3:720:TRP:CZ3	1.67	1.10
1:A:73:HIS:HD2	1:A:81:PHE:CD2	1.69	1.10
1:A:264:PHE:HE1	1:A:455:VAL:HG13	1.15	1.10
1:A:1505:LYS:CE	37:Z:615:SER:OG	1.99	1.10
1:A:349:ALA:HB2	1:A:399:ALA:HB2	1.27	1.10
1:A:1900:GLU:HG2	37:Z:521:PRO:HG2	1.33	1.10
1:A:2287:ARG:NH2	4:D:1147:ASN:CB	2.14	1.10
28:J:225:LEU:HD21	29:L:211:ASN:HB2	1.29	1.10
1:A:86:ARG:HH22	32:R:211:ARG:HG3	1.08	1.10
1:A:232:LEU:HD23	3:C:388:VAL:CG1	1.80	1.10
1:A:1962:THR:HG22	37:Z:524:ARG:HB2	1.18	1.10
3:C:470:PRO:HB3	3:C:500:THR:HG23	1.34	1.10
1:A:252:ASP:HB2	1:A:334:THR:CG2	1.81	1.09
1:A:73:HIS:NE2	1:A:81:PHE:CE1	2.20	1.09
1:A:299:ILE:HD11	3:C:921:LEU:HB2	1.33	1.09
1:A:762:ARG:NH2	31:P:226:LYS:HE2	1.66	1.09
18:w:485:ASN:HA	23:3:978:LEU:HD21	1.35	1.09
1:A:232:LEU:HD23	3:C:388:VAL:HG12	1.21	1.09
1:A:312:TYR:OH	3:C:853:ARG:NH2	1.85	1.09
1:A:666:LYS:HB2	1:A:668:VAL:HG22	1.18	1.09
3:C:66:TYR:CD2	33:T:457:GLY:HA2	1.87	1.09
36:Y:85:GLU:O	37:Z:502:ALA:N	1.85	1.08
1:A:76:MET:CE	1:A:88:TYR:CD2	2.36	1.08
1:A:393:LEU:N	3:C:379:LYS:CE	2.15	1.08
1:A:349:ALA:CB	1:A:399:ALA:HB2	1.82	1.08
3:C:465:MET:CE	3:C:475:MET:HG3	1.82	1.08
37:Z:566:TYR:CE2	37:Z:584:TRP:HZ3	1.71	1.08
1:A:384:VAL:HG21	3:C:334:ILE:HG21	1.21	1.08
1:A:529:THR:HG22	30:M:197:TYR:O	1.52	1.08
1:A:783:TYR:CE1	31:P:228:ILE:HG21	1.88	1.08
1:A:666:LYS:HB2	1:A:668:VAL:CG2	1.82	1.08
28:J:259:GLN:HE22	29:L:220:PRO:CD	1.66	1.08
1:A:417:ARG:NH1	2:B:58:U:O3'	1.87	1.07
3:C:497:LEU:CD1	3:C:577:PHE:CZ	2.36	1.07
1:A:395:THR:CG2	3:C:383:GLN:HE22	1.65	1.07

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:4:17:VAL:HA	24:4:85:ARG:O	1.53	1.07
3:C:670:SER:CB	3:C:823:ALA:HB3	1.85	1.07
15:H:45:C:H2'	18:w:394:TYR:CE2	1.90	1.07
1:A:546:LEU:HD11	1:A:595:LYS:HD2	1.12	1.06
1:A:744:LYS:CE	31:P:213:ASP:HA	1.84	1.06
18:w:485:ASN:O	23:3:978:LEU:CD2	2.03	1.06
1:A:1146:ASP:OD2	1:A:1182:ASN:ND2	1.89	1.06
13:F:68:C:C4	31:P:33:ARG:CB	2.38	1.06
1:A:369:GLU:O	1:A:371:LEU:N	1.88	1.06
1:A:393:LEU:HA	3:C:379:LYS:HG2	1.34	1.06
1:A:264:PHE:CE1	1:A:455:VAL:HG13	1.90	1.05
2:B:39:C:H4'	2:B:40:U:OP1	1.23	1.05
1:A:168:PRO:HG3	1:A:559:ASP:HB3	1.39	1.05
1:A:387:PHE:HE1	3:C:327:TYR:HA	1.14	1.05
1:A:705:LYS:CG	32:R:251:ILE:HD12	1.86	1.05
3:C:452:THR:HG22	3:C:577:PHE:HD2	1.21	1.05
1:A:664:HIS:CE1	1:A:668:VAL:HG23	1.92	1.04
1:A:664:HIS:HE1	1:A:668:VAL:HG23	1.21	1.04
33:T:399:LYS:CG	33:T:406:ILE:HD11	1.87	1.04
1:A:692:ASP:HA	33:T:376:ARG:HH22	1.18	1.04
3:C:228:PHE:HA	3:C:256:CYS:O	1.57	1.04
32:R:178:ARG:HD3	32:R:194:GLN:HE22	1.17	1.04
1:A:1449:LYS:HE3	32:R:428:GLY:HA3	1.37	1.04
3:C:78:GLU:HG2	3:C:80:ILE:HD11	1.06	1.04
1:A:331:TRP:CE3	3:C:179:VAL:HG21	1.91	1.04
1:A:755:HIS:ND1	31:P:223:PHE:CD1	2.26	1.04
3:C:488:VAL:HG13	3:C:609:LYS:HE2	1.39	1.04
13:F:25:C:H4'	13:F:26:U:OP2	1.22	1.04
7:i:88:LYS:CB	18:w:173:ILE:CB	2.34	1.04
32:R:436:VAL:HG23	32:R:437:TYR:CD1	1.93	1.04
1:A:232:LEU:HD12	1:A:404:LEU:HD12	1.04	1.04
24:4:70:ALA:O	24:4:74:MET:CB	2.04	1.03
1:A:168:PRO:CG	1:A:559:ASP:HB3	1.87	1.03
1:A:755:HIS:CE1	31:P:223:PHE:CD2	2.46	1.03
29:L:224:PHE:CD1	32:R:86:LEU:HD12	1.93	1.03
18:w:485:ASN:CA	23:3:978:LEU:CD2	2.36	1.03
18:w:485:ASN:C	23:3:978:LEU:HD21	1.82	1.03
28:J:273:TYR:CZ	32:R:228:PRO:HB3	1.94	1.03
4:D:754:GLU:CB	23:3:662:PHE:CZ	2.41	1.03
15:H:105:G:H2'	15:H:106:G:H5''	1.37	1.03
1:A:254:TYR:CZ	1:A:434:HIS:HB3	1.93	1.02

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:452:THR:HG22	3:C:577:PHE:CD2	1.94	1.02
28:J:331:GLN:HG2	32:R:98:TYR:OH	1.59	1.02
37:Z:564:PRO:CB	37:Z:582:TYR:CG	2.41	1.02
1:A:91:ALA:HA	32:R:207:MET:HE3	1.37	1.02
1:A:250:VAL:HB	1:A:337:VAL:HG11	1.41	1.02
1:A:844:GLU:CB	32:R:422:MET:HE1	1.87	1.02
3:C:387:ASP:O	3:C:388:VAL:CG1	2.07	1.02
32:R:420:LYS:HG3	32:R:421:GLY:H	1.20	1.02
1:A:338:VAL:HG23	3:C:867:PRO:HG3	1.39	1.02
13:F:68:C:C5	31:P:33:ARG:CB	2.42	1.02
32:R:434:TYR:O	32:R:435:ASN:ND2	1.90	1.02
36:Y:37:TRP:CD1	36:Y:83:CYS:HB2	1.92	1.02
1:A:254:TYR:CE2	1:A:434:HIS:HB2	1.94	1.02
13:F:36:A:H3'	13:F:37:C:H5''	1.39	1.02
18:w:411:CYS:SG	18:w:425:HIS:CE1	2.52	1.02
32:R:442:ARG:HD2	32:R:444:GLY:H	0.97	1.02
1:A:299:ILE:HD11	3:C:921:LEU:CB	1.90	1.01
1:A:305:ARG:CB	3:C:879:ASP:OD1	2.07	1.01
23:3:440:HIS:CE1	23:3:720:TRP:CZ3	2.47	1.01
37:Z:525:TYR:CD1	37:Z:526:ILE:HG23	1.95	1.01
3:C:511:GLY:O	3:C:576:ILE:CD1	2.07	1.01
1:A:1457:HIS:HE1	1:A:1459:ARG:CG	1.74	1.01
1:A:1900:GLU:HG2	37:Z:521:PRO:CG	1.91	1.01
3:C:132:VAL:HG12	3:C:226:VAL:HG23	1.43	1.01
3:C:349:PHE:CD1	3:C:356:PHE:CE1	2.49	1.01
1:A:299:ILE:HD11	3:C:921:LEU:CA	1.91	1.00
1:A:1900:GLU:CD	37:Z:522:LEU:HB2	1.85	1.00
1:A:1900:GLU:OE2	37:Z:521:PRO:HB2	1.59	1.00
23:3:440:HIS:O	23:3:733:PRO:HG2	1.61	1.00
3:C:261:ASP:OD2	41:C:1500:GTP:N1	1.92	1.00
3:C:703:GLU:OE2	3:C:740:THR:HG21	1.61	1.00
15:H:179:C:H2'	15:H:180:G:H8	1.25	1.00
1:A:312:TYR:CZ	3:C:882:GLY:CA	2.45	1.00
1:A:1301:ILE:CD1	1:A:1306:LYS:HE2	1.92	1.00
2:B:42:U:N3	14:G:-3:A:H2	1.50	1.00
3:C:705:VAL:CG2	3:C:717:PHE:CD2	2.39	1.00
31:P:193:VAL:HG21	31:P:194:PHE:HD2	1.26	1.00
33:T:352:THR:HG22	33:T:373:LYS:C	1.86	1.00
1:A:264:PHE:CE1	1:A:459:LEU:HD13	1.96	1.00
3:C:81:VAL:CG1	33:T:201:SER:HB3	1.90	1.00
23:3:303:ALA:O	23:3:310:ILE:HA	1.61	1.00

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:85:ASP:HB3	33:T:238:LEU:HG	1.43	1.00
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.44	1.00
1:A:1162:PRO:HG2	31:P:194:PHE:CE2	1.97	1.00
37:Z:525:TYR:CE1	37:Z:526:ILE:HG23	1.96	1.00
1:A:779:LEU:HD21	31:P:223:PHE:CE2	1.97	0.99
23:3:440:HIS:CE1	23:3:733:PRO:CG	2.45	0.99
32:R:414:ARG:NE	37:Z:598:PHE:HZ	1.38	0.99
1:A:783:TYR:HB2	31:P:228:ILE:HG12	1.43	0.99
28:J:270:ASP:OD2	32:R:222:PRO:CG	2.10	0.99
1:A:232:LEU:HD12	1:A:404:LEU:CD1	1.91	0.99
1:A:267:LYS:NZ	2:B:49:A:OP1	1.94	0.99
1:A:1505:LYS:HE3	37:Z:615:SER:OG	1.62	0.99
1:A:76:MET:HE1	1:A:88:TYR:CD2	1.98	0.99
1:A:696:MET:CB	33:T:415:ILE:HD13	1.89	0.99
33:T:434:GLY:HA2	33:T:464:GLY:HA2	1.41	0.99
1:A:715:GLU:OE2	32:R:258:TRP:HZ3	1.43	0.99
18:w:411:CYS:SG	18:w:425:HIS:HE1	1.84	0.99
37:Z:600:ARG:HB3	37:Z:600:ARG:HH11	1.24	0.99
1:A:384:VAL:CG1	3:C:332:GLY:H	1.76	0.99
3:C:64:LYS:HE3	31:P:206:LYS:HE2	1.45	0.99
3:C:137:HIS:CD2	3:C:236:MET:CB	2.45	0.99
13:F:68:C:C5	31:P:33:ARG:HB2	1.97	0.99
1:A:1457:HIS:NE2	32:R:425:GLY:N	2.09	0.99
1:A:2287:ARG:HH21	4:D:1147:ASN:CB	1.72	0.99
18:w:485:ASN:HB3	23:3:978:LEU:CD2	1.92	0.99
1:A:232:LEU:CD1	1:A:404:LEU:CD1	2.41	0.99
1:A:1900:GLU:OE1	37:Z:522:LEU:CB	2.10	0.98
3:C:78:GLU:O	33:T:198:ARG:CA	2.11	0.98
1:A:1084:PRO:HG2	31:P:188:TRP:HZ2	1.26	0.98
23:3:440:HIS:CE1	23:3:733:PRO:HG3	1.99	0.98
31:P:210:PHE:CD2	33:T:455:GLN:OE1	2.16	0.98
32:R:420:LYS:HB2	37:Z:610:LEU:HD11	1.44	0.98
3:C:306:ASN:OD1	3:C:437:HIS:CE1	2.16	0.98
31:P:30:TYR:OH	32:R:162:ALA:HA	1.63	0.98
1:A:417:ARG:NH2	2:B:58:U:H5''	1.79	0.98
1:A:2074:ARG:NH2	4:D:1044:VAL:O	1.96	0.98
18:w:485:ASN:HB3	23:3:978:LEU:HD21	1.41	0.98
1:A:369:GLU:OE2	1:A:369:GLU:N	1.97	0.98
15:H:83:A:H2'	15:H:84:C:O4'	1.64	0.98
3:C:84:GLU:O	33:T:238:LEU:CD2	2.12	0.97
3:C:670:SER:CA	3:C:823:ALA:HB3	1.94	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:412:ASP:CG	32:R:413:GLN:H	1.69	0.97
3:C:66:TYR:HB3	33:T:456:PRO:O	1.64	0.97
3:C:81:VAL:HG13	33:T:201:SER:HB3	0.99	0.97
36:Y:37:TRP:CZ3	37:Z:498:GLY:HA3	2.00	0.97
1:A:1900:GLU:OE2	37:Z:521:PRO:C	2.06	0.97
34:V:548:ALA:CB	34:V:585:ILE:CB	2.42	0.97
37:Z:566:TYR:HE2	37:Z:584:TRP:HZ3	1.05	0.97
3:C:711:ARG:HD3	3:C:730:ARG:HH11	1.29	0.97
3:C:500:THR:HG22	3:C:545:PRO:HA	1.47	0.97
3:C:670:SER:HA	3:C:823:ALA:HB3	1.43	0.97
1:A:299:ILE:HG12	3:C:920:PRO:O	1.64	0.97
1:A:546:LEU:HD11	1:A:595:LYS:CD	1.94	0.97
1:A:1320:LYS:HE2	32:R:434:TYR:HE1	1.15	0.97
1:A:2328:ALA:HB2	4:D:788:GLY:HA2	1.43	0.97
1:A:256:TYR:CE1	3:C:888:ARG:NH1	2.33	0.96
3:C:670:SER:CA	3:C:823:ALA:CB	2.43	0.96
28:J:300:ASP:OD2	32:R:101:ILE:HG13	1.65	0.96
23:3:440:HIS:NE2	23:3:733:PRO:HD3	1.70	0.96
1:A:121:HIS:NE2	1:A:481:PHE:CB	2.29	0.96
3:C:855:GLY:O	3:C:856:HIS:HB3	1.63	0.96
33:T:352:THR:HG22	33:T:373:LYS:O	1.65	0.96
36:Y:37:TRP:HH2	37:Z:498:GLY:CA	1.70	0.96
1:A:47:GLU:O	1:A:50:LYS:HB2	1.64	0.96
3:C:135:CYS:SG	3:C:227:LEU:HD12	2.06	0.96
15:H:78:C:H2'	15:H:79:G:H8	1.27	0.96
1:A:748:ASP:OD1	31:P:214:THR:HG22	1.64	0.96
16:o:46:ALA:HB1	16:o:68:THR:O	1.64	0.96
3:C:115:GLU:O	3:C:118:PHE:N	1.98	0.95
1:A:232:LEU:CD2	3:C:388:VAL:CG1	2.43	0.95
1:A:783:TYR:CD1	31:P:228:ILE:HG21	2.01	0.95
1:A:2298:LEU:CB	4:D:1283:PRO:CB	2.44	0.95
5:E:146:ARG:HH11	5:E:148:LYS:HE2	1.27	0.95
14:G:11:A:N3	14:G:12:G:H8	1.64	0.95
36:Y:37:TRP:CH2	37:Z:498:GLY:HA3	1.96	0.95
23:3:440:HIS:NE2	23:3:733:PRO:HD2	1.77	0.95
32:R:442:ARG:HD3	32:R:443:GLY:CA	1.96	0.95
15:H:45:C:H42	18:w:395:TRP:CD1	1.83	0.95
1:A:171:ASP:O	1:A:520:TYR:CD2	2.20	0.95
1:A:664:HIS:CE1	1:A:666:LYS:HB2	2.02	0.95
15:H:156:U:H5''	15:H:156:U:C6	2.02	0.95
1:A:2335:ALA:O	4:D:570:THR:HA	1.65	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:145:PHE:CB	3:C:312:SER:HB3	1.97	0.95
32:R:442:ARG:HH11	32:R:444:GLY:N	1.64	0.95
1:A:86:ARG:HH22	32:R:211:ARG:CG	1.79	0.95
3:C:700:ILE:HG23	3:C:735:PHE:CD2	2.01	0.95
1:A:393:LEU:CA	3:C:379:LYS:CG	2.45	0.95
1:A:705:LYS:HG2	32:R:251:ILE:HB	1.49	0.95
1:A:221:ASN:OD1	2:B:12:U:OP1	1.83	0.95
1:A:1426:ASP:CG	32:R:421:GLY:HA3	1.91	0.95
1:A:1505:LYS:HE2	37:Z:615:SER:OG	1.65	0.95
1:A:305:ARG:HH21	3:C:854:ARG:NH1	1.65	0.94
1:A:785:LYS:CE	31:P:215:LEU:HD11	1.97	0.94
14:G:11:A:C2	14:G:12:G:N7	2.34	0.94
1:A:384:VAL:CG2	3:C:334:ILE:CG2	2.42	0.94
1:A:1162:PRO:HG3	31:P:194:PHE:CD2	2.02	0.94
1:A:1457:HIS:CE1	32:R:424:SER:HA	2.01	0.94
28:J:339:TRP:CA	32:R:116:TYR:CE2	2.48	0.94
3:C:711:ARG:NH2	3:C:730:ARG:O	2.00	0.94
1:A:151:MET:HE3	1:A:628:GLY:O	1.67	0.94
13:F:49:G:N7	29:L:33:ARG:NH1	2.15	0.94
1:A:278:LYS:NZ	14:G:-9:C:OP1	1.99	0.94
1:A:386:PRO:HD3	3:C:372:PHE:HE1	1.28	0.94
5:E:119:THR:CG2	5:E:161:ARG:HB3	1.97	0.94
15:H:180:G:H2'	15:H:181:G:H8	1.30	0.94
1:A:264:PHE:CZ	1:A:459:LEU:CD1	2.50	0.94
1:A:402:ILE:HG13	3:C:385:VAL:HG21	1.45	0.94
1:A:530:LEU:N	30:M:198:GLN:HE22	1.52	0.94
1:A:1405:LEU:CB	32:R:415:LEU:CD2	2.45	0.94
1:A:1459:ARG:HE	32:R:423:ASP:HB2	1.31	0.94
1:A:1962:THR:CG2	37:Z:524:ARG:CB	2.45	0.94
3:C:145:PHE:HA	3:C:312:SER:HB2	0.95	0.94
3:C:445:ALA:HB3	3:C:466:SER:HA	1.50	0.94
15:H:79:G:H2'	15:H:80:A:H8	1.33	0.94
24:4:69:TYR:CZ	24:4:73:ILE:HG13	2.03	0.94
3:C:349:PHE:HD1	3:C:356:PHE:CD1	1.85	0.94
1:A:151:MET:CE	1:A:628:GLY:O	2.15	0.94
1:A:2113:LYS:CE	4:D:1229:ASP:O	2.16	0.93
13:F:8:C:H6	13:F:8:C:H5''	1.31	0.93
14:G:131:U:OP1	18:w:396:LEU:CD1	2.15	0.93
1:A:2268:LEU:CD2	4:D:1261:PRO:CB	2.46	0.93
1:A:158:ARG:NH2	1:A:570:ASP:OD2	2.01	0.93
1:A:256:TYR:CZ	3:C:888:ARG:NH1	2.36	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:25:C:C4'	13:F:26:U:OP2	2.16	0.93
18:w:485:ASN:HD22	23:3:976:LYS:CG	1.81	0.93
32:R:171:LEU:HD12	32:R:201:GLU:OE1	1.67	0.93
1:A:73:HIS:CD2	1:A:81:PHE:CE1	2.56	0.93
1:A:366:LYS:HE3	1:A:366:LYS:H	1.29	0.93
3:C:76:GLU:OE1	3:C:76:GLU:N	2.01	0.93
5:E:146:ARG:NH1	5:E:148:LYS:HE2	1.82	0.93
3:C:149:LEU:CD1	3:C:427:PHE:HD2	1.80	0.93
1:A:695:ASP:CB	33:T:374:SER:OG	2.15	0.93
3:C:449:ILE:HG21	3:C:457:VAL:CG1	1.99	0.93
28:J:259:GLN:NE2	29:L:220:PRO:CD	2.30	0.93
28:J:294:HIS:CE1	29:L:227:THR:HB	2.04	0.93
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.02	0.93
1:A:2314:PHE:CB	4:D:1125:SER:CA	2.47	0.93
3:C:497:LEU:HD13	3:C:577:PHE:HZ	1.17	0.93
13:F:68:C:C4	31:P:33:ARG:CG	2.52	0.93
1:A:1118:PRO:C	1:A:1120:PRO:HA	1.94	0.92
2:B:40:U:H3	14:G:-1:G:H1	1.14	0.92
2:B:64:G:H5'	5:E:106:LYS:NZ	1.83	0.92
31:P:224:MET:HA	31:P:224:MET:HE3	1.51	0.92
32:R:101:ILE:O	32:R:104:GLN:CG	2.16	0.92
3:C:69:ALA:HA	33:T:456:PRO:HG3	1.49	0.92
3:C:449:ILE:CG2	3:C:457:VAL:CG1	2.46	0.92
3:C:678:THR:HG21	3:C:683:ASN:HD22	1.35	0.92
1:A:228:TRP:O	1:A:415:SER:HA	1.70	0.92
1:A:402:ILE:HG12	3:C:265:LEU:CD2	1.99	0.92
1:A:548:ARG:NH2	1:A:549:GLU:OE2	2.01	0.92
1:A:2113:LYS:HE2	4:D:1229:ASP:CB	1.98	0.92
2:B:43:U:N3	14:G:-4:A:N1	2.17	0.92
3:C:140:HIS:CG	3:C:230:ASP:HB3	2.03	0.92
32:R:414:ARG:NH1	37:Z:598:PHE:HE2	1.58	0.92
1:A:305:ARG:HA	1:A:305:ARG:HH11	1.33	0.92
2:B:44:A:C2	14:G:-5:G:N1	2.36	0.92
3:C:445:ALA:O	3:C:449:ILE:N	2.03	0.92
3:C:476:CYS:HB3	3:C:565:ILE:HB	1.51	0.92
28:J:339:TRP:CA	32:R:116:TYR:CD2	2.51	0.92
1:A:1301:ILE:HD11	1:A:1306:LYS:HE2	1.51	0.92
23:3:440:HIS:HE1	23:3:720:TRP:HZ3	1.06	0.92
1:A:387:PHE:CE1	3:C:327:TYR:HA	2.05	0.92
1:A:539:ARG:NH2	13:F:64:U:O2'	2.02	0.92
2:B:39:C:C4'	2:B:40:U:OP1	2.16	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:670:SER:HB3	3:C:823:ALA:HB3	1.48	0.92
28:J:259:GLN:HE22	29:L:220:PRO:HD2	1.32	0.92
1:A:762:ARG:HH22	31:P:226:LYS:HZ1	1.08	0.92
3:C:77:VAL:CG1	33:T:196:LEU:CB	2.45	0.92
1:A:779:LEU:HD21	31:P:223:PHE:CZ	2.05	0.92
3:C:244:LYS:HA	3:C:292:TYR:HD2	1.34	0.91
32:R:106:GLN:HG2	32:R:110:LYS:HE2	1.51	0.91
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.51	0.91
1:A:235:MET:CE	1:A:411:PHE:HA	1.99	0.91
3:C:483:SER:HA	3:C:490:PHE:HB3	1.52	0.91
3:C:674:CYS:SG	3:C:822:MET:SD	2.67	0.91
3:C:86:THR:O	33:T:239:LYS:O	1.88	0.91
3:C:132:VAL:CG1	3:C:226:VAL:HG23	2.00	0.91
2:B:41:U:O4	14:G:-2:C:N4	2.03	0.91
1:A:1761:PRO:HB2	1:A:1930:TYR:OH	1.71	0.91
1:A:1962:THR:HG22	37:Z:524:ARG:CB	2.00	0.91
1:A:417:ARG:HH12	2:B:58:U:C3'	1.84	0.91
1:A:463:PRO:HB3	2:B:20:G:O2'	1.69	0.91
1:A:1320:LYS:CE	32:R:434:TYR:CE1	2.54	0.91
23:3:699:VAL:HG22	23:3:716:SER:HB2	1.53	0.91
1:A:1757:GLU:CD	32:R:451:ILE:HG12	1.96	0.91
1:A:2328:ALA:CB	4:D:788:GLY:HA2	1.99	0.91
3:C:452:THR:HG22	3:C:577:PHE:HB3	1.52	0.91
29:L:224:PHE:CD1	32:R:86:LEU:CD1	2.53	0.91
1:A:384:VAL:HA	3:C:331:PHE:HD2	1.03	0.90
3:C:145:PHE:N	3:C:312:SER:HB2	1.85	0.90
13:F:35:A:C8	14:G:12:G:C6	2.59	0.90
18:w:485:ASN:CB	23:3:978:LEU:CD2	2.49	0.90
23:3:34:ARG:HB2	23:3:37:ILE:HB	1.51	0.90
1:A:393:LEU:CA	3:C:379:LYS:CE	2.48	0.90
1:A:666:LYS:HB3	1:A:668:VAL:HG22	1.52	0.90
3:C:230:ASP:OD2	3:C:233:GLU:HG2	1.70	0.90
1:A:1457:HIS:CE1	32:R:425:GLY:H	1.88	0.90
3:C:678:THR:OG1	3:C:680:ASN:O	1.89	0.90
1:A:171:ASP:HB3	1:A:519:ASP:HB2	1.53	0.90
1:A:1320:LYS:CE	32:R:434:TYR:HE1	1.85	0.90
36:Y:37:TRP:NE1	36:Y:83:CYS:HB2	1.87	0.90
1:A:312:TYR:CE2	3:C:882:GLY:CA	2.53	0.90
1:A:254:TYR:CZ	1:A:434:HIS:CB	2.54	0.90
3:C:221:ILE:CD1	3:C:479:THR:OG1	2.19	0.90
13:F:94:C:P	28:J:351:ASN:HD22	1.95	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:82:MET:HE3	32:R:82:MET:C	1.97	0.90
1:A:782:LEU:HD13	31:P:220:HIS:HE1	1.34	0.90
3:C:711:ARG:HD3	3:C:730:ARG:NH1	1.86	0.90
3:C:228:PHE:CA	3:C:256:CYS:O	2.20	0.90
1:A:705:LYS:HG2	32:R:251:ILE:CB	2.01	0.89
33:T:399:LYS:HG3	33:T:406:ILE:HD11	1.54	0.89
1:A:419:ARG:NH2	1:A:423:ASP:O	2.06	0.89
18:w:485:ASN:ND2	23:3:976:LYS:HG2	1.87	0.89
36:Y:36:ALA:HB2	37:Z:499:LYS:O	1.72	0.89
1:A:744:LYS:HE2	31:P:213:ASP:HA	1.52	0.89
1:A:227:ARG:CA	1:A:416:GLY:O	2.20	0.89
1:A:91:ALA:HB1	32:R:207:MET:HE3	1.52	0.89
31:P:192:VAL:HG12	31:P:194:PHE:H	1.35	0.89
1:A:748:ASP:HA	31:P:214:THR:HG21	1.54	0.89
15:H:80:A:H2'	15:H:81:G:H8	1.36	0.89
32:R:81:LYS:HA	32:R:81:LYS:CE	2.02	0.89
1:A:232:LEU:CD2	3:C:388:VAL:HG11	2.03	0.89
28:J:220:LEU:HD11	28:J:224:LYS:HE3	1.53	0.89
1:A:76:MET:HE1	1:A:88:TYR:CG	2.08	0.89
1:A:90:GLY:HA3	32:R:207:MET:O	1.73	0.89
1:A:175:PRO:HG2	1:A:498:ARG:NH2	1.88	0.89
1:A:333:HIS:CA	3:C:139:HIS:NE2	2.36	0.89
15:H:81:G:H2'	15:H:82:G:H8	1.35	0.89
15:H:82:G:H2'	15:H:83:A:H8	1.38	0.89
32:R:442:ARG:CD	32:R:444:GLY:H	1.85	0.89
31:P:193:VAL:HG21	31:P:194:PHE:CD2	2.02	0.88
14:G:11:A:N3	14:G:12:G:C8	2.38	0.88
32:R:81:LYS:HA	32:R:81:LYS:NZ	1.88	0.88
1:A:785:LYS:HE2	31:P:215:LEU:HD11	1.54	0.88
3:C:78:GLU:O	33:T:199:VAL:N	2.06	0.88
3:C:140:HIS:CE1	3:C:233:GLU:HB2	2.07	0.88
3:C:79:THR:C	3:C:80:ILE:HD12	1.98	0.88
3:C:465:MET:HE1	3:C:475:MET:CG	2.01	0.88
3:C:679:PRO:CG	3:C:807:GLN:OE1	2.21	0.88
3:C:678:THR:CG2	3:C:683:ASN:HB2	2.04	0.88
13:F:68:C:C4	31:P:33:ARG:HG2	2.07	0.88
1:A:251:ASP:HB3	1:A:337:VAL:HG23	1.54	0.88
1:A:1757:GLU:CD	32:R:451:ILE:CG1	2.47	0.88
18:w:485:ASN:O	23:3:978:LEU:HD22	1.70	0.88
32:R:442:ARG:CD	32:R:444:GLY:N	2.34	0.88
39:x:664:PRO:O	39:x:667:ALA:CB	2.22	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:GLU:OE2	32:R:258:TRP:CZ3	2.25	0.88
1:A:2314:PHE:HB2	4:D:1125:SER:CA	2.02	0.88
22:2:614:ARG:HH11	22:2:614:ARG:HG3	1.38	0.88
3:C:261:ASP:OD1	41:C:1500:GTP:O6	1.92	0.88
1:A:1457:HIS:CE1	32:R:425:GLY:N	2.41	0.88
1:A:1459:ARG:HG3	32:R:422:MET:O	1.74	0.88
23:3:440:HIS:O	23:3:733:PRO:CG	2.22	0.88
28:J:270:ASP:CG	32:R:222:PRO:HB3	1.99	0.88
31:P:224:MET:CE	31:P:228:ILE:HD13	2.04	0.88
1:A:305:ARG:NH2	3:C:854:ARG:HH11	1.72	0.87
3:C:97:VAL:CG2	31:P:45:GLN:HG3	2.03	0.87
15:H:179:C:O2'	15:H:180:G:H5'	1.74	0.87
1:A:48:LYS:O	1:A:53:PHE:CD2	2.27	0.87
3:C:149:LEU:HD12	3:C:427:PHE:HD2	1.39	0.87
3:C:700:ILE:HG23	3:C:735:PHE:CE2	2.09	0.87
23:3:812:LYS:O	23:3:816:LYS:HB2	1.74	0.87
2:B:42:U:N3	14:G:-3:A:N1	2.16	0.87
3:C:64:LYS:HZ1	31:P:206:LYS:HG2	1.39	0.87
14:G:137:C:H42	15:H:40:C:H42	1.22	0.87
23:3:545:VAL:HG12	23:3:546:LYS:HG2	1.57	0.87
24:4:75:ASN:OD1	24:4:86:VAL:HB	1.74	0.87
3:C:523:GLN:OE1	3:C:524:ILE:N	2.07	0.87
1:A:393:LEU:CA	3:C:379:LYS:HG2	2.02	0.87
3:C:705:VAL:HG21	3:C:717:PHE:CE2	2.07	0.87
5:E:243:LEU:CD1	5:E:247:GLY:HA2	2.04	0.87
15:H:68:G:O2'	15:H:69:U:H5'	1.74	0.87
15:H:78:C:H2'	15:H:79:G:C8	2.10	0.87
1:A:1162:PRO:CG	31:P:194:PHE:CE2	2.57	0.87
3:C:488:VAL:HG13	3:C:609:LYS:CE	2.05	0.87
15:H:154:C:O2	15:H:176:G:N2	2.07	0.87
28:J:339:TRP:CD2	32:R:116:TYR:HD2	1.93	0.87
32:R:423:ASP:O	32:R:424:SER:OG	1.92	0.87
1:A:86:ARG:NH2	32:R:211:ARG:HG3	1.88	0.87
1:A:384:VAL:HG12	3:C:332:GLY:H	1.38	0.87
1:A:395:THR:HG21	3:C:383:GLN:HE22	1.38	0.87
15:H:180:G:H2'	15:H:181:G:C8	2.10	0.87
3:C:701:GLU:HA	3:C:740:THR:OG1	1.75	0.87
28:J:255:LEU:HD22	29:L:235:LEU:HD13	1.56	0.87
3:C:216:THR:CG2	3:C:245:HIS:HE1	1.84	0.86
32:R:442:ARG:NH1	32:R:443:GLY:O	2.07	0.86
1:A:420:ARG:NH1	2:B:56:C:O2'	2.07	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:TRP:CE3	3:C:179:VAL:CG2	2.59	0.86
15:H:179:C:H2'	15:H:180:G:C8	2.09	0.86
1:A:2113:LYS:HE3	4:D:1229:ASP:C	2.01	0.86
18:w:485:ASN:HA	23:3:978:LEU:CD2	2.03	0.86
15:H:148:C:O2'	15:H:149:A:H5'	1.75	0.86
21:1:1179:ASP:OD2	21:1:1185:ARG:NH1	2.08	0.86
32:R:125:MET:HE3	32:R:131:ASP:OD1	1.76	0.86
33:T:399:LYS:HG2	33:T:406:ILE:HD11	1.53	0.86
1:A:401:GLY:HA3	3:C:386:GLY:CA	2.03	0.86
5:E:269:PRO:O	5:E:270:LYS:HB3	1.76	0.86
13:F:26:U:H3'	13:F:27:A:H5''	1.56	0.86
28:J:256:LYS:O	29:L:232:TYR:CE2	2.29	0.86
31:P:210:PHE:HD2	33:T:455:GLN:OE1	1.53	0.86
32:R:147:THR:HG23	33:T:360:VAL:HG12	1.57	0.86
23:3:442:LEU:HD12	23:3:733:PRO:O	1.76	0.86
33:T:417:ASN:OD1	33:T:432:ASP:OD1	1.94	0.86
1:A:386:PRO:HA	3:C:327:TYR:CE2	2.10	0.86
1:A:152:ARG:HB3	1:A:152:ARG:HH11	1.39	0.85
32:R:135:PRO:O	32:R:136:ASP:OD1	1.94	0.85
1:A:433:GLU:OE1	1:A:436:PRO:HB3	1.74	0.85
20:v:164:ARG:O	20:v:165:ARG:CB	2.24	0.85
32:R:420:LYS:HE3	32:R:420:LYS:CA	1.98	0.85
1:A:252:ASP:HB2	1:A:334:THR:HG21	0.90	0.85
3:C:72:VAL:HG22	33:T:453:ALA:HB1	1.58	0.85
3:C:149:LEU:HD12	3:C:427:PHE:CD2	2.07	0.85
15:H:79:G:O2'	15:H:80:A:H5'	1.76	0.85
2:B:64:G:H5'	5:E:106:LYS:HZ3	1.38	0.85
3:C:145:PHE:HB2	3:C:312:SER:HB3	1.57	0.85
15:H:45:C:C4	18:w:395:TRP:HD1	1.93	0.85
21:1:672:ALA:HA	21:1:679:ILE:HD11	1.58	0.85
1:A:363:HIS:NE2	3:C:287:GLY:HA3	1.91	0.85
2:B:95:G:H4'	2:B:96:A:O4'	1.76	0.85
32:R:414:ARG:NH1	37:Z:598:PHE:HZ	1.44	0.85
5:E:162:ARG:NH2	5:E:203:ASP:O	2.10	0.85
1:A:388:LEU:HD11	3:C:399:LEU:HD21	0.86	0.85
32:R:414:ARG:HB2	32:R:414:ARG:NH2	1.92	0.85
3:C:133:THR:O	3:C:226:VAL:N	2.10	0.85
1:A:386:PRO:HA	3:C:327:TYR:CZ	2.11	0.85
2:B:42:U:H3	14:G:-3:A:H2	0.90	0.85
14:G:1:G:N2	30:M:202:CYS:SG	2.50	0.85
1:A:232:LEU:CD2	3:C:388:VAL:HG12	2.05	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:595:LYS:HE3	1:A:644:ILE:HD11	1.58	0.84
1:A:1900:GLU:CG	37:Z:521:PRO:CG	2.55	0.84
3:C:94:ILE:HD13	31:P:44:ARG:NH1	1.92	0.84
15:H:156:U:H6	15:H:156:U:C5'	1.88	0.84
37:Z:600:ARG:HH11	37:Z:600:ARG:CB	1.90	0.84
1:A:73:HIS:CD2	1:A:81:PHE:CD2	2.57	0.84
1:A:1370:ARG:HH11	34:V:467:LEU:CA	1.89	0.84
38:z:85:ASP:OD1	38:z:109:ASN:ND2	2.10	0.84
1:A:1900:GLU:OE2	37:Z:522:LEU:N	2.11	0.84
3:C:444:GLY:O	3:C:447:PRO:HD2	1.77	0.84
3:C:516:LEU:HD12	3:C:517:GLU:HG3	1.59	0.84
1:A:121:HIS:CG	1:A:481:PHE:O	2.30	0.84
13:F:36:A:H2'	13:F:38:G:OP2	1.78	0.84
15:H:80:A:O2'	15:H:81:G:H5'	1.78	0.84
15:H:181:G:O2'	15:H:182:U:H5'	1.77	0.84
15:H:182:U:O2'	15:H:183:G:H5'	1.75	0.84
23:3:356:HIS:HB2	23:3:401:LEU:HB2	1.60	0.84
3:C:80:ILE:O	33:T:200:ILE:HA	1.78	0.84
32:R:415:LEU:O	32:R:417:ASN:N	2.09	0.84
1:A:755:HIS:CE1	31:P:223:PHE:CB	2.60	0.84
3:C:711:ARG:HD3	3:C:730:ARG:HE	1.42	0.84
1:A:232:LEU:HD11	3:C:412:ILE:HD11	1.59	0.84
1:A:1505:LYS:HE2	37:Z:615:SER:CB	2.07	0.84
3:C:244:LYS:HA	3:C:292:TYR:CD2	2.13	0.84
3:C:365:SER:OG	3:C:371:GLU:OE2	1.95	0.84
3:C:725:ASP:OD1	3:C:727:LEU:N	2.10	0.84
15:H:78:C:O2'	15:H:79:G:H5'	1.77	0.84
32:R:178:ARG:HD3	32:R:194:GLN:NE2	1.91	0.84
1:A:393:LEU:CA	3:C:379:LYS:HE3	2.07	0.84
1:A:1426:ASP:CB	32:R:421:GLY:HA3	2.08	0.84
1:A:1457:HIS:CE1	1:A:1459:ARG:CG	2.61	0.84
1:A:1457:HIS:NE2	32:R:424:SER:HA	1.93	0.83
3:C:705:VAL:HG21	3:C:717:PHE:HE2	1.40	0.83
1:A:333:HIS:O	3:C:139:HIS:CE1	2.31	0.83
3:C:348:TYR:CD1	3:C:359:LYS:HB3	2.13	0.83
15:H:71:C:O2'	15:H:72:U:H5'	1.78	0.83
37:Z:566:TYR:CE2	37:Z:584:TRP:CE3	2.66	0.83
1:A:168:PRO:HG3	1:A:559:ASP:CB	2.07	0.83
1:A:254:TYR:CE2	1:A:434:HIS:CB	2.61	0.83
1:A:1301:ILE:HD12	2:B:39:C:H5''	1.60	0.83
3:C:488:VAL:CG1	3:C:609:LYS:HE2	2.08	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:22:C:O2'	14:G:23:U:OP1	1.95	0.83
15:H:152:G:N2	15:H:153:A:N7	2.27	0.83
1:A:338:VAL:CG2	3:C:867:PRO:HG3	2.07	0.83
5:E:74:PHE:CE1	5:E:81:LEU:CD2	2.62	0.83
36:Y:37:TRP:CZ2	37:Z:498:GLY:HA2	2.08	0.83
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.11	0.83
15:H:70:C:O2'	15:H:71:C:H5'	1.78	0.83
23:3:442:LEU:O	23:3:735:SER:N	2.10	0.83
32:R:117:THR:O	32:R:120:VAL:HG12	1.78	0.83
3:C:77:VAL:CG1	33:T:196:LEU:CG	2.35	0.83
1:A:1301:ILE:CD1	2:B:39:C:H5''	2.09	0.83
3:C:80:ILE:N	33:T:199:VAL:O	2.12	0.83
1:A:387:PHE:CZ	3:C:326:ILE:HG22	2.13	0.83
3:C:824:THR:HG23	3:C:824:THR:O	1.77	0.83
32:R:134:ARG:O	32:R:136:ASP:N	2.12	0.83
1:A:1457:HIS:HE1	1:A:1459:ARG:HG2	1.43	0.83
1:A:1900:GLU:OE2	37:Z:521:PRO:CB	2.26	0.83
18:w:485:ASN:HD21	23:3:976:LYS:H	1.22	0.83
3:C:145:PHE:CA	3:C:312:SER:HB3	2.04	0.83
15:H:72:U:O2'	15:H:73:C:H5'	1.77	0.83
18:w:485:ASN:HA	23:3:978:LEU:HD11	1.59	0.83
28:J:406:PHE:CD2	28:J:411:MET:HE3	2.13	0.83
3:C:470:PRO:HB3	3:C:500:THR:CG2	2.08	0.82
21:1:1108:ASN:ND2	21:1:1111:CYS:SG	2.52	0.82
1:A:91:ALA:HB1	32:R:207:MET:CE	2.09	0.82
1:A:529:THR:CG2	30:M:197:TYR:O	2.26	0.82
1:A:615:ARG:O	1:A:618:THR:OG1	1.96	0.82
15:H:73:C:O2'	15:H:74:U:H5'	1.79	0.82
1:A:319:LEU:HD11	3:C:590:ILE:HD11	1.60	0.82
1:A:1084:PRO:HG2	31:P:188:TRP:CZ2	2.12	0.82
3:C:220:ARG:NH1	3:C:578:ARG:O	2.12	0.82
3:C:228:PHE:CB	3:C:256:CYS:O	2.27	0.82
3:C:482:TYR:HE2	3:C:493:PHE:CG	1.97	0.82
5:E:165:GLN:O	5:E:166:LEU:HD23	1.79	0.82
28:J:259:GLN:NE2	29:L:220:PRO:HD2	1.94	0.82
2:B:42:U:C2	14:G:-3:A:H2	1.97	0.82
3:C:705:VAL:CB	3:C:717:PHE:CE2	2.61	0.82
15:H:45:C:H2'	18:w:394:TYR:HE2	1.39	0.82
14:G:11:A:C4	14:G:12:G:C8	2.67	0.82
15:H:69:U:O2'	15:H:70:C:H5'	1.80	0.82
16:o:46:ALA:CB	16:o:68:THR:O	2.27	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:103:ARG:HB3	32:R:103:ARG:HH11	1.44	0.82
15:H:81:G:O2'	15:H:82:G:H5'	1.78	0.82
3:C:140:HIS:ND1	3:C:230:ASP:HB3	1.94	0.82
23:3:304:GLN:HE21	23:3:308:GLY:HA2	1.44	0.82
1:A:393:LEU:HD12	3:C:379:LYS:HG3	1.60	0.82
1:A:417:ARG:HH12	2:B:58:U:C4'	1.92	0.82
1:A:1370:ARG:HH12	34:V:468:ASP:N	1.77	0.82
3:C:489:GLN:O	3:C:489:GLN:NE2	2.13	0.82
15:H:105:G:C2'	15:H:106:G:H5''	2.10	0.82
31:P:30:TYR:OH	32:R:162:ALA:CA	2.27	0.82
1:A:1457:HIS:CE1	1:A:1459:ARG:HG2	2.15	0.82
3:C:259:LYS:HG2	3:C:262:ARG:CD	2.09	0.82
31:P:212:ASN:HB3	33:T:458:SER:HB2	1.61	0.82
2:B:18:C:O2'	2:B:19:A:O5'	1.98	0.82
1:A:331:TRP:CZ3	3:C:179:VAL:HG21	2.14	0.81
5:E:74:PHE:CE2	5:E:343:ILE:HG12	2.14	0.81
14:G:132:G:O4'	18:w:399:LEU:HD13	1.80	0.81
36:Y:37:TRP:HA	36:Y:82:LEU:O	1.80	0.81
1:A:164:MET:HE1	1:A:560:SER:HA	1.62	0.81
1:A:305:ARG:HG2	3:C:878:ILE:HG21	1.60	0.81
1:A:331:TRP:CZ3	3:C:179:VAL:CG2	2.64	0.81
1:A:1900:GLU:CG	37:Z:521:PRO:HG2	2.09	0.81
3:C:64:LYS:HE3	31:P:206:LYS:CE	2.10	0.81
3:C:244:LYS:HB2	3:C:292:TYR:CE2	2.15	0.81
3:C:306:ASN:OD1	3:C:437:HIS:ND1	2.14	0.81
3:C:507:VAL:CG1	3:C:565:ILE:HG23	2.10	0.81
22:2:643:PRO:HD2	24:4:69:TYR:CD2	2.16	0.81
23:3:42:ARG:HE	23:3:53:LEU:HD11	1.45	0.81
23:3:210:PHE:HB2	23:3:224:TYR:HB2	1.60	0.81
26:6:49:CYS:HB3	26:6:87:LYS:HD3	1.61	0.81
1:A:247:THR:OG1	1:A:429:ASN:HB3	1.80	0.81
31:P:193:VAL:HG23	31:P:194:PHE:CG	2.15	0.81
1:A:232:LEU:HD11	3:C:412:ILE:CD1	2.10	0.81
1:A:250:VAL:HG23	1:A:337:VAL:HB	1.60	0.81
23:3:772:ALA:HB1	23:3:775:ASN:HD21	1.44	0.81
33:T:213:GLU:HG3	33:T:218:TRP:CE2	2.16	0.81
1:A:95:MET:HE2	1:A:503:MET:HE1	1.63	0.81
1:A:1301:ILE:HD13	1:A:1306:LYS:HE2	1.63	0.81
3:C:511:GLY:O	3:C:576:ILE:HD13	1.79	0.81
32:R:443:GLY:HA2	32:R:446:ASP:HB3	1.62	0.81
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.14	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1426:ASP:HB2	32:R:421:GLY:CA	2.11	0.81
3:C:261:ASP:CG	41:C:1500:GTP:HN1	1.88	0.81
3:C:452:THR:HG21	3:C:577:PHE:HD2	1.43	0.81
5:E:74:PHE:CZ	5:E:81:LEU:HD21	2.16	0.81
1:A:705:LYS:HB2	32:R:251:ILE:CD1	2.07	0.81
1:A:439:GLN:O	1:A:444:ARG:NH1	2.14	0.81
1:A:907:PRO:HD3	31:P:229:LYS:HB2	1.63	0.81
3:C:96:PRO:HA	31:P:48:GLN:HE21	1.44	0.81
3:C:140:HIS:NE2	3:C:233:GLU:HG3	1.95	0.81
1:A:660:PHE:CD2	32:R:209:PRO:HB2	2.16	0.81
3:C:140:HIS:ND1	3:C:230:ASP:N	2.28	0.81
3:C:452:THR:CB	3:C:577:PHE:HD2	1.93	0.81
3:C:507:VAL:HG11	3:C:565:ILE:CG2	2.09	0.81
3:C:711:ARG:HD3	3:C:730:ARG:NE	1.96	0.81
1:A:228:TRP:N	1:A:416:GLY:O	2.14	0.80
15:H:183:G:H2'	15:H:184:C:H6	1.44	0.80
1:A:245:LEU:HA	1:A:430:TRP:HZ2	1.46	0.80
15:H:83:A:H2'	15:H:84:C:C1'	2.10	0.80
23:3:440:HIS:CG	23:3:733:PRO:HG3	2.15	0.80
1:A:91:ALA:CB	32:R:207:MET:CE	2.56	0.80
13:F:68:C:H41	31:P:33:ARG:HB3	1.45	0.80
28:J:273:TYR:CE1	32:R:228:PRO:HB3	2.17	0.80
14:G:134:U:H3	15:H:42:G:H1	1.24	0.80
23:3:979:ARG:HD2	23:3:982:GLU:HB2	1.63	0.80
32:R:65:PRO:HG2	32:R:66:GLU:OE2	1.79	0.80
15:H:149:A:H2'	15:H:150:U:H6	1.44	0.80
22:2:682:LEU:HD13	22:2:687:PHE:HA	1.63	0.80
1:A:357:ASN:O	3:C:865:GLY:N	2.15	0.80
1:A:417:ARG:HH22	2:B:58:U:H5''	1.42	0.80
1:A:748:ASP:CA	31:P:214:THR:HG21	2.11	0.80
3:C:705:VAL:CG2	3:C:717:PHE:HE2	1.84	0.80
15:H:82:G:O2'	15:H:83:A:H5'	1.81	0.80
1:A:121:HIS:HA	1:A:482:PHE:HA	1.62	0.80
1:A:384:VAL:CG1	3:C:332:GLY:N	2.45	0.80
3:C:87:GLN:OE1	3:C:91:GLU:HG2	1.82	0.80
3:C:140:HIS:CE1	3:C:230:ASP:HB3	2.16	0.80
3:C:776:GLU:O	3:C:781:ASP:OD1	2.00	0.80
5:E:265:ARG:H	5:E:272:ARG:NH2	1.80	0.80
13:F:68:C:N3	31:P:33:ARG:HG2	1.97	0.80
15:H:152:G:H5''	15:H:153:A:OP2	1.80	0.80
21:1:732:TRP:HE1	21:1:768:GLU:HG2	1.47	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:MET:HE1	1:A:411:PHE:HA	1.61	0.80
1:A:1144:LYS:O	1:A:1147:VAL:HG22	1.82	0.80
1:A:1764:SER:HB3	1:A:1766:GLN:HG2	1.64	0.80
3:C:445:ALA:HB1	3:C:449:ILE:HD11	1.63	0.80
3:C:738:ASP:HB2	3:C:740:THR:O	1.82	0.80
1:A:221:ASN:CG	2:B:12:U:OP1	2.25	0.80
1:A:305:ARG:NH2	3:C:854:ARG:NH1	2.29	0.80
1:A:401:GLY:CA	3:C:386:GLY:HA2	2.08	0.80
1:A:402:ILE:HG12	3:C:265:LEU:HD23	1.61	0.80
1:A:1370:ARG:HH11	34:V:467:LEU:HA	1.43	0.80
1:A:2314:PHE:HB3	4:D:1125:SER:CA	2.11	0.80
5:E:248:SER:HB2	5:E:249:TYR:CD1	2.17	0.80
14:G:130:A:N1	18:w:400:HIS:CE1	2.50	0.80
7:i:85:PRO:CA	18:w:187:GLU:CB	2.58	0.80
23:3:637:PRO:HA	23:3:669:LEU:HA	1.63	0.80
24:4:28:LEU:O	24:4:32:LEU:CB	2.27	0.80
2:B:90:U:H5''	2:B:91:U:H5'	1.65	0.79
5:E:209:ILE:HG21	5:E:250:LEU:CD1	2.12	0.79
23:3:442:LEU:HD12	23:3:734:LEU:HD23	1.64	0.79
23:3:477:SER:HA	23:3:482:THR:HG22	1.65	0.79
29:L:222:LEU:H	29:L:222:LEU:HD22	1.45	0.79
1:A:264:PHE:HE1	1:A:455:VAL:CG1	1.94	0.79
1:A:299:ILE:CG1	3:C:920:PRO:O	2.30	0.79
1:A:362:ARG:NH2	3:C:284:GLU:OE2	2.15	0.79
1:A:825:ILE:HB	1:A:1001:VAL:HG12	1.65	0.79
3:C:145:PHE:N	3:C:312:SER:CB	2.41	0.79
33:T:292:TYR:CZ	33:T:308:ARG:HG3	2.18	0.79
1:A:168:PRO:HG2	1:A:559:ASP:HB3	1.64	0.79
1:A:232:LEU:HD13	1:A:404:LEU:CD1	2.12	0.79
1:A:318:TYR:N	3:C:638:ASP:OD1	2.14	0.79
3:C:77:VAL:HG11	33:T:196:LEU:HG	0.79	0.79
5:E:310:TYR:CE1	5:E:322:LYS:HD2	2.18	0.79
33:T:306:CYS:SG	33:T:336:VAL:HB	2.22	0.79
23:3:772:ALA:CB	23:3:775:ASN:HD21	1.95	0.79
1:A:312:TYR:CD2	3:C:882:GLY:HA3	2.16	0.79
1:A:1876:LEU:HD12	1:A:1884:ILE:HD11	1.65	0.79
3:C:244:LYS:HB2	3:C:292:TYR:HE2	1.47	0.79
1:A:283:VAL:O	1:A:284:ARG:NE	2.15	0.79
15:H:153:A:H2'	15:H:154:C:H5'	1.65	0.79
32:R:67:ILE:HG22	32:R:69:VAL:HG23	1.65	0.79
31:P:212:ASN:O	33:T:458:SER:CA	2.23	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:420:LYS:HG3	32:R:421:GLY:N	1.97	0.79
33:T:351:ASP:O	33:T:352:THR:OG1	1.98	0.79
3:C:515:THR:O	3:C:517:GLU:N	2.16	0.79
3:C:705:VAL:HB	3:C:717:PHE:CE2	2.18	0.79
1:A:393:LEU:HB2	3:C:379:LYS:HE3	1.65	0.79
3:C:140:HIS:ND1	3:C:230:ASP:CB	2.46	0.79
3:C:259:LYS:HE2	3:C:262:ARG:CD	2.13	0.79
15:H:68:G:H1	15:H:84:C:H42	1.29	0.79
15:H:79:G:H2'	15:H:80:A:C8	2.17	0.79
1:A:256:TYR:CD1	3:C:888:ARG:NH2	2.51	0.78
1:A:293:TRP:CZ3	1:A:295:GLU:OE1	2.35	0.78
1:A:435:CYS:HB2	3:C:892:GLN:NE2	1.98	0.78
13:F:34:G:N7	14:G:12:G:O6	2.16	0.78
15:H:101:U:H5''	15:H:102:U:H5'	1.64	0.78
37:Z:593:PHE:O	37:Z:597:ARG:HB2	1.83	0.78
1:A:1767:ASN:O	1:A:1771:LEU:HB2	1.82	0.78
1:A:48:LYS:O	1:A:53:PHE:CG	2.37	0.78
1:A:173:GLU:OE2	38:z:7:GLN:CB	2.32	0.78
1:A:718:ARG:NH2	32:R:259:LYS:HE3	1.98	0.78
15:H:82:G:H2'	15:H:83:A:C8	2.17	0.78
23:3:1109:LEU:HD11	23:3:1128:ILE:HG21	1.65	0.78
1:A:250:VAL:CB	1:A:337:VAL:HG11	2.14	0.78
1:A:695:ASP:OD2	33:T:350:HIS:HB3	1.83	0.78
23:3:641:CYS:HB2	23:3:701:LEU:HB3	1.64	0.78
23:3:435:LEU:HD22	23:3:799:ILE:HD11	1.66	0.78
23:3:440:HIS:HE1	23:3:733:PRO:HD3	1.46	0.78
1:A:1370:ARG:NH1	34:V:468:ASP:N	2.32	0.78
32:R:132:LEU:HB3	33:T:399:LYS:NZ	1.99	0.78
1:A:705:LYS:HG2	32:R:251:ILE:HD12	1.65	0.78
1:A:758:ARG:CB	31:P:227:TYR:CE2	2.64	0.78
2:B:43:U:H4'	13:F:67:G:H1	1.48	0.78
33:T:387:PHE:CE1	33:T:398:TRP:CD1	2.72	0.78
1:A:152:ARG:HH11	1:A:152:ARG:CB	1.96	0.78
1:A:1900:GLU:CD	37:Z:522:LEU:CB	2.55	0.78
24:4:17:VAL:HG22	24:4:86:VAL:HG22	1.66	0.78
33:T:434:GLY:HA2	33:T:464:GLY:CA	2.14	0.78
1:A:1505:LYS:HD2	37:Z:615:SER:HB3	1.66	0.78
3:C:133:THR:HB	3:C:225:VAL:HG23	1.65	0.78
23:3:295:THR:HG22	23:3:297:SER:H	1.48	0.78
1:A:2325:VAL:HG13	4:D:788:GLY:C	2.07	0.78
3:C:452:THR:HG21	3:C:577:PHE:CD2	2.16	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:2:649:LYS:HB3	22:2:655:SER:HB2	1.65	0.78
24:4:17:VAL:O	24:4:56:TYR:HA	1.83	0.78
33:T:267:ASP:HB3	33:T:269:GLN:HG2	1.64	0.78
1:A:468:LYS:HD3	1:A:469:LYS:N	1.99	0.77
1:A:692:ASP:CA	33:T:376:ARG:HH22	1.97	0.77
1:A:919:ASP:OD2	1:A:1012:LYS:NZ	2.17	0.77
1:A:1838:LYS:HG2	1:A:1871:PRO:HG2	1.66	0.77
21:1:1053:ARG:NH1	22:2:559:PRO:O	2.17	0.77
23:3:590:MET:HG2	23:3:607:VAL:HA	1.63	0.77
23:3:805:ASN:ND2	23:3:858:GLY:O	2.14	0.77
1:A:398:THR:HG23	3:C:382:ALA:HB1	1.67	0.77
2:B:42:U:C4	14:G:-3:A:N1	2.53	0.77
1:A:329:LEU:HB3	3:C:177:ARG:NE	1.98	0.77
3:C:449:ILE:HG21	3:C:457:VAL:HG12	1.66	0.77
3:C:677:GLU:OE2	3:C:684:LYS:HG2	1.83	0.77
21:1:941:ASN:HA	21:1:948:ARG:HH22	1.48	0.77
1:A:203:VAL:HG21	1:A:237:THR:CG2	2.14	0.77
1:A:1405:LEU:CA	32:R:415:LEU:CD2	2.62	0.77
1:A:2166:HIS:CD2	1:A:2272:MET:HE1	2.18	0.77
3:C:449:ILE:CD1	3:C:466:SER:OG	2.33	0.77
15:H:80:A:H2'	15:H:81:G:C8	2.19	0.77
24:4:69:TYR:CE1	24:4:73:ILE:HG13	2.19	0.77
37:Z:595:GLN:O	37:Z:599:ALA:N	2.14	0.77
1:A:456:LEU:O	1:A:460:LYS:HG2	1.84	0.77
3:C:349:PHE:CD1	3:C:356:PHE:CD1	2.68	0.77
5:E:277:PHE:HE2	5:E:300:ILE:CD1	1.98	0.77
13:F:8:C:H5''	13:F:8:C:C6	2.19	0.77
23:3:474:ILE:O	23:3:485:LEU:HB2	1.83	0.77
23:3:772:ALA:HB1	23:3:775:ASN:ND2	1.99	0.77
3:C:85:ASP:CB	33:T:238:LEU:HG	2.14	0.77
3:C:140:HIS:HA	3:C:259:LYS:HZ3	1.48	0.77
3:C:151:GLU:OE1	3:C:417:ARG:CZ	2.33	0.77
14:G:11:A:H2'	14:G:12:G:O4'	1.84	0.77
36:Y:86:ASP:HA	37:Z:502:ALA:HB3	1.65	0.77
1:A:1505:LYS:CE	37:Z:615:SER:CB	2.62	0.77
28:J:291:GLN:NE2	29:L:230:GLU:OE2	2.17	0.77
33:T:318:ARG:HG3	33:T:319:THR:HG23	1.67	0.77
33:T:352:THR:CG2	33:T:373:LYS:C	2.58	0.77
1:A:664:HIS:CE1	1:A:668:VAL:CG2	2.66	0.77
1:A:1757:GLU:OE2	32:R:451:ILE:HD11	1.85	0.77
3:C:482:TYR:HE2	3:C:493:PHE:CB	1.98	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Z:603:SER:O	37:Z:607:VAL:HG23	1.84	0.77
1:A:1426:ASP:HB2	32:R:421:GLY:HA3	1.64	0.77
3:C:145:PHE:CZ	3:C:427:PHE:CE1	2.73	0.77
3:C:471:ASP:H	3:C:499:GLY:HA2	1.47	0.77
5:E:74:PHE:CD1	5:E:81:LEU:CD2	2.67	0.77
23:3:785:PRO:HA	23:3:800:ILE:O	1.84	0.77
3:C:567:GLU:HG2	3:C:572:GLU:OE2	1.85	0.77
15:H:177:A:H5''	15:H:178:A:OP1	1.84	0.77
23:3:981:CYS:SG	23:3:982:GLU:N	2.57	0.77
1:A:232:LEU:HD21	3:C:388:VAL:HG11	1.67	0.76
1:A:630:TRP:O	1:A:632:ALA:N	2.18	0.76
1:A:782:LEU:HD13	31:P:220:HIS:CE1	2.18	0.76
3:C:82:GLN:CB	33:T:231:TRP:HZ3	1.98	0.76
3:C:711:ARG:HD3	3:C:730:ARG:CZ	2.16	0.76
5:E:146:ARG:HH12	5:E:148:LYS:HE3	1.49	0.76
1:A:232:LEU:HD13	1:A:404:LEU:HD13	1.66	0.76
21:1:473:GLN:HE22	25:5:93:ASN:H	1.33	0.76
32:R:420:LYS:HG2	32:R:423:ASP:OD2	1.84	0.76
1:A:705:LYS:CB	32:R:251:ILE:CD1	2.59	0.76
2:B:44:A:H2	14:G:-5:G:N1	1.81	0.76
3:C:449:ILE:HD11	3:C:466:SER:N	1.99	0.76
15:H:143:A:H3'	15:H:143:A:N3	2.01	0.76
1:A:362:ARG:O	1:A:362:ARG:NE	2.18	0.76
5:E:162:ARG:NH2	5:E:204:THR:HA	1.99	0.76
15:H:148:C:H2'	15:H:149:A:H8	1.48	0.76
1:A:417:ARG:CZ	2:B:58:U:H5''	2.14	0.76
3:C:471:ASP:OD1	3:C:472:GLY:N	2.19	0.76
22:2:611:ASP:O	22:2:614:ARG:HB3	1.86	0.76
1:A:755:HIS:HA	31:P:223:PHE:CE1	2.20	0.76
1:A:1119:ASP:N	1:A:1120:PRO:HA	2.01	0.76
23:3:423:LEU:HB2	23:3:438:LEU:HB2	1.66	0.76
34:V:548:ALA:HB1	34:V:586:PHE:N	2.00	0.76
1:A:529:THR:HG22	30:M:197:TYR:C	2.11	0.76
15:H:168:A:H5'	15:H:169:C:OP2	1.86	0.76
18:w:176:GLU:O	18:w:177:ARG:CB	2.33	0.76
37:Z:566:TYR:HD2	37:Z:580:PRO:HG2	1.50	0.76
1:A:91:ALA:HA	32:R:207:MET:CE	2.14	0.76
3:C:750:LEU:O	3:C:754:VAL:HG23	1.84	0.76
13:F:40:U:H2'	13:F:41:A:C8	2.20	0.76
23:3:328:LYS:HB2	23:3:372:GLU:HG3	1.68	0.76
1:A:229:GLN:HG2	1:A:415:SER:HB2	1.68	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:LEU:CD1	3:C:265:LEU:HD13	2.15	0.76
1:A:779:LEU:CD2	31:P:223:PHE:CE2	2.69	0.76
5:E:231:MET:HB3	5:E:262:TRP:CZ3	2.21	0.76
18:w:283:GLN:O	18:w:284:ARG:CB	2.32	0.76
18:w:485:ASN:C	23:3:978:LEU:CD2	2.48	0.76
1:A:305:ARG:HH21	3:C:854:ARG:HH11	1.28	0.75
1:A:435:CYS:SG	3:C:892:GLN:NE2	2.57	0.75
1:A:1162:PRO:CG	31:P:194:PHE:CD2	2.69	0.75
23:3:11:ALA:O	23:3:34:ARG:NH1	2.17	0.75
37:Z:594:GLU:O	37:Z:598:PHE:HB2	1.86	0.75
3:C:149:LEU:CD1	3:C:427:PHE:CG	2.53	0.75
3:C:593:GLU:HG3	3:C:594:PRO:HD2	1.67	0.75
14:G:132:G:H1	15:H:44:U:H3	1.34	0.75
23:3:784:THR:O	23:3:786:ARG:NH1	2.18	0.75
32:R:66:GLU:OE2	32:R:66:GLU:N	2.19	0.75
32:R:181:PRO:O	32:R:182:SER:HB2	1.84	0.75
1:A:319:LEU:HD11	3:C:590:ILE:CD1	2.16	0.75
1:A:378:PHE:HZ	3:C:335:ASN:HB2	1.51	0.75
14:G:11:A:C4	14:G:12:G:H8	2.04	0.75
15:H:81:G:H2'	15:H:82:G:C8	2.19	0.75
23:3:905:VAL:HB	23:3:928:TYR:HB2	1.68	0.75
1:A:1951:LYS:HD3	37:Z:521:PRO:O	1.85	0.75
18:w:485:ASN:ND2	23:3:976:LYS:H	1.83	0.75
23:3:720:TRP:HB3	23:3:731:LEU:HD11	1.69	0.75
39:x:876:GLY:O	39:x:880:VAL:N	2.14	0.75
1:A:230:PHE:N	1:A:414:ARG:O	2.18	0.75
1:A:305:ARG:HD3	3:C:933:PHE:CZ	2.22	0.75
3:C:470:PRO:HA	3:C:499:GLY:HA2	1.67	0.75
3:C:711:ARG:CD	3:C:730:ARG:HE	1.99	0.75
15:H:10:C:H2'	15:H:11:G:H8	1.52	0.75
16:o:45:ASP:O	16:o:67:LYS:N	2.18	0.75
23:3:441:GLY:HA3	23:3:734:LEU:O	1.85	0.75
23:3:1105:GLN:O	23:3:1118:VAL:HB	1.87	0.75
1:A:119:LEU:HD12	1:A:484:SER:HB2	1.67	0.75
1:A:1762:TYR:O	1:A:1768:TYR:OH	2.05	0.75
13:F:36:A:C3'	13:F:37:C:H5''	2.16	0.75
15:H:45:C:C2'	18:w:394:TYR:CE2	2.69	0.75
28:J:339:TRP:CE3	32:R:116:TYR:HD2	2.04	0.75
34:V:515:CYS:HA	34:V:521:TYR:CB	2.17	0.75
38:z:57:VAL:HG22	38:z:63:VAL:HG23	1.68	0.75
38:z:136[B]:ASP:OD1	38:z:136[B]:ASP:N	2.18	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:MET:HE2	1:A:88:TYR:CD2	2.21	0.75
3:C:82:GLN:HB2	33:T:231:TRP:HZ3	1.50	0.75
15:H:71:C:H2'	15:H:72:U:C6	2.21	0.75
32:R:412:ASP:CG	32:R:413:GLN:N	2.39	0.75
1:A:384:VAL:HG21	3:C:334:ILE:HG12	1.69	0.75
15:H:153:A:C2'	15:H:154:C:H5'	2.17	0.75
34:V:538:ARG:HA	37:Z:534:MET:CB	2.16	0.75
1:A:405:LEU:HD13	3:C:265:LEU:HD13	1.68	0.74
3:C:348:TYR:CE1	3:C:359:LYS:HB3	2.22	0.74
3:C:510:LEU:HD22	3:C:514:TYR:CE2	2.22	0.74
28:J:256:LYS:O	29:L:232:TYR:HD2	1.66	0.74
28:J:273:TYR:CG	32:R:228:PRO:HG2	2.21	0.74
1:A:231:THR:HA	3:C:389:ASP:OD2	1.86	0.74
1:A:1405:LEU:CA	32:R:415:LEU:HD21	2.15	0.74
1:A:1784:ASN:HD22	1:A:1897:LEU:HD12	1.50	0.74
1:A:2073:TRP:CD1	1:A:2074:ARG:HD2	2.22	0.74
3:C:449:ILE:CG2	3:C:457:VAL:HG12	2.17	0.74
1:A:203:VAL:CG2	1:A:237:THR:CG2	2.66	0.74
1:A:783:TYR:CB	31:P:228:ILE:HG12	2.17	0.74
37:Z:525:TYR:HD1	37:Z:526:ILE:HG23	1.52	0.74
23:3:437:VAL:O	23:3:776:GLN:HA	1.87	0.74
1:A:463:PRO:CB	2:B:20:G:O2'	2.35	0.74
1:A:1457:HIS:CD2	32:R:425:GLY:H	2.04	0.74
3:C:137:HIS:CG	3:C:236:MET:HB2	2.22	0.74
15:H:180:G:O2'	15:H:181:G:H5'	1.88	0.74
18:w:476:GLU:CB	23:3:978:LEU:HD22	2.17	0.74
28:J:406:PHE:CD2	28:J:411:MET:CE	2.70	0.74
32:R:70:ALA:O	32:R:71:GLN:O	2.05	0.74
1:A:1301:ILE:HG13	2:B:39:C:OP1	1.87	0.74
1:A:1405:LEU:HA	32:R:415:LEU:CD2	2.17	0.74
23:3:294:LYS:O	23:3:343:LYS:NZ	2.21	0.74
23:3:931:VAL:HG12	23:3:932:ASN:H	1.53	0.74
28:J:270:ASP:OD2	32:R:222:PRO:HG2	1.88	0.74
1:A:168:PRO:CG	1:A:559:ASP:CB	2.64	0.74
1:A:388:LEU:CD1	3:C:399:LEU:CD2	2.41	0.74
5:E:258:THR:HG22	5:E:260:ARG:HG2	1.68	0.74
32:R:132:LEU:HB3	33:T:399:LYS:HZ2	1.52	0.74
1:A:744:LYS:HE3	31:P:213:ASP:HA	1.70	0.74
3:C:140:HIS:CA	3:C:230:ASP:HB2	2.17	0.74
13:F:34:G:H5''	13:F:34:G:N3	2.03	0.74
32:R:422:MET:O	32:R:424:SER:N	2.17	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:T:385:TYR:O	33:T:400:PHE:HB2	1.88	0.74
3:C:445:ALA:HB1	3:C:449:ILE:CD1	2.17	0.74
15:H:45:C:N3	18:w:395:TRP:CD1	2.55	0.74
1:A:748:ASP:OD1	31:P:214:THR:CG2	2.36	0.73
5:E:243:LEU:HD11	5:E:247:GLY:HA2	1.68	0.73
3:C:89:LEU:HD23	3:C:89:LEU:C	2.14	0.73
18:w:482:SER:CB	23:3:975:LYS:CB	2.65	0.73
23:3:555:VAL:HG23	23:3:592:LEU:HD22	1.70	0.73
1:A:546:LEU:CD1	1:A:595:LYS:HD2	2.06	0.73
5:E:119:THR:HG21	5:E:161:ARG:CB	2.17	0.73
1:A:76:MET:CE	1:A:88:TYR:CG	2.70	0.73
1:A:378:PHE:CZ	3:C:335:ASN:HB2	2.22	0.73
3:C:97:VAL:HG21	31:P:45:GLN:HG3	1.69	0.73
15:H:45:C:C2'	18:w:394:TYR:HE2	2.01	0.73
21:1:563:LEU:HD22	21:1:566:LEU:HD22	1.70	0.73
1:A:231:THR:CB	3:C:389:ASP:OD2	2.37	0.73
1:A:253:ASN:ND2	1:A:334:THR:O	2.21	0.73
3:C:94:ILE:HD11	31:P:44:ARG:NH2	2.03	0.73
23:3:772:ALA:O	23:3:775:ASN:ND2	2.21	0.73
1:A:260:LEU:HD23	1:A:455:VAL:HG22	1.70	0.73
2:B:42:U:O4	14:G:-3:A:N1	2.21	0.73
3:C:516:LEU:CD1	3:C:517:GLU:HG3	2.18	0.73
3:C:671:SER:O	3:C:672:LEU:HD13	1.89	0.73
15:H:69:U:H2'	15:H:70:C:C6	2.23	0.73
15:H:165:A:O2'	15:H:166:G:H5'	1.88	0.73
23:3:441:GLY:O	23:3:775:ASN:CG	2.31	0.73
5:E:287:ASN:O	5:E:289:LEU:HD23	1.88	0.73
26:6:51:TYR:H	26:6:54:TYR:HB2	1.53	0.73
32:R:67:ILE:HG22	32:R:69:VAL:CG2	2.18	0.73
32:R:420:LYS:HG2	32:R:423:ASP:CG	2.13	0.73
1:A:1301:ILE:O	1:A:1303:LEU:O	2.06	0.73
1:A:2078:ILE:CG2	4:D:1047:PRO:CB	2.66	0.73
15:H:106:G:H4'	15:H:107:A:O4'	1.89	0.73
7:i:85:PRO:N	18:w:184:ARG:O	2.22	0.73
23:3:1145:GLU:OE2	23:3:1149:ARG:NH2	2.21	0.73
28:J:339:TRP:CE3	32:R:116:TYR:CD2	2.76	0.73
3:C:711:ARG:CD	3:C:730:ARG:HH11	2.01	0.73
28:J:259:GLN:NE2	29:L:220:PRO:HD3	2.02	0.73
3:C:449:ILE:HG22	3:C:457:VAL:CG1	2.18	0.72
5:E:146:ARG:HH12	5:E:148:LYS:CE	1.99	0.72
5:E:250:LEU:HD23	5:E:250:LEU:O	1.88	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:70:C:H2'	15:H:71:C:C6	2.24	0.72
1:A:434:HIS:ND1	1:A:435:CYS:SG	2.62	0.72
3:C:508:LYS:HE3	3:C:566:THR:HG21	1.70	0.72
23:3:547:CYS:HA	23:3:555:VAL:O	1.89	0.72
33:T:434:GLY:CA	33:T:464:GLY:HA2	2.19	0.72
3:C:93:ILE:HD13	33:T:230:ILE:HD13	1.72	0.72
15:H:106:G:H21	15:H:107:A:N6	1.87	0.72
15:H:182:U:H2'	15:H:183:G:H8	1.53	0.72
21:1:428:ALA:O	21:1:432:THR:N	2.21	0.72
38:z:38:ARG:NH1	38:z:173:ASP:OD1	2.21	0.72
1:A:368:GLN:OE1	1:A:368:GLN:HA	1.88	0.72
1:A:392:PRO:C	3:C:379:LYS:CE	2.48	0.72
1:A:541:GLY:HA3	13:F:66:C:OP1	1.87	0.72
1:A:675:GLN:OE1	13:F:70:A:OP1	2.08	0.72
3:C:519:GLU:N	3:C:519:GLU:OE2	2.21	0.72
13:F:34:G:N3	13:F:34:G:H3'	2.05	0.72
1:A:1457:HIS:HE2	32:R:424:SER:CA	2.02	0.72
1:A:2324:GLU:HG2	1:A:2330:ARG:HH12	1.54	0.72
3:C:125:ASN:O	3:C:126:SER:OG	2.04	0.72
3:C:726:LEU:HD12	3:C:726:LEU:O	1.89	0.72
1:A:712:HIS:CE1	32:R:254:CYS:HB2	2.24	0.72
3:C:77:VAL:CG1	33:T:196:LEU:CA	2.68	0.72
3:C:449:ILE:HG21	3:C:457:VAL:HG11	1.70	0.72
13:F:5:U:H3'	13:F:7:G:H5"	1.71	0.72
1:A:107:PRO:O	1:A:111:GLU:OE1	2.08	0.72
1:A:193:LEU:HD12	1:A:194:GLU:H	1.55	0.72
1:A:462:ARG:HD2	1:A:462:ARG:N	2.05	0.72
1:A:1413:ASP:O	1:A:1418:ARG:NH1	2.21	0.72
1:A:2325:VAL:CG1	4:D:789:MET:HA	2.20	0.72
3:C:250:ARG:HE	3:C:451:HIS:CD2	2.07	0.72
23:3:442:LEU:CD1	23:3:734:LEU:HD23	2.19	0.72
34:V:548:ALA:HB3	34:V:585:ILE:CB	2.19	0.72
1:A:150:MET:SD	1:A:153:ARG:NH2	2.62	0.72
1:A:335:PRO:HG3	3:C:139:HIS:HB3	1.70	0.72
13:F:39:A:H61	14:G:8:C:H42	1.36	0.72
22:2:614:ARG:HG3	22:2:614:ARG:NH1	1.98	0.72
1:A:332:TYR:CB	3:C:177:ARG:O	2.38	0.72
1:A:718:ARG:CZ	32:R:259:LYS:HE3	2.20	0.72
1:A:2078:ILE:HG21	4:D:1047:PRO:CB	2.20	0.72
5:E:264:VAL:HA	5:E:272:ARG:HH21	1.55	0.72
23:3:783:TYR:HB2	23:3:801:GLU:HB3	1.72	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:PRO:HD3	3:C:372:PHE:CE1	2.20	0.72
1:A:785:LYS:HE3	31:P:215:LEU:HD11	1.71	0.72
15:H:165:A:C2'	15:H:166:G:H5'	2.20	0.72
23:3:440:HIS:CE1	23:3:720:TRP:HZ3	1.96	0.72
1:A:228:TRP:O	1:A:415:SER:CA	2.38	0.71
1:A:480:LYS:HE2	32:R:203:GLN:OE1	1.90	0.71
3:C:64:LYS:NZ	31:P:206:LYS:HG2	2.05	0.71
3:C:129:ILE:HA	3:C:199:LEU:O	1.90	0.71
1:A:176:LEU:HD13	1:A:181:ASN:HD22	1.52	0.71
1:A:549:GLU:OE1	1:A:552:ARG:NH1	2.23	0.71
1:A:696:MET:C	1:A:698:PRO:HD3	2.15	0.71
1:A:1301:ILE:CG1	2:B:39:C:OP1	2.38	0.71
28:J:273:TYR:CE1	32:R:228:PRO:CB	2.72	0.71
29:L:224:PHE:CE1	32:R:86:LEU:CD1	2.73	0.71
31:P:66:ARG:HB2	31:P:66:ARG:HH11	1.55	0.71
1:A:231:THR:HB	3:C:389:ASP:OD2	1.89	0.71
1:A:730:GLY:O	32:R:252:PRO:HG2	1.90	0.71
1:A:1364:LEU:HD22	34:V:465:SER:CB	2.20	0.71
1:A:1402:ARG:HH22	37:Z:572:PRO:HA	1.53	0.71
2:B:44:A:H2	14:G:-5:G:C6	2.08	0.71
21:1:1206:ASP:OD1	21:1:1207:SER:N	2.21	0.71
23:3:446:GLU:OE1	23:3:763:ARG:NH1	2.24	0.71
1:A:264:PHE:CE2	1:A:459:LEU:CD1	2.73	0.71
1:A:384:VAL:HG12	3:C:332:GLY:N	2.04	0.71
15:H:153:A:H2'	15:H:154:C:C5'	2.19	0.71
21:1:405:ASP:HA	25:5:49:ARG:HH22	1.55	0.71
32:R:135:PRO:O	32:R:136:ASP:CG	2.33	0.71
39:x:640:ARG:CB	39:x:667:ALA:HA	2.19	0.71
1:A:406:TRP:CZ3	3:C:265:LEU:C	2.69	0.71
3:C:706:GLN:HE21	3:C:708:THR:H	1.38	0.71
5:E:74:PHE:CE2	5:E:343:ILE:CG1	2.73	0.71
18:w:485:ASN:HA	23:3:978:LEU:CD1	2.20	0.71
31:P:224:MET:HA	31:P:224:MET:CE	2.21	0.71
32:R:414:ARG:CZ	32:R:414:ARG:HB2	2.18	0.71
1:A:1962:THR:HG23	37:Z:524:ARG:HB2	1.68	0.71
3:C:700:ILE:HA	3:C:705:VAL:CG1	2.21	0.71
3:C:705:VAL:HG23	3:C:717:PHE:HD2	1.48	0.71
15:H:72:U:H2'	15:H:73:C:C6	2.26	0.71
1:A:203:VAL:HG23	1:A:237:THR:HG21	1.72	0.71
1:A:393:LEU:CB	3:C:379:LYS:HE3	2.21	0.71
1:A:1529:ILE:O	1:A:1532:ARG:N	2.24	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:80:ILE:HD12	3:C:80:ILE:N	2.05	0.71
3:C:94:ILE:HD13	31:P:44:ARG:CZ	2.20	0.71
3:C:441:PRO:O	3:C:444:GLY:HA3	1.90	0.71
3:C:490:PHE:CZ	3:C:612:LYS:HD2	2.26	0.71
31:P:191:ASP:N	31:P:191:ASP:OD1	2.23	0.71
37:Z:612:TYR:O	37:Z:614:TRP:N	2.23	0.71
2:B:43:U:C4	14:G:-4:A:N1	2.58	0.71
1:A:81:PHE:O	1:A:83:HIS:N	2.24	0.71
1:A:171:ASP:O	1:A:520:TYR:CG	2.44	0.71
1:A:1459:ARG:CG	32:R:422:MET:O	2.39	0.71
1:A:2156:THR:OG1	1:A:2157:VAL:N	2.21	0.71
3:C:679:PRO:HG2	3:C:807:GLN:OE1	1.91	0.71
28:J:270:ASP:OD2	32:R:222:PRO:HG3	1.88	0.71
32:R:422:MET:HG2	32:R:423:ASP:N	2.05	0.71
34:V:549:LYS:O	34:V:552:ALA:HB3	1.91	0.71
1:A:377:GLU:O	1:A:378:PHE:HB3	1.91	0.71
1:A:705:LYS:HG2	32:R:251:ILE:CD1	2.21	0.71
1:A:1085:ILE:HG12	1:A:1099:PHE:HE1	1.56	0.71
1:A:1306:LYS:NZ	2:B:38:C:H2'	2.05	0.71
3:C:474:LEU:HD23	3:C:474:LEU:C	2.16	0.71
21:1:1221:GLU:HG3	21:1:1223:SER:H	1.56	0.71
28:J:353:GLU:OE1	28:J:358:GLU:HB3	1.91	0.71
31:P:189:ASP:OD2	31:P:192:VAL:HG21	1.91	0.71
33:T:366:VAL:HG21	33:T:402:ASP:HA	1.72	0.71
1:A:73:HIS:NE2	1:A:81:PHE:CZ	2.51	0.70
1:A:181:ASN:O	1:A:185:VAL:HG22	1.90	0.70
1:A:719:CYS:SG	32:R:258:TRP:CH2	2.84	0.70
1:A:1370:ARG:NH1	34:V:467:LEU:C	2.49	0.70
3:C:259:LYS:HG3	41:C:1500:GTP:C6	2.26	0.70
1:A:301:LYS:HG2	3:C:940:ARG:N	2.06	0.70
1:A:2328:ALA:HB3	4:D:788:GLY:N	2.05	0.70
15:H:160:A:O2'	15:H:161:U:H5'	1.90	0.70
14:G:11:A:N3	14:G:11:A:H5''	2.05	0.70
15:H:168:A:N3	15:H:168:A:H2'	2.06	0.70
13:F:24:A:H2	13:F:26:U:C2	2.09	0.70
7:i:85:PRO:CA	18:w:184:ARG:HA	2.22	0.70
32:R:189:ASN:HD21	32:R:195:ARG:NH2	1.90	0.70
33:T:267:ASP:O	33:T:268:LYS:HG3	1.91	0.70
1:A:251:ASP:CB	1:A:337:VAL:HG23	2.20	0.70
1:A:316:PHE:CE1	3:C:635:LEU:HA	2.27	0.70
2:B:40:U:H4'	2:B:41:U:OP2	1.89	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:43:U:N3	14:G:-4:A:C2	2.51	0.70
3:C:449:ILE:HD13	3:C:466:SER:OG	1.92	0.70
13:F:94:C:OP1	28:J:351:ASN:ND2	2.25	0.70
15:H:181:G:H2'	15:H:182:U:C6	2.26	0.70
21:1:901:GLN:HA	21:1:939:ARG:NH2	2.07	0.70
32:R:103:ARG:HH11	32:R:103:ARG:CB	2.04	0.70
34:V:536:ILE:O	34:V:578:SER:CB	2.39	0.70
1:A:76:MET:CE	1:A:506:LEU:HD11	2.21	0.70
3:C:457:VAL:CB	3:C:462:GLY:HA3	2.22	0.70
13:F:38:G:P	13:F:38:G:H8	2.14	0.70
13:F:68:C:C2	31:P:33:ARG:HG2	2.27	0.70
14:G:12:G:N3	14:G:12:G:H2'	2.07	0.70
21:1:1108:ASN:OD1	21:1:1110:VAL:N	2.25	0.70
1:A:333:HIS:C	3:C:139:HIS:NE2	2.49	0.70
1:A:1860:GLN:HG2	1:A:1883:VAL:HB	1.74	0.70
2:B:40:U:C4'	2:B:41:U:OP2	2.39	0.70
3:C:132:VAL:CG1	3:C:226:VAL:CG2	2.70	0.70
3:C:135:CYS:SG	3:C:227:LEU:CD1	2.80	0.70
32:R:220:ARG:NH1	32:R:220:ARG:HB2	2.06	0.70
39:x:831:SER:CB	39:x:942:ALA:CA	2.70	0.70
1:A:664:HIS:NE2	1:A:666:LYS:HG2	2.06	0.70
1:A:675:GLN:O	13:F:55:C:O2'	2.10	0.70
1:A:1318:THR:HB	1:A:1324:GLY:HA3	1.73	0.70
15:H:154:C:H2'	15:H:155:C:C6	2.27	0.70
21:1:1155:PHE:HA	21:1:1158:ILE:HG12	1.73	0.70
32:R:80:LYS:O	32:R:81:LYS:NZ	2.25	0.70
1:A:76:MET:HE3	1:A:506:LEU:HD11	1.74	0.70
1:A:231:THR:CA	3:C:389:ASP:OD2	2.40	0.70
1:A:719:CYS:SG	32:R:258:TRP:HH2	2.13	0.70
3:C:137:HIS:CE1	3:C:236:MET:SD	2.85	0.70
1:A:299:ILE:HD12	3:C:921:LEU:HB2	1.74	0.69
1:A:718:ARG:NE	32:R:259:LYS:HE3	2.06	0.69
3:C:452:THR:HB	3:C:577:PHE:CD2	2.26	0.69
23:3:722:SER:HA	23:3:730:HIS:O	1.92	0.69
1:A:76:MET:SD	1:A:88:TYR:CG	2.85	0.69
1:A:363:HIS:CE1	3:C:287:GLY:HA3	2.27	0.69
1:A:673:THR:O	1:A:677:VAL:HG23	1.91	0.69
3:C:64:LYS:NZ	31:P:206:LYS:CG	2.55	0.69
3:C:452:THR:O	3:C:577:PHE:HA	1.92	0.69
5:E:74:PHE:HE2	5:E:343:ILE:HG12	1.54	0.69
5:E:264:VAL:HA	5:E:272:ARG:NH2	2.07	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:LEU:HD23	3:C:387:ASP:O	1.92	0.69
1:A:250:VAL:CG2	1:A:337:VAL:CG1	2.70	0.69
1:A:311:GLU:HB3	3:C:885:THR:CG2	2.21	0.69
1:A:461:HIS:CD2	2:B:26:A:H61	2.10	0.69
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	1.73	0.69
1:A:1705:ILE:HD11	1:A:1730:MET:HE1	1.75	0.69
1:A:439:GLN:NE2	1:A:614:TYR:CE2	2.49	0.69
1:A:805:GLU:CB	31:P:194:PHE:HZ	2.04	0.69
1:A:2314:PHE:HD2	4:D:1123:TRP:CB	2.05	0.69
3:C:709:TRP:HB3	3:C:713:LYS:HD2	1.73	0.69
23:3:280:ASP:H	23:3:857:ALA:HB3	1.58	0.69
31:P:30:TYR:OH	32:R:161:ALA:O	2.10	0.69
32:R:436:VAL:HG23	32:R:437:TYR:CE1	2.26	0.69
1:A:645:THR:HB	1:A:646:PRO:HD3	1.74	0.69
1:A:755:HIS:HE1	31:P:223:PHE:CD2	2.06	0.69
15:H:149:A:H2'	15:H:150:U:C6	2.27	0.69
15:H:153:A:N6	15:H:177:A:C2	2.60	0.69
15:H:183:G:H2'	15:H:184:C:C6	2.26	0.69
32:R:408:GLU:CG	32:R:409:VAL:H	2.04	0.69
1:A:71:ARG:HD2	1:A:177:ASP:OD2	1.91	0.69
1:A:1180:LYS:HA	1:A:1201:ARG:HH12	1.58	0.69
3:C:141:GLY:C	3:C:258:ASN:HD22	2.01	0.69
16:o:46:ALA:HB2	16:o:68:THR:CB	2.23	0.69
23:3:428:GLY:HA3	23:3:433:SER:HA	1.73	0.69
1:A:76:MET:HE1	1:A:88:TYR:CB	2.22	0.69
1:A:203:VAL:CG2	1:A:237:THR:HG21	2.23	0.69
1:A:256:TYR:CE1	3:C:888:ARG:CZ	2.76	0.69
1:A:367:SER:CB	3:C:299:ILE:HD12	2.23	0.69
1:A:384:VAL:CA	3:C:331:PHE:CD2	2.61	0.69
1:A:762:ARG:NH2	31:P:226:LYS:HZ3	1.87	0.69
1:A:1505:LYS:CD	37:Z:615:SER:HB3	2.22	0.69
3:C:482:TYR:CE2	3:C:493:PHE:HB2	2.28	0.69
5:E:178:LEU:CD1	5:E:222:LEU:CD2	2.71	0.69
15:H:83:A:C2'	15:H:84:C:O4'	2.39	0.69
23:3:452:LEU:HD11	23:3:762:LEU:HB2	1.74	0.69
25:5:18:ASN:OD1	25:5:19:ARG:N	2.25	0.69
35:X:185:ARG:O	35:X:189:HIS:HB2	1.93	0.69
1:A:1459:ARG:HG3	32:R:424:SER:H	1.57	0.69
1:A:2267:PHE:HA	4:D:1261:PRO:CB	2.23	0.69
3:C:93:ILE:CG2	33:T:218:TRP:CE2	2.76	0.69
3:C:736:GLY:CA	3:C:770:PHE:CE2	2.75	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:152:G:O3'	15:H:153:A:O4'	2.11	0.69
23:3:236:ILE:HB	23:3:249:LEU:HB2	1.75	0.69
28:J:353:GLU:OE1	28:J:358:GLU:CB	2.41	0.69
31:P:30:TYR:CZ	32:R:162:ALA:HA	2.28	0.69
31:P:224:MET:CE	31:P:228:ILE:CD1	2.71	0.69
39:x:726:ALA:HB1	39:x:732:GLY:HA3	1.75	0.69
1:A:299:ILE:HD11	3:C:921:LEU:HA	1.74	0.69
3:C:72:VAL:HG22	33:T:453:ALA:CB	2.23	0.69
3:C:256:CYS:SG	3:C:308:CYS:HB2	2.33	0.69
5:E:74:PHE:CD1	5:E:81:LEU:HD23	2.28	0.69
1:A:229:GLN:CG	1:A:415:SER:HB2	2.21	0.68
1:A:253:ASN:OD1	1:A:334:THR:OG1	2.03	0.68
1:A:388:LEU:HD12	3:C:399:LEU:HD21	1.72	0.68
1:A:755:HIS:CE1	31:P:223:PHE:HB3	2.28	0.68
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.11	0.68
13:F:37:C:H4'	13:F:38:G:OP2	1.91	0.68
22:2:487:LEU:O	22:2:490:HIS:N	2.26	0.68
23:3:718:ARG:NH2	23:3:734:LEU:O	2.25	0.68
1:A:255:PHE:HE1	1:A:432:ARG:O	1.75	0.68
3:C:140:HIS:CD2	3:C:230:ASP:HB3	2.28	0.68
3:C:445:ALA:CB	3:C:466:SER:HA	2.20	0.68
3:C:725:ASP:OD1	3:C:728:ALA:N	2.25	0.68
32:R:434:TYR:HE2	32:R:436:VAL:HG22	1.57	0.68
1:A:73:HIS:NE2	1:A:81:PHE:CD1	2.59	0.68
1:A:1301:ILE:CD1	1:A:1306:LYS:CE	2.70	0.68
2:B:21:A:O3'	2:B:22:U:H4'	1.94	0.68
18:w:478:GLU:CB	23:3:978:LEU:HD12	2.23	0.68
22:2:643:PRO:HD2	24:4:69:TYR:CG	2.27	0.68
31:P:72:ARG:NH1	31:P:72:ARG:HB2	2.08	0.68
32:R:106:GLN:CG	32:R:110:LYS:HE2	2.22	0.68
36:Y:33:LYS:HA	36:Y:87:GLN:HE22	1.59	0.68
1:A:32:GLU:HG3	1:A:36:LYS:HE3	1.74	0.68
1:A:402:ILE:HG12	3:C:265:LEU:HD22	1.75	0.68
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.28	0.68
36:Y:86:ASP:HB2	37:Z:502:ALA:CB	2.23	0.68
1:A:44:ARG:HD2	1:A:45:TYR:CE2	2.28	0.68
1:A:1900:GLU:OE2	37:Z:522:LEU:HB2	1.93	0.68
1:A:2146:VAL:HG22	1:A:2272:MET:HB2	1.74	0.68
3:C:482:TYR:CE2	3:C:493:PHE:CB	2.77	0.68
3:C:678:THR:HG21	3:C:683:ASN:ND2	2.06	0.68
14:G:-2:C:H2'	14:G:-1:G:C8	2.28	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:868:VAL:O	23:3:877:LEU:N	2.27	0.68
1:A:530:LEU:H	30:M:198:GLN:CD	1.96	0.68
5:E:108:HIS:CE1	5:E:128:SER:CB	2.77	0.68
15:H:147:G:O2'	15:H:148:C:H5'	1.94	0.68
23:3:524:ILE:HD11	23:3:556:ILE:HG21	1.74	0.68
31:P:63:LEU:O	31:P:63:LEU:HD23	1.94	0.68
32:R:414:ARG:NE	37:Z:598:PHE:CE1	2.47	0.68
1:A:338:VAL:HG21	3:C:867:PRO:CD	2.24	0.68
1:A:779:LEU:CD2	31:P:223:PHE:HE2	2.06	0.68
1:A:1457:HIS:HE2	32:R:424:SER:HA	1.55	0.68
13:F:68:C:C5	31:P:33:ARG:HB3	2.20	0.68
32:R:88:ILE:CG2	32:R:96:ILE:CG2	2.71	0.68
1:A:779:LEU:HD22	31:P:224:MET:HE1	1.75	0.68
3:C:79:THR:HG23	33:T:199:VAL:CG2	2.24	0.68
3:C:350:ASN:CG	3:C:353:THR:HG23	2.19	0.68
3:C:452:THR:HG22	3:C:577:PHE:CB	2.23	0.68
5:E:74:PHE:CD1	5:E:81:LEU:HD21	2.29	0.68
34:V:547:VAL:O	34:V:550:MET:N	2.27	0.68
37:Z:597:ARG:NH1	37:Z:601:LEU:CD1	2.57	0.68
1:A:660:PHE:CD2	32:R:209:PRO:CB	2.76	0.68
1:A:758:ARG:HG3	1:A:779:LEU:HD11	1.75	0.68
1:A:1210:LYS:NZ	1:A:1369:TYR:OH	2.27	0.68
2:B:19:A:O2'	2:B:20:G:OP1	2.12	0.68
3:C:141:GLY:O	3:C:258:ASN:ND2	2.27	0.68
22:2:614:ARG:NH2	22:2:685:ASP:OD1	2.26	0.68
23:3:301:PHE:HB2	23:3:313:ILE:HB	1.76	0.68
27:7:48:ASP:O	27:7:51:ASN:N	2.27	0.68
28:J:360:ASP:O	28:J:363:ARG:HG3	1.93	0.68
36:Y:86:ASP:CA	37:Z:502:ALA:HB3	2.23	0.68
1:A:91:ALA:O	1:A:93:LYS:N	2.27	0.68
1:A:121:HIS:HE2	1:A:481:PHE:HB3	1.51	0.68
1:A:245:LEU:HA	1:A:430:TRP:CZ2	2.28	0.68
3:C:94:ILE:CD1	31:P:44:ARG:NH1	2.57	0.68
13:F:35:A:H5''	13:F:35:A:N3	2.09	0.68
15:H:159:U:O2'	15:H:160:A:H5'	1.94	0.68
23:3:374:SER:HB3	23:3:377:MET:HG3	1.76	0.68
28:J:353:GLU:OE2	28:J:361:ARG:NH2	2.27	0.68
3:C:94:ILE:CD1	31:P:44:ARG:CZ	2.72	0.67
3:C:360:ALA:H	3:C:361:PRO:HD3	1.59	0.67
3:C:534:VAL:HG12	3:C:535:ALA:H	1.59	0.67
32:R:420:LYS:HB2	37:Z:610:LEU:CD1	2.22	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ILE:CD1	1:A:483:GLN:HG3	2.24	0.67
1:A:298:ASP:O	1:A:302:ILE:HG12	1.95	0.67
1:A:305:ARG:HG3	3:C:878:ILE:HB	1.77	0.67
1:A:2270:PHE:HD1	4:D:1264:PRO:CB	1.96	0.67
3:C:140:HIS:HB3	3:C:230:ASP:HB2	1.71	0.67
21:1:498:MET:HE1	21:1:530:PRO:HB2	1.76	0.67
23:3:18:ILE:HD12	23:3:67:ALA:HB2	1.77	0.67
32:R:147:THR:CG2	33:T:360:VAL:HG12	2.23	0.67
3:C:140:HIS:CD2	3:C:230:ASP:CB	2.77	0.67
3:C:737:PRO:HG3	3:C:774:THR:OG1	1.93	0.67
21:1:437:PRO:O	35:X:262:TYR:HA	1.94	0.67
23:3:753:GLY:HA3	23:3:765:LEU:O	1.94	0.67
1:A:228:TRP:O	1:A:416:GLY:N	2.26	0.67
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.76	0.67
1:A:1118:PRO:HD2	1:A:1119:ASP:H	1.59	0.67
1:A:1962:THR:HG23	37:Z:524:ARG:HG3	1.74	0.67
3:C:259:LYS:HE2	3:C:262:ARG:HD2	1.74	0.67
18:w:434:GLY:O	18:w:438:LEU:HB2	1.94	0.67
21:1:1097:LEU:O	21:1:1100:ASN:ND2	2.24	0.67
23:3:412:ILE:HG12	23:3:423:LEU:HG	1.76	0.67
1:A:76:MET:SD	1:A:88:TYR:CD1	2.88	0.67
1:A:89:LEU:HD22	1:A:656:LEU:HD22	1.76	0.67
1:A:1422:LEU:HD22	21:1:88:VAL:CB	2.25	0.67
1:A:2113:LYS:CE	4:D:1229:ASP:CB	2.71	0.67
3:C:389:ASP:OD1	3:C:389:ASP:N	2.26	0.67
5:E:66:GLU:HB2	5:E:87:ASP:OD2	1.94	0.67
21:1:474:TYR:OH	25:5:93:ASN:ND2	2.27	0.67
21:1:798:THR:HG22	21:1:800:GLY:H	1.60	0.67
32:R:119:LEU:CB	32:R:232:MET:HG3	2.24	0.67
32:R:285:ASN:OD1	32:R:286:GLU:N	2.27	0.67
33:T:185:MET:CB	33:T:186:PRO:HD3	2.24	0.67
1:A:1281:THR:HG22	1:A:1284:LEU:H	1.59	0.67
3:C:94:ILE:HD11	31:P:44:ARG:HH22	1.60	0.67
3:C:132:VAL:HG12	3:C:226:VAL:CG2	2.23	0.67
5:E:246:GLU:HB2	5:E:248:SER:OG	1.94	0.67
33:T:455:GLN:HG3	33:T:485:THR:HG21	1.76	0.67
1:A:435:CYS:CB	3:C:892:GLN:NE2	2.57	0.67
1:A:1258:LYS:HE2	32:R:432:GLU:HA	1.77	0.67
1:A:1661:TRP:CE2	1:A:1700:GLY:HA3	2.30	0.67
1:A:2300:ASN:OD1	4:D:1228:VAL:O	2.12	0.67
3:C:736:GLY:CA	3:C:770:PHE:HE2	2.07	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Y:62:ILE:HA	36:Y:84:TYR:HA	1.75	0.67
36:Y:100:ILE:O	36:Y:106:THR:HA	1.94	0.67
37:Z:597:ARG:NH1	37:Z:601:LEU:HD12	2.08	0.67
1:A:171:ASP:OD2	1:A:519:ASP:OD2	2.12	0.67
1:A:299:ILE:CD1	3:C:920:PRO:O	2.43	0.67
1:A:393:LEU:HA	3:C:379:LYS:CD	2.24	0.67
2:B:40:U:C5'	2:B:41:U:OP2	2.43	0.67
3:C:572:GLU:HG3	3:C:573:GLU:H	1.60	0.67
15:H:151:C:C2	15:H:152:G:C8	2.83	0.67
32:R:81:LYS:HA	32:R:81:LYS:HZ1	1.59	0.67
32:R:119:LEU:HA	32:R:232:MET:SD	2.34	0.67
33:T:272:CYS:HB3	33:T:282:ARG:HG3	1.76	0.67
1:A:229:GLN:HA	1:A:414:ARG:O	1.94	0.67
1:A:282:LEU:C	1:A:282:LEU:HD23	2.20	0.67
1:A:293:TRP:HZ3	1:A:295:GLU:OE1	1.76	0.67
3:C:452:THR:CB	3:C:577:PHE:CD2	2.73	0.67
5:E:243:LEU:HD12	5:E:247:GLY:HA2	1.76	0.67
14:G:10:U:O5'	14:G:10:U:H6	1.78	0.67
15:H:169:C:O2'	15:H:170:C:H5'	1.95	0.67
23:3:63:ARG:NH2	23:3:119:GLN:OE1	2.22	0.67
23:3:470:PHE:HB3	23:3:747:SER:HA	1.75	0.67
23:3:802:THR:HA	23:3:863:ALA:O	1.95	0.67
1:A:439:GLN:NE2	1:A:614:TYR:OH	2.27	0.67
3:C:149:LEU:HD13	3:C:427:PHE:CE2	2.22	0.67
3:C:510:LEU:HD22	3:C:514:TYR:CD2	2.30	0.67
15:H:153:A:C3'	15:H:154:C:H5'	2.25	0.67
21:1:1126:PHE:HA	21:1:1165:TYR:OH	1.94	0.67
1:A:417:ARG:HH22	2:B:58:U:C5'	2.07	0.66
1:A:1984:LYS:HG3	1:A:2011:ILE:HD11	1.76	0.66
1:A:2306:HIS:CD2	1:A:2308:VAL:H	2.13	0.66
3:C:77:VAL:CG1	33:T:196:LEU:HB3	2.24	0.66
3:C:129:ILE:HG22	3:C:199:LEU:CB	2.23	0.66
23:3:1035:THR:HG21	23:3:1103:SER:HA	1.75	0.66
24:4:17:VAL:HG13	24:4:84:ILE:HG23	1.77	0.66
1:A:398:THR:CG2	3:C:382:ALA:HB1	2.23	0.66
3:C:230:ASP:OD1	3:C:259:LYS:CB	2.43	0.66
15:H:143:A:H2'	15:H:144:C:H6	1.59	0.66
15:H:151:C:O2	15:H:152:G:C8	2.48	0.66
1:A:676:ARG:NE	13:F:56:A:OP1	2.28	0.66
1:A:1768:TYR:HA	1:A:1771:LEU:HB3	1.75	0.66
3:C:62:ASP:OD1	3:C:62:ASP:N	2.28	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:244:LYS:CB	3:C:292:TYR:CE2	2.79	0.66
15:H:151:C:H2'	15:H:152:G:H8	1.59	0.66
23:3:147:ASP:OD1	23:3:151:ARG:N	2.25	0.66
23:3:546:LYS:O	23:3:556:ILE:HA	1.94	0.66
23:3:947:GLU:HB3	23:3:963:VAL:HG22	1.75	0.66
1:A:338:VAL:CG2	3:C:867:PRO:CG	2.73	0.66
1:A:377:GLU:O	1:A:378:PHE:CB	2.44	0.66
1:A:748:ASP:OD2	33:T:204:LEU:O	2.13	0.66
1:A:1386:TRP:HE1	1:A:1417:PRO:HD2	1.61	0.66
1:A:1457:HIS:CE1	1:A:1459:ARG:HB2	2.30	0.66
3:C:141:GLY:C	3:C:258:ASN:ND2	2.53	0.66
5:E:146:ARG:HH11	5:E:148:LYS:CE	1.83	0.66
15:H:73:C:H2'	15:H:74:U:C6	2.30	0.66
15:H:114:A:H61	15:H:142:C:H42	1.44	0.66
21:1:397:ARG:HD3	21:1:398:PRO:HD2	1.78	0.66
23:3:187:MET:HE3	23:3:206:GLN:HB3	1.78	0.66
26:6:25:LYS:NZ	26:6:26:CYS:SG	2.68	0.66
1:A:75:ASP:OD1	1:A:75:ASP:N	2.26	0.66
1:A:480:LYS:HG2	32:R:203:GLN:OE1	1.95	0.66
2:B:19:A:H2'	2:B:20:G:H5''	1.78	0.66
31:P:224:MET:HE3	31:P:228:ILE:HD13	1.74	0.66
1:A:134:TRP:HB3	1:A:418:THR:CG2	2.25	0.66
1:A:630:TRP:O	1:A:631:ALA:C	2.37	0.66
3:C:473:PRO:O	3:C:474:LEU:HB3	1.96	0.66
15:H:47:U:H1'	15:H:48:A:H8	1.61	0.66
23:3:1017:ASN:OD1	23:3:1018:GLU:N	2.29	0.66
31:P:212:ASN:OD1	33:T:483:ASP:HA	1.96	0.66
33:T:314:ILE:HD12	33:T:324:HIS:HB2	1.75	0.66
36:Y:39:PHE:O	36:Y:109:VAL:HA	1.95	0.66
36:Y:98:ASN:OD1	36:Y:99:GLY:N	2.25	0.66
37:Z:525:TYR:HE1	37:Z:526:ILE:HG23	1.57	0.66
3:C:145:PHE:CE1	3:C:427:PHE:HE1	2.14	0.66
3:C:221:ILE:CG1	3:C:479:THR:OG1	2.43	0.66
33:T:342:GLU:HB3	33:T:343:PRO:CD	2.26	0.66
34:V:548:ALA:HB1	34:V:585:ILE:CB	2.25	0.66
1:A:271:MET:HE1	1:A:313:LYS:HD2	1.78	0.66
1:A:312:TYR:CE1	3:C:882:GLY:CA	2.78	0.66
1:A:395:THR:CG2	3:C:383:GLN:NE2	2.49	0.66
1:A:718:ARG:HH21	32:R:259:LYS:HE3	1.58	0.66
1:A:785:LYS:HE3	31:P:215:LEU:CD1	2.26	0.66
3:C:140:HIS:HA	3:C:259:LYS:NZ	2.10	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:116:HIS:O	5:E:124:LEU:HD12	1.95	0.66
23:3:355:ASN:OD1	23:3:436:ARG:NH2	2.26	0.66
33:T:355:ARG:C	33:T:356:LEU:HD12	2.21	0.66
1:A:366:LYS:HE3	1:A:366:LYS:N	2.07	0.66
14:G:146:C:H41	21:1:1107:GLN:HG3	1.60	0.66
23:3:952:ILE:HG12	23:3:961:ILE:HG12	1.78	0.66
27:7:63:ARG:O	27:7:67:ASN:ND2	2.29	0.66
28:J:300:ASP:OD2	32:R:101:ILE:CG1	2.44	0.66
1:A:225:TYR:O	1:A:418:THR:OG1	2.11	0.66
1:A:755:HIS:HE1	31:P:223:PHE:HB3	1.61	0.66
1:A:829:PRO:O	1:A:882:LYS:NZ	2.27	0.66
1:A:1457:HIS:NE2	32:R:424:SER:CA	2.59	0.66
3:C:87:GLN:HE21	33:T:239:LYS:HD3	1.61	0.66
3:C:750:LEU:C	3:C:750:LEU:HD12	2.21	0.66
23:3:330:PHE:O	23:3:394:ASN:ND2	2.29	0.66
3:C:77:VAL:HG12	33:T:197:TYR:CA	2.25	0.65
3:C:136:GLY:HA2	3:C:239:THR:HG22	1.77	0.65
5:E:178:LEU:HD11	5:E:222:LEU:CD2	2.26	0.65
32:R:124:VAL:HG13	32:R:125:MET:H	1.60	0.65
1:A:333:HIS:O	3:C:139:HIS:NE2	2.29	0.65
1:A:1459:ARG:HE	32:R:423:ASP:CB	2.06	0.65
14:G:-12:G:H2'	14:G:-11:G:C8	2.30	0.65
23:3:440:HIS:CG	23:3:733:PRO:CG	2.79	0.65
33:T:439:TRP:CZ3	33:T:446:ASN:HB2	2.32	0.65
21:1:1171:PRO:O	21:1:1174:GLU:HB2	1.96	0.65
31:P:210:PHE:HB3	33:T:455:GLN:HE22	1.61	0.65
1:A:344:ASP:N	1:A:344:ASP:OD1	2.28	0.65
1:A:1459:ARG:CD	32:R:422:MET:O	2.45	0.65
1:A:1962:THR:O	37:Z:524:ARG:CG	2.45	0.65
21:1:713:ALA:HA	21:1:716:ALA:HB3	1.77	0.65
31:P:66:ARG:HH11	31:P:66:ARG:CB	2.09	0.65
1:A:151:MET:SD	1:A:628:GLY:C	2.80	0.65
3:C:457:VAL:HB	3:C:462:GLY:HA3	1.78	0.65
15:H:45:C:N3	18:w:395:TRP:HB3	2.11	0.65
33:T:327:SER:O	33:T:357:TRP:HH2	1.79	0.65
1:A:254:TYR:OH	1:A:434:HIS:HB3	1.95	0.65
1:A:435:CYS:CB	3:C:892:GLN:HE22	2.09	0.65
3:C:700:ILE:HG21	3:C:741:GLY:O	1.97	0.65
14:G:137:C:H42	15:H:40:C:N4	1.95	0.65
21:1:584:ASP:OD1	21:1:585:GLU:N	2.29	0.65
22:2:487:LEU:HD12	27:7:28:LYS:HE3	1.78	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:2:511:LEU:HD23	22:2:593:GLU:HG3	1.79	0.65
23:3:458:ALA:HA	23:3:741:PHE:HB3	1.78	0.65
33:T:459:LEU:HD12	33:T:460:ASP:H	1.61	0.65
38:z:53:ILE:HG22	38:z:160:LYS:HG2	1.77	0.65
1:A:95:MET:HE2	1:A:503:MET:CE	2.26	0.65
1:A:361:HIS:HD2	3:C:279:ARG:NH1	1.95	0.65
5:E:108:HIS:CE1	5:E:128:SER:HB3	2.31	0.65
13:F:24:A:H2	13:F:26:U:N3	1.94	0.65
32:R:171:LEU:CD1	32:R:201:GLU:CD	2.70	0.65
38:z:13:GLY:HA2	38:z:168:PHE:HD2	1.62	0.65
1:A:134:TRP:HB3	1:A:418:THR:HG21	1.79	0.65
1:A:405:LEU:HD11	3:C:385:VAL:HG11	1.78	0.65
2:B:40:U:H5'	2:B:41:U:OP2	1.97	0.65
3:C:572:GLU:HG3	3:C:573:GLU:N	2.12	0.65
23:3:866:ILE:HB	23:3:880:VAL:HB	1.79	0.65
29:L:11:TRP:CG	29:L:49:ARG:HE	2.15	0.65
32:R:451:ILE:HD13	32:R:451:ILE:N	2.12	0.65
33:T:458:SER:OG	33:T:459:LEU:N	2.30	0.65
2:B:43:U:O4	14:G:-4:A:N1	2.29	0.65
14:G:130:A:H5''	18:w:396:LEU:HD21	1.78	0.65
23:3:791:HIS:HE1	23:3:934:GLY:HA3	1.62	0.65
24:4:75:ASN:OD1	24:4:86:VAL:CB	2.45	0.65
1:A:97:HIS:HD2	1:A:473:PHE:CZ	2.15	0.65
1:A:2314:PHE:CD2	4:D:1123:TRP:CB	2.80	0.65
3:C:749:THR:O	3:C:753:GLU:N	2.27	0.65
13:F:33:G:OP2	13:F:33:G:H8	1.80	0.65
15:H:153:A:H3'	15:H:154:C:H5'	1.79	0.65
15:H:156:U:C6	15:H:156:U:C5'	2.72	0.65
21:1:1026:ASN:HD22	21:1:1031:VAL:HG11	1.60	0.65
31:P:210:PHE:CE2	33:T:455:GLN:OE1	2.50	0.65
3:C:97:VAL:CG1	31:P:47:THR:OG1	2.45	0.64
3:C:463:GLU:OE1	3:C:463:GLU:N	2.29	0.64
3:C:488:VAL:HG13	3:C:609:LYS:NZ	2.12	0.64
5:E:277:PHE:HE2	5:E:300:ILE:HD13	1.61	0.64
21:1:912:ASN:OD1	21:1:957:ARG:NH1	2.30	0.64
32:R:171:LEU:CD1	32:R:201:GLU:OE1	2.44	0.64
1:A:664:HIS:NE2	1:A:666:LYS:HB2	2.11	0.64
3:C:72:VAL:CG2	33:T:453:ALA:HB1	2.26	0.64
14:G:11:A:N3	14:G:11:A:H3'	2.12	0.64
15:H:148:C:H2'	15:H:149:A:C8	2.30	0.64
1:A:378:PHE:CD1	1:A:379:GLU:N	2.65	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:153:PHE:O	5:E:171:SER:HB2	1.97	0.64
7:i:84:GLY:HA2	18:w:188:MET:CB	2.27	0.64
23:3:429:ARG:HH12	27:7:58:ASN:HA	1.62	0.64
23:3:635:ALA:HB3	23:3:669:LEU:HD23	1.79	0.64
1:A:363:HIS:CD2	3:C:283:ASP:O	2.50	0.64
1:A:779:LEU:HD21	31:P:223:PHE:HE2	1.59	0.64
1:A:1051:LEU:CD2	31:P:193:VAL:HG11	2.27	0.64
3:C:256:CYS:SG	3:C:308:CYS:CB	2.86	0.64
23:3:206:GLN:HG3	23:3:228:LEU:HD12	1.78	0.64
23:3:670:GLN:HA	23:3:698:PRO:HA	1.78	0.64
32:R:88:ILE:H	32:R:88:ILE:HD12	1.61	0.64
36:Y:24:ASP:O	36:Y:27:SER:N	2.30	0.64
37:Z:594:GLU:O	37:Z:598:PHE:N	2.25	0.64
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.78	0.64
1:A:1069:ASN:OD1	1:A:1075:GLN:NE2	2.31	0.64
1:A:2328:ALA:CB	4:D:788:GLY:CA	2.74	0.64
3:C:97:VAL:HG22	31:P:45:GLN:HG3	1.77	0.64
3:C:482:TYR:HE2	3:C:493:PHE:CD2	2.14	0.64
37:Z:574:ASN:O	37:Z:575:ARG:C	2.40	0.64
1:A:305:ARG:HA	1:A:305:ARG:NH1	2.09	0.64
15:H:68:G:H1	15:H:84:C:N4	1.95	0.64
23:3:184:CYS:SG	23:3:209:THR:OG1	2.56	0.64
23:3:714:ALA:O	23:3:720:TRP:HB2	1.97	0.64
32:R:419:SER:O	32:R:420:LYS:O	2.16	0.64
1:A:303:ILE:CG2	3:C:933:PHE:CE1	2.81	0.64
3:C:350:ASN:ND2	3:C:353:THR:HG23	2.13	0.64
3:C:705:VAL:HB	3:C:717:PHE:CZ	2.33	0.64
14:G:149:G:C2	14:G:150:U:H2'	2.32	0.64
21:1:847:ALA:O	21:1:851:SER:CB	2.46	0.64
32:R:433:ILE:HD12	32:R:435:ASN:ND2	2.12	0.64
1:A:250:VAL:CG2	1:A:337:VAL:HG11	2.28	0.64
1:A:305:ARG:HG2	3:C:878:ILE:CG2	2.27	0.64
1:A:435:CYS:HB2	3:C:892:GLN:CD	2.22	0.64
1:A:1118:PRO:O	1:A:1119:ASP:CB	2.44	0.64
3:C:824:THR:O	3:C:824:THR:CG2	2.45	0.64
13:F:38:G:H8	13:F:38:G:O5'	1.79	0.64
21:1:599:ASN:O	21:1:603:ALA:HB2	1.98	0.64
21:1:702:ARG:O	21:1:705:SER:OG	2.13	0.64
23:3:525:ARG:HG3	23:3:533:VAL:HG13	1.78	0.64
24:4:15:VAL:O	24:4:58:PHE:HA	1.97	0.64
29:L:224:PHE:HD1	32:R:86:LEU:HD12	1.54	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:TRP:CH2	3:C:266:GLU:HB2	2.33	0.64
1:A:1252:GLY:HA2	1:A:1298:ARG:NH2	2.13	0.64
1:A:1370:ARG:NH1	34:V:467:LEU:HA	2.12	0.64
3:C:363:SER:O	3:C:364:SER:OG	2.11	0.64
15:H:25:G:H2'	15:H:26:A:H8	1.62	0.64
28:J:294:HIS:CE1	29:L:227:THR:CB	2.80	0.64
32:R:110:LYS:HD2	32:R:110:LYS:C	2.23	0.64
39:x:936:TYR:O	39:x:939:VAL:N	2.30	0.64
1:A:176:LEU:HD13	1:A:181:ASN:ND2	2.13	0.64
1:A:338:VAL:HG23	3:C:867:PRO:CG	2.24	0.64
1:A:384:VAL:CG1	3:C:331:PHE:CB	2.46	0.64
1:A:393:LEU:HA	3:C:379:LYS:CE	2.18	0.64
1:A:1215:ASN:HB3	1:A:1224:ARG:HD2	1.79	0.64
1:A:1457:HIS:CE1	32:R:424:SER:CA	2.79	0.64
3:C:678:THR:HG21	3:C:683:ASN:HB2	1.76	0.64
14:G:155:U:H4'	14:G:156:U:H5'	1.79	0.64
18:w:445:HIS:CG	18:w:446:PHE:CD2	2.86	0.64
1:A:1962:THR:HG23	37:Z:524:ARG:CG	2.27	0.63
1:A:2319:LEU:HG	1:A:2320:LEU:N	2.11	0.63
3:C:482:TYR:CE2	3:C:493:PHE:CD2	2.86	0.63
4:D:1992:GLU:HA	4:D:1995:ALA:HB3	1.80	0.63
23:3:673:VAL:HA	23:3:691:THR:H	1.63	0.63
28:J:406:PHE:CG	28:J:411:MET:HE2	2.33	0.63
1:A:175:PRO:HG2	1:A:498:ARG:CZ	2.27	0.63
1:A:366:LYS:H	1:A:366:LYS:CE	2.09	0.63
1:A:1370:ARG:HH11	34:V:467:LEU:C	2.06	0.63
2:B:12:U:O2'	2:B:13:C:O5'	2.14	0.63
3:C:481:MET:SD	3:C:492:ALA:HB2	2.37	0.63
3:C:596:ASN:HD22	3:C:596:ASN:N	1.96	0.63
13:F:94:C:OP1	28:J:351:ASN:HB2	1.98	0.63
15:H:152:G:C2	15:H:153:A:C5	2.87	0.63
23:3:524:ILE:HD11	23:3:556:ILE:HD13	1.80	0.63
24:4:75:ASN:OD1	24:4:86:VAL:N	2.31	0.63
32:R:415:LEU:C	32:R:417:ASN:H	2.05	0.63
1:A:109:PRO:HD3	1:A:630:TRP:CZ2	2.33	0.63
3:C:77:VAL:HG12	33:T:196:LEU:O	1.70	0.63
5:E:119:THR:HG23	5:E:161:ARG:HB3	1.80	0.63
13:F:35:A:H2'	13:F:36:A:C5'	2.28	0.63
23:3:931:VAL:N	23:3:936:LYS:O	2.29	0.63
25:5:20:ILE:HG12	25:5:63:VAL:HG22	1.78	0.63
1:A:305:ARG:HD3	3:C:933:PHE:HZ	1.64	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:695:ASP:CG	33:T:374:SER:OG	2.41	0.63
1:A:755:HIS:CD2	31:P:219:PHE:HE2	2.15	0.63
3:C:78:GLU:CD	33:T:198:ARG:HE	2.07	0.63
13:F:58:G:H2'	13:F:59:G:C8	2.32	0.63
7:i:85:PRO:C	18:w:184:ARG:HA	2.24	0.63
23:3:86:ARG:HA	23:3:105:GLU:O	1.98	0.63
23:3:174:ASP:OD2	23:3:240:GLY:N	2.31	0.63
23:3:489:GLU:HG2	23:3:748:GLU:HB3	1.80	0.63
35:X:241:GLY:N	35:X:262:TYR:O	2.31	0.63
1:A:44:ARG:HD2	1:A:45:TYR:CZ	2.34	0.63
3:C:129:ILE:CG2	3:C:199:LEU:HB3	2.27	0.63
3:C:295:ASP:OD1	3:C:297:ASN:N	2.32	0.63
3:C:456:GLY:O	3:C:457:VAL:HG22	1.99	0.63
13:F:36:A:C5'	13:F:36:A:H8	2.12	0.63
31:P:210:PHE:HD2	33:T:455:GLN:CD	2.05	0.63
32:R:132:LEU:HD23	32:R:132:LEU:H	1.63	0.63
1:A:251:ASP:HB3	1:A:337:VAL:CG2	2.25	0.63
1:A:468:LYS:HD3	1:A:469:LYS:H	1.61	0.63
1:A:1852:LEU:HD12	1:A:1853:PRO:HD2	1.80	0.63
3:C:137:HIS:NE2	3:C:236:MET:HE2	2.14	0.63
23:3:794:SER:OG	23:3:796:ASN:OD1	2.15	0.63
32:R:123:GLU:OE1	32:R:124:VAL:N	2.30	0.63
1:A:97:HIS:CD2	1:A:473:PHE:CZ	2.87	0.63
1:A:1260:VAL:HG21	1:A:1325:LEU:HB3	1.80	0.63
1:A:1787:ARG:NH2	1:A:1804:ASN:O	2.31	0.63
5:E:178:LEU:HD21	5:E:208:ILE:CD1	2.28	0.63
15:H:47:U:H1'	15:H:48:A:C8	2.34	0.63
21:1:812:PRO:HB2	21:1:813:PRO:HD3	1.81	0.63
23:3:1182:PHE:HA	23:3:1185:MET:HE2	1.81	0.63
25:5:23:ILE:HD12	25:5:89:VAL:HG12	1.81	0.63
1:A:331:TRP:CZ3	3:C:179:VAL:HG22	2.33	0.63
1:A:693:ILE:HG13	1:A:738:MET:SD	2.38	0.63
1:A:1000:ILE:HG22	1:A:1001:VAL:HG13	1.81	0.63
3:C:93:ILE:CD1	33:T:230:ILE:HD13	2.29	0.63
3:C:476:CYS:CB	3:C:565:ILE:HB	2.27	0.63
7:i:85:PRO:CA	18:w:184:ARG:O	2.47	0.63
21:1:698:GLN:O	21:1:702:ARG:NH1	2.32	0.63
23:3:399:ASP:OD1	23:3:400:GLU:N	2.32	0.63
23:3:521:PRO:HA	23:3:544:ILE:HG22	1.81	0.63
32:R:67:ILE:HD13	32:R:67:ILE:N	2.13	0.63
1:A:155:LYS:NZ	1:A:624:GLY:O	2.29	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:259:LYS:HE2	3:C:262:ARG:HD3	1.79	0.63
13:F:26:U:C3'	13:F:27:A:H5''	2.29	0.63
13:F:40:U:H2'	13:F:41:A:H8	1.61	0.63
32:R:418:GLN:O	37:Z:606:ALA:HB2	1.97	0.63
1:A:768:ASP:HB2	1:A:771:VAL:HG12	1.79	0.62
3:C:250:ARG:NE	3:C:451:HIS:NE2	2.47	0.62
5:E:265:ARG:H	5:E:272:ARG:HH21	1.47	0.62
15:H:179:C:C2	15:H:180:G:N7	2.67	0.62
32:R:250:LYS:HD3	32:R:251:ILE:N	2.13	0.62
34:V:549:LYS:O	34:V:552:ALA:N	2.32	0.62
37:Z:566:TYR:HB2	37:Z:581:GLY:O	1.98	0.62
1:A:1085:ILE:HG12	1:A:1099:PHE:CE1	2.34	0.62
2:B:47:A:HO2'	2:B:48:A:H8	1.47	0.62
5:E:251:LEU:HG	5:E:291:CYS:SG	2.39	0.62
1:A:203:VAL:HG21	1:A:237:THR:HG22	1.81	0.62
1:A:312:TYR:CE1	3:C:882:GLY:O	2.52	0.62
1:A:312:TYR:CE1	3:C:882:GLY:HA3	2.28	0.62
3:C:64:LYS:HZ2	31:P:206:LYS:HG3	1.62	0.62
3:C:79:THR:HG23	33:T:199:VAL:HB	0.68	0.62
21:1:1010:THR:OG1	21:1:1011:PRO:HD3	1.98	0.62
1:A:299:ILE:HD11	3:C:920:PRO:C	2.25	0.62
1:A:395:THR:HG23	3:C:383:GLN:HE22	1.58	0.62
1:A:417:ARG:NH1	2:B:58:U:H5''	2.14	0.62
1:A:755:HIS:ND1	31:P:223:PHE:CD2	2.60	0.62
1:A:1301:ILE:HD11	1:A:1306:LYS:CE	2.25	0.62
3:C:360:ALA:N	3:C:361:PRO:HD3	2.14	0.62
15:H:45:C:H42	18:w:395:TRP:NE1	1.81	0.62
21:1:1257:PRO:HG3	22:2:482:ALA:HB2	1.81	0.62
23:3:553:GLN:NE2	23:3:565:TYR:OH	2.31	0.62
37:Z:566:TYR:CD2	37:Z:584:TRP:CE3	2.88	0.62
1:A:386:PRO:CD	3:C:372:PHE:HE1	2.07	0.62
3:C:132:VAL:HG11	3:C:434:CYS:SG	2.39	0.62
23:3:27:GLN:OE1	23:3:42:ARG:NH1	2.32	0.62
23:3:380:GLU:O	23:3:383:ASP:N	2.32	0.62
31:P:188:TRP:O	31:P:189:ASP:C	2.42	0.62
31:P:188:TRP:C	31:P:190:ASP:N	2.52	0.62
32:R:250:LYS:HA	32:R:250:LYS:HE3	1.81	0.62
33:T:185:MET:HB3	33:T:186:PRO:HD3	1.81	0.62
1:A:755:HIS:HE1	31:P:223:PHE:CG	2.11	0.62
3:C:259:LYS:HG2	3:C:262:ARG:HD2	1.81	0.62
15:H:182:U:H2'	15:H:183:G:C8	2.34	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:273:ARG:O	23:3:386:PHE:HA	2.00	0.62
1:A:361:HIS:CD2	3:C:279:ARG:NH1	2.68	0.62
1:A:393:LEU:HD11	3:C:378:TYR:HB2	1.81	0.62
1:A:414:ARG:HD3	3:C:410:LEU:O	1.99	0.62
1:A:800:TYR:CG	3:C:59:LEU:HD13	2.34	0.62
1:A:2105:ILE:HD13	1:A:2266:ARG:HH22	1.64	0.62
5:E:119:THR:HG21	5:E:161:ARG:HB3	1.72	0.62
23:3:440:HIS:CD2	23:3:733:PRO:CD	2.82	0.62
23:3:567:GLU:OE2	23:3:601:ARG:NE	2.29	0.62
31:P:211:VAL:HG13	33:T:457:GLY:HA3	0.75	0.62
32:R:171:LEU:HD12	32:R:201:GLU:CD	2.25	0.62
33:T:351:ASP:C	33:T:352:THR:HG1	2.05	0.62
33:T:356:LEU:HD12	33:T:356:LEU:N	2.15	0.62
1:A:50:LYS:O	1:A:51:PHE:C	2.43	0.62
5:E:146:ARG:CZ	5:E:148:LYS:HE3	2.27	0.62
21:1:847:ALA:O	21:1:851:SER:HB3	1.99	0.62
23:3:440:HIS:CE1	23:3:720:TRP:CH2	2.87	0.62
37:Z:600:ARG:HH11	37:Z:600:ARG:CG	2.13	0.62
1:A:155:LYS:HD2	1:A:626:GLY:O	2.00	0.62
1:A:303:ILE:HG21	3:C:933:PHE:CE1	2.34	0.62
1:A:344:ASP:OD1	1:A:347:LEU:HD12	2.00	0.62
1:A:762:ARG:NH2	31:P:226:LYS:HZ1	1.79	0.62
1:A:2328:ALA:HB3	4:D:788:GLY:CA	2.30	0.62
15:H:154:C:H2'	15:H:155:C:H6	1.63	0.62
15:H:161:U:H6	15:H:161:U:O5'	1.83	0.62
21:1:664:GLY:HA2	21:1:667:ILE:HD12	1.80	0.62
21:1:696:ASP:OD1	21:1:697:GLU:N	2.33	0.62
21:1:1052:ALA:HA	21:1:1055:TRP:HD1	1.64	0.62
22:2:612:GLU:O	22:2:615:ILE:N	2.33	0.62
23:3:642:ILE:O	23:3:703:ARG:NH2	2.32	0.62
28:J:406:PHE:CE2	28:J:411:MET:CE	2.83	0.62
1:A:141:ILE:HG12	1:A:426:LEU:CD2	2.30	0.62
1:A:173:GLU:CD	38:z:7:GLN:CB	2.72	0.62
3:C:230:ASP:OD1	3:C:259:LYS:HB3	2.00	0.62
4:D:754:GLU:CB	23:3:662:PHE:CE1	2.83	0.62
25:5:53:THR:OG1	25:5:56:THR:OG1	2.14	0.62
1:A:256:TYR:CD1	3:C:888:ARG:CZ	2.83	0.61
1:A:329:LEU:CD1	3:C:173:THR:HG23	2.30	0.61
1:A:835:ASP:OD1	1:A:836:THR:N	2.32	0.61
5:E:277:PHE:HE2	5:E:300:ILE:HD12	1.63	0.61
17:p:194:PHE:O	17:p:196:ASN:N	2.33	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:811:THR:OG1	23:3:884:GLN:OE1	2.14	0.61
23:3:1004:ASP:OD1	23:3:1005:VAL:N	2.33	0.61
1:A:260:LEU:CD2	1:A:455:VAL:HG22	2.30	0.61
1:A:2068:SER:HB2	1:A:2072:GLU:HB2	1.81	0.61
13:F:24:A:C2	13:F:26:U:C2	2.88	0.61
14:G:13:C:H2'	14:G:14:A:C8	2.36	0.61
21:1:624:VAL:O	21:1:628:THR:OG1	2.14	0.61
23:3:786:ARG:NH1	23:3:802:THR:O	2.33	0.61
28:J:262:ARG:HD3	29:L:220:PRO:HG2	1.82	0.61
37:Z:597:ARG:HH12	37:Z:601:LEU:HD12	1.66	0.61
1:A:783:TYR:HB2	31:P:228:ILE:CG1	2.26	0.61
3:C:619:THR:C	3:C:620:LYS:HG3	2.25	0.61
13:F:38:G:P	13:F:38:G:C8	2.94	0.61
21:1:866:LYS:HG3	21:1:909:VAL:HG11	1.82	0.61
23:3:317:THR:HA	23:3:322:VAL:HA	1.81	0.61
1:A:203:VAL:CG2	1:A:237:THR:HB	2.30	0.61
1:A:1900:GLU:HG2	37:Z:521:PRO:HG3	1.82	0.61
14:G:146:C:H1'	15:H:33:G:N2	2.15	0.61
15:H:165:A:H8	15:H:165:A:O5'	1.84	0.61
32:R:55:LEU:O	32:R:73:PRO:O	2.19	0.61
35:X:343:ARG:HB3	35:X:378:GLU:HG3	1.83	0.61
37:Z:566:TYR:CD1	37:Z:567:SER:N	2.69	0.61
1:A:378:PHE:C	1:A:379:GLU:HG2	2.25	0.61
1:A:2106:LEU:HD12	1:A:2107:PRO:HD2	1.83	0.61
3:C:679:PRO:HD3	3:C:811:THR:OG1	1.99	0.61
15:H:56:A:H61	22:2:505:CYS:HA	1.66	0.61
15:H:68:G:H2'	15:H:69:U:C6	2.35	0.61
21:1:648:LEU:O	21:1:651:VAL:N	2.33	0.61
23:3:288:VAL:HG23	23:3:289:CYS:H	1.65	0.61
23:3:994:GLN:NE2	23:3:1036:ALA:O	2.33	0.61
33:T:327:SER:O	33:T:357:TRP:CH2	2.53	0.61
1:A:158:ARG:HH12	1:A:573:GLN:HE21	1.48	0.61
3:C:97:VAL:HG13	31:P:47:THR:OG1	2.00	0.61
3:C:140:HIS:CG	3:C:230:ASP:H	2.18	0.61
3:C:809:ILE:HB	3:C:810:PRO:HD3	1.82	0.61
23:3:1191:LYS:NZ	23:3:1195:GLU:OE2	2.33	0.61
1:A:349:ALA:HB1	1:A:399:ALA:HB2	1.78	0.61
2:B:43:U:H3	14:G:-4:A:H2	1.45	0.61
3:C:471:ASP:N	3:C:499:GLY:HA2	2.15	0.61
3:C:495:ARG:HD2	3:C:497:LEU:HD23	1.81	0.61
21:1:720:GLY:N	23:3:216:GLY:O	2.29	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:185:GLY:O	32:R:186:VAL:HG22	2.00	0.61
33:T:339:GLN:NE2	33:T:342:GLU:O	2.34	0.61
34:V:537:HIS:HA	34:V:578:SER:CB	2.31	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CD1	2.88	0.61
1:A:283:VAL:HG13	1:A:284:ARG:H	1.64	0.61
1:A:1286:ASP:OD1	1:A:1354:ARG:NH2	2.33	0.61
3:C:151:GLU:OE1	3:C:417:ARG:NH1	2.34	0.61
3:C:470:PRO:HA	3:C:499:GLY:CA	2.29	0.61
3:C:675:PHE:HD1	3:C:675:PHE:H	1.47	0.61
3:C:701:GLU:HA	3:C:740:THR:HG1	1.65	0.61
14:G:8:C:H2'	14:G:9:C:C6	2.35	0.61
15:H:106:G:N2	15:H:107:A:C6	2.67	0.61
15:H:142:C:C2'	15:H:143:A:H5'	2.30	0.61
15:H:157:G:H5''	15:H:157:G:H8	1.65	0.61
28:J:408:ASP:OD1	28:J:442:ARG:HG2	2.01	0.61
3:C:478:THR:OG1	3:C:563:ALA:O	2.14	0.61
3:C:705:VAL:HG22	3:C:705:VAL:O	2.00	0.61
15:H:153:A:N6	15:H:177:A:H2	1.98	0.61
21:1:608:THR:O	21:1:612:THR:OG1	2.15	0.61
23:3:452:LEU:HB3	23:3:478:PHE:HE1	1.66	0.61
29:L:74:LEU:HD23	29:L:77:LEU:HD12	1.83	0.61
36:Y:87:GLN:O	36:Y:90:THR:N	2.33	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CG	2.89	0.61
1:A:402:ILE:CG1	3:C:385:VAL:HG21	2.25	0.61
5:E:108:HIS:CE1	5:E:128:SER:HB2	2.35	0.61
13:F:6:C:OP2	13:F:6:C:H4'	1.99	0.61
21:1:1203:GLY:O	23:3:1171:LYS:NZ	2.34	0.61
23:3:226:GLU:HG3	23:3:261:PHE:HZ	1.65	0.61
24:4:71:ILE:HD11	24:4:88:LYS:HB3	1.83	0.61
32:R:241:MET:HE2	32:R:241:MET:HA	1.82	0.61
33:T:349:SER:OG	33:T:351:ASP:OD1	2.18	0.61
1:A:122:ILE:N	1:A:481:PHE:O	2.34	0.60
1:A:1405:LEU:HA	32:R:415:LEU:HD21	1.78	0.60
3:C:133:THR:O	3:C:226:VAL:HB	2.01	0.60
3:C:135:CYS:O	3:C:228:PHE:N	2.28	0.60
3:C:449:ILE:HD11	3:C:466:SER:CA	2.31	0.60
3:C:710:ASN:O	3:C:713:LYS:N	2.31	0.60
15:H:143:A:H2'	15:H:144:C:C6	2.35	0.60
21:1:1293:ASN:HB3	27:7:76:CYS:HB3	1.83	0.60
37:Z:524:ARG:NE	37:Z:524:ARG:O	2.34	0.60
1:A:121:HIS:CE1	1:A:481:PHE:CB	2.68	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:800:TYR:CD2	3:C:59:LEU:HD13	2.36	0.60
1:A:1457:HIS:CE1	1:A:1459:ARG:CB	2.83	0.60
13:F:26:U:O2'	13:F:27:A:OP1	2.18	0.60
21:1:918:VAL:HG12	21:1:961:VAL:HG21	1.83	0.60
23:3:505:THR:HG21	23:3:508:CYS:SG	2.40	0.60
28:J:338:GLU:O	32:R:116:TYR:CD1	2.54	0.60
37:Z:491:ASP:O	37:Z:495:ALA:CB	2.48	0.60
1:A:387:PHE:CZ	3:C:330:THR:HB	2.35	0.60
28:J:291:GLN:OE1	29:L:230:GLU:HG3	2.01	0.60
33:T:339:GLN:HG2	33:T:340:ALA:N	2.16	0.60
37:Z:491:ASP:O	37:Z:495:ALA:HB2	2.01	0.60
37:Z:612:TYR:O	37:Z:613:LYS:C	2.43	0.60
1:A:82:ARG:HB3	1:A:83:HIS:ND1	2.17	0.60
1:A:301:LYS:HG2	3:C:940:ARG:CA	2.31	0.60
14:G:13:C:H2'	14:G:14:A:H8	1.66	0.60
23:3:441:GLY:O	23:3:775:ASN:HB2	2.00	0.60
24:4:31:GLU:O	24:4:35:GLN:HG2	2.02	0.60
33:T:292:TYR:CE2	33:T:308:ARG:HG3	2.36	0.60
1:A:351:TYR:HA	3:C:270:PRO:HG3	1.84	0.60
1:A:461:HIS:CD2	2:B:26:A:N6	2.68	0.60
1:A:664:HIS:HE1	1:A:668:VAL:CG2	2.04	0.60
1:A:1827:TRP:HH2	1:A:1837:ALA:HB2	1.67	0.60
1:A:2073:TRP:CZ3	1:A:2310:ARG:HG2	2.36	0.60
3:C:779:LEU:HB3	3:C:934:MET:HE1	1.83	0.60
5:E:178:LEU:HD21	5:E:208:ILE:HD13	1.82	0.60
23:3:833:GLU:HA	23:3:834:LEU:HB2	1.84	0.60
29:L:233:GLN:OE1	29:L:233:GLN:HA	2.01	0.60
37:Z:573:PRO:HD2	37:Z:573:PRO:O	1.99	0.60
1:A:91:ALA:O	1:A:92:LEU:C	2.45	0.60
1:A:392:PRO:O	3:C:379:LYS:HG2	2.01	0.60
1:A:1447:VAL:HG11	1:A:1449:LYS:HE2	1.82	0.60
3:C:86:THR:HG22	33:T:238:LEU:O	2.01	0.60
3:C:452:THR:HG22	3:C:577:PHE:CG	2.37	0.60
3:C:706:GLN:NE2	3:C:708:THR:OG1	2.35	0.60
18:w:422:PHE:HZ	18:w:450:THR:HG22	1.67	0.60
34:V:483:GLU:O	34:V:486:THR:CB	2.49	0.60
1:A:344:ASP:OD1	1:A:347:LEU:CD1	2.49	0.60
1:A:924:GLN:HE22	1:A:1439:ARG:CZ	2.14	0.60
3:C:221:ILE:HD11	3:C:479:THR:HG1	1.65	0.60
3:C:456:GLY:C	3:C:457:VAL:HG13	2.25	0.60
14:G:130:A:H5''	18:w:396:LEU:CD2	2.32	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:898:ASN:OD1	23:3:899:THR:N	2.34	0.60
1:A:384:VAL:HG12	3:C:331:PHE:HB3	0.71	0.60
1:A:705:LYS:HE2	32:R:251:ILE:HB	1.82	0.60
1:A:960:ASN:ND2	1:A:1225:THR:OG1	2.32	0.60
1:A:2298:LEU:CD1	4:D:1265:GLN:CB	2.79	0.60
3:C:77:VAL:HG21	33:T:196:LEU:HD23	1.83	0.60
3:C:148:CYS:HA	3:C:417:ARG:NH2	2.16	0.60
23:3:325:ILE:O	23:3:375:SER:N	2.35	0.60
33:T:267:ASP:O	33:T:268:LYS:CB	2.47	0.60
33:T:455:GLN:HG2	33:T:456:PRO:HD3	1.83	0.60
1:A:661:GLU:HG3	32:R:210:PRO:CB	2.32	0.60
3:C:140:HIS:HA	3:C:230:ASP:HB2	1.83	0.60
3:C:567:GLU:OE2	3:C:570:GLY:HA3	2.02	0.60
13:F:7:G:H5'	13:F:7:G:H8	1.66	0.60
13:F:37:C:H41	14:G:5:G:P	2.24	0.60
15:H:83:A:C2	15:H:84:C:C2	2.90	0.60
29:L:77:LEU:HD22	32:R:289:ALA:HA	1.84	0.60
33:T:342:GLU:HB3	33:T:343:PRO:HD3	1.83	0.60
37:Z:563:ARG:HH21	37:Z:563:ARG:CG	2.14	0.60
38:z:56:ARG:HB3	38:z:64:GLN:HB3	1.84	0.60
1:A:1384:ARG:HH21	1:A:1414:ARG:HH12	1.50	0.60
1:A:1426:ASP:OD2	32:R:421:GLY:HA3	2.01	0.60
3:C:79:THR:CG2	33:T:199:VAL:CB	2.37	0.60
3:C:82:GLN:HB2	33:T:231:TRP:CZ3	2.36	0.60
3:C:94:ILE:CD1	31:P:44:ARG:NH2	2.65	0.60
3:C:443:VAL:O	3:C:447:PRO:HD3	2.02	0.60
3:C:516:LEU:HD13	3:C:516:LEU:C	2.26	0.60
3:C:678:THR:CG2	3:C:683:ASN:CB	2.79	0.60
18:w:411:CYS:HG	18:w:425:HIS:CE1	2.19	0.60
21:1:862:GLU:OE1	21:1:904:THR:OG1	2.19	0.60
23:3:457:ASN:ND2	23:3:478:PHE:O	2.35	0.60
32:R:106:GLN:HG2	32:R:110:LYS:CE	2.28	0.60
33:T:185:MET:SD	33:T:442:ARG:NH1	2.71	0.60
23:3:968:ARG:HD3	23:3:979:ARG:HD3	1.84	0.59
1:A:329:LEU:HD13	3:C:173:THR:HG23	1.82	0.59
1:A:715:GLU:CD	32:R:258:TRP:CZ3	2.79	0.59
3:C:73:TYR:CD2	33:T:199:VAL:HG21	2.36	0.59
3:C:73:TYR:CZ	33:T:487:LYS:HE3	2.37	0.59
3:C:669:THR:HG22	3:C:690:GLU:HB3	1.84	0.59
31:P:72:ARG:HB2	31:P:72:ARG:HH11	1.66	0.59
33:T:455:GLN:HG2	33:T:456:PRO:CD	2.32	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:MET:CE	1:A:628:GLY:C	2.75	0.59
1:A:718:ARG:HE	32:R:259:LYS:HE3	1.67	0.59
3:C:186:VAL:HG22	3:C:535:ALA:HA	1.85	0.59
5:E:114:GLU:CD	5:E:116:HIS:HE2	2.09	0.59
23:3:883:GLU:HG3	23:3:884:GLN:H	1.66	0.59
32:R:104:GLN:NE2	32:R:105:GLY:N	2.50	0.59
2:B:64:G:H5'	5:E:106:LYS:HZ2	1.65	0.59
5:E:233:GLY:O	5:E:260:ARG:NH2	2.35	0.59
14:G:22:C:O2'	14:G:23:U:P	2.60	0.59
28:J:493:ALA:HB1	28:J:499:ARG:CB	2.32	0.59
31:P:228:ILE:O	31:P:229:LYS:C	2.45	0.59
32:R:74:LEU:HD23	32:R:74:LEU:C	2.27	0.59
32:R:124:VAL:HG22	32:R:125:MET:N	2.16	0.59
32:R:420:LYS:HA	32:R:420:LYS:CE	2.12	0.59
1:A:398:THR:HG23	3:C:382:ALA:CB	2.32	0.59
1:A:944:ASP:OD2	1:A:1435:GLY:N	2.34	0.59
1:A:1262:LYS:CG	32:R:431:ASP:CB	2.69	0.59
1:A:1405:LEU:HA	32:R:415:LEU:HD22	1.84	0.59
1:A:1962:THR:O	37:Z:524:ARG:HG3	2.02	0.59
3:C:298:LEU:HD13	3:C:298:LEU:N	2.18	0.59
15:H:56:A:H2'	15:H:57:A:C8	2.38	0.59
18:w:485:ASN:HB3	23:3:978:LEU:HD23	1.83	0.59
23:3:895:ARG:NH2	23:3:901:GLU:OE1	2.34	0.59
23:3:1040:ASP:OD1	23:3:1043:THR:N	2.35	0.59
34:V:514:PHE:O	34:V:521:TYR:CB	2.51	0.59
1:A:181:ASN:N	1:A:181:ASN:OD1	2.35	0.59
1:A:692:ASP:O	1:A:696:MET:CB	2.50	0.59
1:A:942:PRO:HB2	1:A:1438:VAL:HG12	1.84	0.59
1:A:1076:ASP:OD1	1:A:1077:ILE:N	2.35	0.59
1:A:1363:GLN:HG2	1:A:1364:LEU:H	1.66	0.59
3:C:66:TYR:HE2	31:P:211:VAL:HG11	1.67	0.59
3:C:91:GLU:OE1	3:C:91:GLU:HA	2.01	0.59
3:C:145:PHE:CB	3:C:312:SER:CB	2.65	0.59
13:F:36:A:C5'	13:F:36:A:C8	2.85	0.59
15:H:112:G:H2'	15:H:113:G:H8	1.65	0.59
21:1:936:VAL:O	21:1:940:LEU:HB2	2.03	0.59
21:1:1125:PRO:HA	21:1:1128:VAL:HG22	1.84	0.59
23:3:740:GLU:HB2	23:3:757:ILE:HD12	1.83	0.59
33:T:345:ILE:HB	33:T:357:TRP:HB2	1.85	0.59
1:A:86:ARG:HG3	1:A:87:VAL:N	2.17	0.59
1:A:132:ILE:HD13	2:B:57:G:OP1	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:SER:HB3	3:C:299:ILE:HD12	1.85	0.59
1:A:1405:LEU:CB	32:R:415:LEU:HD22	2.33	0.59
1:A:2095:ASP:OD2	1:A:2258:ARG:NE	2.36	0.59
3:C:149:LEU:CD1	3:C:427:PHE:CB	2.80	0.59
23:3:224:TYR:HB3	23:3:261:PHE:HE2	1.66	0.59
23:3:1015:LYS:HE2	23:3:1065:GLU:HG2	1.85	0.59
28:J:225:LEU:CD2	29:L:211:ASN:HB2	2.20	0.59
32:R:90:VAL:CG1	32:R:94:GLY:O	2.50	0.59
36:Y:88:ARG:HH11	37:Z:576:PHE:HB3	1.68	0.59
1:A:44:ARG:CG	1:A:45:TYR:CD2	2.85	0.59
1:A:417:ARG:NH1	2:B:58:U:C4'	2.65	0.59
1:A:569:VAL:O	1:A:570:ASP:CB	2.50	0.59
1:A:888:GLN:NE2	1:A:890:ALA:O	2.19	0.59
1:A:1199:LYS:NZ	1:A:1206:GLU:OE2	2.32	0.59
3:C:227:LEU:O	3:C:255:VAL:HA	2.03	0.59
23:3:613:THR:HG22	23:3:632:ALA:HA	1.84	0.59
23:3:784:THR:HB	23:3:786:ARG:HH12	1.67	0.59
23:3:1027:ASP:OD1	23:3:1028:THR:N	2.35	0.59
26:6:56:GLY:O	26:6:65:GLY:N	2.21	0.59
31:P:63:LEU:HD23	31:P:63:LEU:C	2.28	0.59
32:R:420:LYS:HG2	32:R:423:ASP:OD1	2.02	0.59
32:R:421:GLY:O	32:R:423:ASP:N	2.35	0.59
1:A:122:ILE:HD13	1:A:483:GLN:CG	2.32	0.59
1:A:303:ILE:HG21	3:C:933:PHE:CD1	2.38	0.59
2:B:44:A:C2	14:G:-5:G:C6	2.89	0.59
3:C:137:HIS:CD2	3:C:236:MET:HB3	2.35	0.59
3:C:497:LEU:HD11	3:C:577:PHE:CZ	2.32	0.59
21:1:1223:SER:HB2	21:1:1226:VAL:HG12	1.83	0.59
3:C:145:PHE:CE1	3:C:427:PHE:CE1	2.91	0.59
3:C:230:ASP:CG	3:C:259:LYS:NZ	2.61	0.59
3:C:465:MET:CE	3:C:475:MET:CG	2.70	0.59
3:C:736:GLY:HA2	3:C:770:PHE:CE2	2.38	0.59
13:F:45:A:H1'	13:F:73:A:C2	2.38	0.59
21:1:522:LYS:HD3	21:1:526:PHE:CZ	2.38	0.59
23:3:22:PHE:HD2	23:3:29:GLU:HB2	1.68	0.59
23:3:587:VAL:HG11	23:3:590:MET:HG3	1.85	0.59
28:J:259:GLN:HE22	29:L:220:PRO:CG	2.15	0.59
32:R:125:MET:CE	32:R:131:ASP:OD1	2.51	0.59
32:R:148:ARG:HG3	32:R:148:ARG:HH11	1.68	0.59
1:A:44:ARG:HG3	1:A:45:TYR:CD2	2.37	0.58
1:A:480:LYS:CD	32:R:203:GLN:OE1	2.50	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:723:ASN:HB2	1:A:785:LYS:HG2	1.83	0.58
3:C:69:ALA:CA	33:T:456:PRO:HG3	2.28	0.58
3:C:359:LYS:HE3	3:C:359:LYS:O	2.02	0.58
13:F:35:A:O2'	13:F:36:A:OP1	2.21	0.58
21:1:1278:ASP:OD2	23:3:112:CYS:N	2.36	0.58
22:2:648:LEU:HD11	22:2:650:ILE:HG13	1.85	0.58
23:3:336:ALA:HA	23:3:351:SER:HA	1.85	0.58
23:3:440:HIS:C	23:3:733:PRO:HG2	2.28	0.58
23:3:463:ARG:HB2	23:3:510:LEU:HD22	1.85	0.58
28:J:339:TRP:CG	32:R:116:TYR:HD2	2.21	0.58
33:T:185:MET:SD	33:T:442:ARG:NH2	2.75	0.58
36:Y:52:ILE:HA	36:Y:55:VAL:HG22	1.84	0.58
1:A:2073:TRP:CD1	1:A:2074:ARG:N	2.71	0.58
1:A:2073:TRP:HD1	1:A:2074:ARG:HD2	1.67	0.58
1:A:2268:LEU:HD22	4:D:1261:PRO:O	1.96	0.58
3:C:474:LEU:HD11	3:C:501:ILE:HG12	1.85	0.58
21:1:982:LEU:HD11	21:1:997:LEU:HD11	1.83	0.58
21:1:1147:VAL:O	21:1:1150:SER:OG	2.17	0.58
23:3:417:ASN:OD1	23:3:418:GLU:N	2.36	0.58
23:3:673:VAL:HG12	23:3:690:ARG:HA	1.84	0.58
23:3:797:LEU:HG	23:3:871:PRO:HG3	1.85	0.58
23:3:903:TRP:HB3	23:3:930:LEU:HD23	1.84	0.58
32:R:433:ILE:CD1	32:R:435:ASN:ND2	2.67	0.58
36:Y:86:ASP:CB	37:Z:502:ALA:HB3	2.33	0.58
39:x:418:LEU:HA	39:x:567:ALA:HB1	1.84	0.58
1:A:32:GLU:OE2	1:A:36:LYS:HE3	2.03	0.58
1:A:305:ARG:HD3	3:C:933:PHE:CE1	2.38	0.58
1:A:316:PHE:HE1	3:C:635:LEU:HA	1.67	0.58
3:C:133:THR:O	3:C:226:VAL:CA	2.51	0.58
5:E:87:ASP:O	5:E:88:ARG:HG3	2.04	0.58
18:w:444:ALA:O	18:w:445:HIS:C	2.45	0.58
21:1:773:LEU:HD21	21:1:792:VAL:HG22	1.84	0.58
23:3:304:GLN:NE2	23:3:335:VAL:HA	2.18	0.58
23:3:638:GLU:H	23:3:669:LEU:HA	1.68	0.58
32:R:233:HIS:CD2	32:R:233:HIS:H	2.22	0.58
34:V:497:CYS:CB	34:V:507:PHE:CB	2.81	0.58
1:A:480:LYS:CE	32:R:203:GLN:OE1	2.50	0.58
1:A:657:ALA:HA	32:R:210:PRO:HG2	1.84	0.58
1:A:849:ALA:O	1:A:1449:LYS:NZ	2.36	0.58
1:A:1180:LYS:HA	1:A:1201:ARG:NH1	2.18	0.58
3:C:679:PRO:HD2	3:C:807:GLN:CB	2.10	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:440:HIS:O	23:3:718:ARG:NH2	2.36	0.58
28:J:338:GLU:O	32:R:116:TYR:CG	2.57	0.58
1:A:388:LEU:HD11	3:C:399:LEU:CG	2.31	0.58
1:A:1367:ASN:OD1	1:A:1368:LEU:N	2.37	0.58
1:A:1900:GLU:OE1	37:Z:522:LEU:HB3	2.00	0.58
3:C:750:LEU:O	3:C:750:LEU:HD12	2.03	0.58
5:E:263:ASP:HB3	5:E:274:VAL:HG21	1.84	0.58
37:Z:566:TYR:CD2	37:Z:584:TRP:HE3	2.20	0.58
1:A:60:ASP:OD1	1:A:60:ASP:N	2.36	0.58
1:A:229:GLN:HA	1:A:415:SER:HA	1.85	0.58
1:A:357:ASN:HB2	3:C:863:ILE:O	2.04	0.58
1:A:1863:VAL:HG11	1:A:1868:MET:HB2	1.84	0.58
1:A:2310:ARG:NH1	1:A:2314:PHE:HE1	2.02	0.58
5:E:87:ASP:O	5:E:88:ARG:CB	2.51	0.58
23:3:224:TYR:HB3	23:3:261:PHE:CE2	2.39	0.58
24:4:18:GLY:H	24:4:85:ARG:HB2	1.67	0.58
31:P:35:LEU:HB3	31:P:36:PRO:HD2	1.86	0.58
31:P:224:MET:HE2	31:P:228:ILE:HD13	1.85	0.58
32:R:82:MET:HE3	32:R:82:MET:O	2.04	0.58
34:V:609:GLN:O	34:V:612:PHE:N	2.36	0.58
1:A:303:ILE:CG2	3:C:933:PHE:CD1	2.87	0.58
1:A:329:LEU:HB3	3:C:177:ARG:CZ	2.33	0.58
1:A:798:GLY:HA2	32:R:288:PHE:CE2	2.39	0.58
1:A:1962:THR:O	37:Z:524:ARG:HG2	2.03	0.58
1:A:2325:VAL:O	4:D:788:GLY:HA2	2.03	0.58
3:C:509:VAL:O	3:C:510:LEU:HD23	2.04	0.58
15:H:147:G:H2'	15:H:148:C:C6	2.38	0.58
30:M:196:ASP:O	30:M:198:GLN:N	2.36	0.58
1:A:76:MET:SD	1:A:88:TYR:CD2	2.95	0.58
1:A:280:GLU:OE2	1:A:281:PRO:HD2	2.03	0.58
1:A:392:PRO:CA	3:C:379:LYS:HE2	2.32	0.58
1:A:417:ARG:NH2	2:B:58:U:OP1	2.37	0.58
1:A:1757:GLU:OE1	32:R:451:ILE:CG1	2.36	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CG	2.66	0.58
15:H:80:A:C2	15:H:81:G:C5	2.92	0.58
23:3:461:THR:HA	23:3:473:TYR:O	2.03	0.58
25:5:24:ARG:HG2	25:5:59:THR:HG22	1.86	0.58
3:C:77:VAL:HG13	33:T:196:LEU:C	1.90	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CB	2.67	0.58
14:G:141:C:H2'	14:G:142:U:H6	1.69	0.58
21:1:415:LEU:O	25:5:36:TYR:OH	2.21	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1109:ARG:NH2	21:1:1142:ASN:HB2	2.19	0.58
21:1:1165:TYR:HE1	22:2:575:PHE:CD1	2.21	0.58
23:3:878:ASP:OD1	23:3:879:LEU:N	2.37	0.58
32:R:124:VAL:HG22	32:R:126:ASN:H	1.68	0.58
37:Z:566:TYR:HE2	37:Z:584:TRP:CZ3	1.92	0.58
1:A:378:PHE:HZ	3:C:335:ASN:CB	2.16	0.58
1:A:593:ARG:HH22	1:A:1551:PHE:CB	2.17	0.58
3:C:115:GLU:O	3:C:116:MET:C	2.43	0.58
3:C:573:GLU:N	3:C:573:GLU:OE1	2.37	0.58
17:p:152:ILE:O	17:p:223:ALA:N	2.36	0.58
23:3:8:LEU:HD23	23:3:774:PHE:HZ	1.68	0.58
23:3:753:GLY:CA	23:3:765:LEU:O	2.51	0.58
32:R:171:LEU:HD23	32:R:171:LEU:O	2.03	0.58
39:x:442:THR:O	39:x:446:MET:N	2.37	0.58
1:A:121:HIS:ND1	1:A:481:PHE:O	2.36	0.57
1:A:301:LYS:HG2	3:C:940:ARG:HA	1.85	0.57
3:C:145:PHE:CD1	3:C:312:SER:HB3	2.39	0.57
5:E:165:GLN:HG3	5:E:181:ILE:HD11	1.85	0.57
32:R:189:ASN:HD21	32:R:195:ARG:HH22	1.50	0.57
33:T:399:LYS:HG2	33:T:406:ILE:CD1	2.31	0.57
5:E:277:PHE:CE2	5:E:300:ILE:CD1	2.85	0.57
13:F:39:A:N6	14:G:8:C:H42	2.02	0.57
14:G:12:G:N2	14:G:13:C:O4'	2.38	0.57
18:w:478:GLU:N	23:3:978:LEU:CD1	2.66	0.57
23:3:440:HIS:CD2	23:3:733:PRO:HD2	2.39	0.57
23:3:781:LEU:HB3	23:3:801:GLU:OE2	2.04	0.57
1:A:152:ARG:HH11	1:A:152:ARG:CG	2.16	0.57
1:A:224:THR:CG2	2:B:13:C:OP2	2.52	0.57
1:A:384:VAL:HG13	3:C:332:GLY:H	1.67	0.57
3:C:749:THR:OG1	3:C:752:SER:HB2	2.04	0.57
35:X:285:ARG:NH1	35:X:304:ALA:O	2.35	0.57
1:A:82:ARG:NH1	14:G:16:G:O6	2.37	0.57
1:A:322:ASN:OD1	3:C:655:VAL:N	2.38	0.57
1:A:535:ARG:CZ	1:A:535:ARG:HB3	2.33	0.57
1:A:800:TYR:HB3	3:C:59:LEU:CD1	2.34	0.57
3:C:617:LEU:HD11	3:C:629:ILE:HG23	1.87	0.57
23:3:306:GLU:OE2	27:7:63:ARG:HG3	2.03	0.57
23:3:1050:PHE:HB3	23:3:1167:TYR:CE2	2.38	0.57
29:L:73:HIS:O	29:L:77:LEU:HG	2.04	0.57
1:A:1771:LEU:HD11	1:A:1777:ILE:HG21	1.86	0.57
3:C:79:THR:HG23	33:T:199:VAL:CG1	2.27	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:671:SER:C	3:C:672:LEU:HD22	2.30	0.57
21:1:850:ILE:O	21:1:854:VAL:HG23	2.04	0.57
23:3:136:GLU:OE2	23:3:189:TYR:OH	2.10	0.57
23:3:791:HIS:CE1	23:3:934:GLY:HA3	2.39	0.57
32:R:55:LEU:CB	32:R:73:PRO:O	2.53	0.57
1:A:785:LYS:CE	31:P:215:LEU:CD1	2.78	0.57
3:C:93:ILE:O	3:C:94:ILE:HB	2.04	0.57
3:C:572:GLU:O	3:C:573:GLU:HB2	2.04	0.57
3:C:669:THR:CG2	3:C:690:GLU:OE1	2.52	0.57
14:G:137:C:N4	15:H:40:C:H42	1.99	0.57
23:3:211:TYR:CE1	23:3:222:ARG:HG2	2.40	0.57
23:3:429:ARG:NH1	27:7:58:ASN:OD1	2.38	0.57
23:3:635:ALA:H	23:3:669:LEU:HD21	1.70	0.57
31:P:73:GLU:O	31:P:76:ARG:HG2	2.04	0.57
31:P:188:TRP:N	31:P:188:TRP:CE3	2.73	0.57
1:A:226:GLN:OE1	1:A:417:ARG:NE	2.31	0.57
1:A:356:ILE:HG22	1:A:357:ASN:N	2.20	0.57
1:A:461:HIS:NE2	2:B:26:A:N6	2.49	0.57
1:A:745:ALA:HB2	33:T:206:TRP:CZ2	2.40	0.57
1:A:783:TYR:CG	31:P:228:ILE:HG12	2.39	0.57
2:B:20:G:O6	2:B:24:G:OP1	2.21	0.57
3:C:140:HIS:HE2	3:C:233:GLU:HG3	1.68	0.57
15:H:166:G:OP2	15:H:166:G:N2	2.27	0.57
29:L:33:ARG:O	29:L:36:SER:OG	2.20	0.57
31:P:31:SER:N	31:P:34:ASP:OD2	2.37	0.57
34:V:483:GLU:O	34:V:486:THR:N	2.33	0.57
1:A:71:ARG:NH1	1:A:177:ASP:OD2	2.32	0.57
1:A:282:LEU:HD23	1:A:282:LEU:O	2.05	0.57
1:A:705:LYS:CG	32:R:251:ILE:HB	2.27	0.57
1:A:1370:ARG:NH1	34:V:467:LEU:CA	2.64	0.57
1:A:2153:THR:HG22	1:A:2154:HIS:H	1.70	0.57
3:C:78:GLU:CD	3:C:80:ILE:HD11	2.30	0.57
3:C:140:HIS:CE1	3:C:233:GLU:CB	2.83	0.57
3:C:487:GLY:HA3	3:C:489:GLN:OE1	2.05	0.57
3:C:490:PHE:HZ	3:C:612:LYS:HD2	1.69	0.57
3:C:511:GLY:O	3:C:576:ILE:HD12	2.02	0.57
15:H:148:C:O5'	15:H:148:C:H6	1.87	0.57
21:1:1109:ARG:HH22	21:1:1142:ASN:HB2	1.69	0.57
21:1:1258:ALA:HB3	21:1:1261:VAL:HG12	1.86	0.57
23:3:275:ARG:HE	23:3:386:PHE:HD2	1.51	0.57
32:R:434:TYR:CD2	32:R:435:ASN:N	2.73	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:V:489:LEU:O	34:V:492:MET:CB	2.53	0.57
1:A:178:TYR:CD2	1:A:491:GLU:HB2	2.40	0.57
1:A:692:ASP:CA	33:T:376:ARG:NH2	2.53	0.57
1:A:705:LYS:CG	32:R:251:ILE:CD1	2.70	0.57
1:A:1757:GLU:HG3	32:R:451:ILE:HG13	1.87	0.57
5:E:310:TYR:CE1	5:E:322:LYS:CD	2.86	0.57
15:H:45:C:H2'	18:w:394:TYR:CD2	2.40	0.57
15:H:152:G:N2	15:H:153:A:C5	2.73	0.57
21:1:1098:LEU:HD13	21:1:1135:GLU:HG3	1.85	0.57
21:1:1126:PHE:CE2	22:2:572:HIS:HA	2.39	0.57
28:J:224:LYS:HE2	28:J:255:LEU:HD13	1.85	0.57
37:Z:525:TYR:CD1	37:Z:526:ILE:N	2.73	0.57
38:z:103:ASN:HB2	38:z:108:ASP:HB3	1.87	0.57
39:x:940:ARG:O	39:x:944:THR:N	2.37	0.57
1:A:249:LEU:HD22	1:A:254:TYR:HB2	1.86	0.57
1:A:250:VAL:HG23	1:A:337:VAL:CB	2.32	0.57
1:A:434:HIS:CE1	1:A:435:CYS:SG	2.98	0.57
1:A:570:ASP:OD1	1:A:571:ALA:N	2.38	0.57
1:A:832:TYR:CE2	1:A:834:HIS:HB2	2.40	0.57
1:A:1113:TYR:C	1:A:1115:THR:H	2.13	0.57
3:C:78:GLU:O	33:T:198:ARG:C	2.47	0.57
3:C:508:LYS:HE3	3:C:566:THR:CG2	2.34	0.57
21:1:807:LYS:HA	21:1:811:LEU:HD12	1.87	0.57
21:1:942:ASN:HD22	21:1:947:VAL:HG11	1.70	0.57
23:3:442:LEU:CD1	23:3:733:PRO:O	2.50	0.57
33:T:347:THR:CG2	33:T:357:TRP:HE1	2.18	0.57
37:Z:611:ALA:O	37:Z:614:TRP:HB3	2.05	0.57
1:A:32:GLU:CG	1:A:36:LYS:HE3	2.35	0.56
1:A:393:LEU:CD1	3:C:375:GLU:O	2.53	0.56
1:A:844:GLU:CB	32:R:422:MET:HE2	2.22	0.56
3:C:261:ASP:OD1	41:C:1500:GTP:C6	2.57	0.56
28:J:270:ASP:OD2	32:R:222:PRO:CB	2.52	0.56
33:T:306:CYS:SG	33:T:336:VAL:CG1	2.93	0.56
1:A:89:LEU:HD13	1:A:660:PHE:CZ	2.41	0.56
1:A:385:GLU:HB3	1:A:386:PRO:HD2	1.86	0.56
1:A:790:ARG:NE	1:A:986:GLU:OE2	2.38	0.56
1:A:1233:ASP:OD1	1:A:1234:ASP:N	2.37	0.56
1:A:1252:GLY:HA2	1:A:1298:ARG:HH21	1.69	0.56
13:F:57:U:H2'	13:F:58:G:H8	1.69	0.56
14:G:7:G:H2'	14:G:8:C:C6	2.40	0.56
15:H:78:C:HO2'	15:H:79:G:H5'	1.70	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:141:C:C2	15:H:142:C:C5	2.94	0.56
23:3:327:LEU:O	23:3:373:PHE:HB2	2.05	0.56
23:3:478:PHE:O	23:3:504:PRO:HB3	2.05	0.56
28:J:273:TYR:CG	32:R:228:PRO:CG	2.88	0.56
32:R:409:VAL:O	32:R:410:GLN:HG2	2.05	0.56
37:Z:524:ARG:HB3	37:Z:524:ARG:CZ	2.35	0.56
1:A:296:PHE:CG	3:C:656:ALA:HB2	2.40	0.56
1:A:339:PHE:C	1:A:340:ILE:HD13	2.31	0.56
1:A:587:GLN:O	1:A:587:GLN:HG2	2.04	0.56
1:A:593:ARG:HH22	1:A:1551:PHE:HB3	1.71	0.56
1:A:1386:TRP:HZ2	1:A:1417:PRO:HB2	1.69	0.56
1:A:1548:TYR:CD2	1:A:1549:VAL:CG2	2.75	0.56
2:B:40:U:H3'	2:B:40:U:O2	2.05	0.56
3:C:426:GLU:O	3:C:427:PHE:HB2	2.05	0.56
3:C:449:ILE:CG2	3:C:457:VAL:HG11	2.30	0.56
5:E:250:LEU:CD2	5:E:262:TRP:HB2	2.35	0.56
15:H:152:G:N2	15:H:153:A:C8	2.73	0.56
21:1:847:ALA:O	21:1:851:SER:OG	2.24	0.56
22:2:643:PRO:CD	24:4:69:TYR:CG	2.88	0.56
23:3:438:LEU:HA	23:3:775:ASN:O	2.06	0.56
23:3:520:TYR:HB2	23:3:521:PRO:HD2	1.87	0.56
23:3:633:LEU:HD13	23:3:667:ILE:HG21	1.87	0.56
31:P:76:ARG:HG3	31:P:77:ASP:N	2.19	0.56
32:R:70:ALA:O	32:R:71:GLN:C	2.48	0.56
32:R:442:ARG:CD	32:R:443:GLY:C	2.77	0.56
1:A:1425:LYS:C	1:A:1425:LYS:HD3	2.31	0.56
3:C:223:ASP:OD1	3:C:495:ARG:NH2	2.38	0.56
3:C:457:VAL:HA	3:C:462:GLY:HA3	1.88	0.56
3:C:673:LYS:HG3	3:C:686:THR:CG2	2.36	0.56
14:G:22:C:O2	14:G:22:C:H2'	2.06	0.56
21:1:944:SER:O	21:1:948:ARG:HG3	2.04	0.56
21:1:1279:ALA:HA	23:3:1167:TYR:CE1	2.41	0.56
24:4:75:ASN:ND2	24:4:86:VAL:O	2.38	0.56
30:M:201:ILE:HA	30:M:220:LEU:HB3	1.85	0.56
1:A:107:PRO:O	1:A:111:GLU:CD	2.48	0.56
1:A:283:VAL:HG22	1:A:284:ARG:HG2	1.88	0.56
1:A:299:ILE:HD11	3:C:921:LEU:N	2.20	0.56
1:A:378:PHE:CZ	3:C:335:ASN:CB	2.89	0.56
1:A:569:VAL:O	1:A:570:ASP:HB2	2.04	0.56
1:A:692:ASP:OD1	33:T:376:ARG:NH2	2.38	0.56
1:A:1163:ARG:NH2	3:C:61:GLU:OE2	2.35	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:550:ASN:HD21	23:3:595:VAL:H	1.53	0.56
27:7:32:LEU:O	27:7:36:HIS:ND1	2.23	0.56
28:J:311:GLN:OE1	28:J:311:GLN:N	2.33	0.56
1:A:226:GLN:HA	1:A:418:THR:OG1	2.06	0.56
1:A:229:GLN:HG2	1:A:415:SER:CB	2.36	0.56
1:A:250:VAL:HG23	1:A:337:VAL:CG1	2.36	0.56
2:B:35:U:H6	2:B:35:U:OP2	1.89	0.56
3:C:301:SER:O	3:C:304:LEU:N	2.30	0.56
13:F:50:A:O2'	13:F:51:U:OP1	2.23	0.56
18:w:411:CYS:SG	18:w:431:HIS:CD2	2.99	0.56
28:J:406:PHE:CE2	28:J:411:MET:HE3	2.41	0.56
1:A:227:ARG:C	1:A:416:GLY:O	2.48	0.56
1:A:402:ILE:HG13	3:C:385:VAL:CG2	2.28	0.56
1:A:579:GLN:NE2	1:A:613:TYR:CE1	2.74	0.56
1:A:812:THR:HG23	1:A:1055:LEU:HD11	1.88	0.56
1:A:2320:LEU:HD23	1:A:2322:GLU:H	1.71	0.56
3:C:140:HIS:CB	3:C:230:ASP:CB	2.66	0.56
15:H:168:A:C5	12:n:54:GLN:CB	2.88	0.56
18:w:477:GLU:HA	23:3:980:LYS:NZ	2.21	0.56
24:4:79:LEU:HB2	24:4:84:ILE:HD11	1.88	0.56
38:z:32:GLU:HB3	38:z:88:HIS:CD2	2.40	0.56
1:A:44:ARG:NH2	5:E:285:GLU:O	2.38	0.56
3:C:85:ASP:HB3	33:T:238:LEU:CG	2.27	0.56
3:C:677:GLU:HA	3:C:683:ASN:O	2.05	0.56
5:E:277:PHE:CE2	5:E:300:ILE:HD13	2.40	0.56
21:1:1026:ASN:ND2	21:1:1031:VAL:HG11	2.21	0.56
23:3:745:PHE:HE2	23:3:750:CYS:HB3	1.71	0.56
1:A:251:ASP:CA	1:A:337:VAL:HG21	2.36	0.56
1:A:1306:LYS:NZ	2:B:38:C:C2'	2.68	0.56
3:C:385:VAL:HG23	3:C:386:GLY:N	2.20	0.56
5:E:153:PHE:HD1	5:E:153:PHE:H	1.54	0.56
15:H:150:U:C2	15:H:151:C:C5	2.94	0.56
21:1:689:ILE:O	21:1:692:HIS:ND1	2.39	0.56
21:1:718:PRO:HA	21:1:756:LEU:HG	1.88	0.56
23:3:669:LEU:HB2	23:3:673:VAL:HG22	1.88	0.56
25:5:93:ASN:OD1	25:5:94:ALA:N	2.34	0.56
28:J:433:ARG:HH12	28:J:461:LYS:CB	2.19	0.56
33:T:342:GLU:CB	33:T:343:PRO:CD	2.83	0.56
1:A:311:GLU:CB	3:C:885:THR:CG2	2.84	0.56
1:A:395:THR:HG21	3:C:383:GLN:NE2	2.15	0.56
1:A:978:GLU:CD	1:A:1188:ASN:H	2.14	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1451:ASN:OD1	1:A:1453:PHE:N	2.39	0.56
3:C:631:GLY:HA3	3:C:637:LEU:HD21	1.88	0.56
15:H:83:A:N1	15:H:84:C:C4	2.74	0.56
18:w:478:GLU:CB	23:3:978:LEU:CD1	2.84	0.56
21:1:1293:ASN:HA	27:7:76:CYS:O	2.05	0.56
21:1:1295:TYR:CE2	27:7:28:LYS:HE2	2.41	0.56
23:3:29:GLU:HB3	23:3:40:LEU:HD11	1.87	0.56
23:3:804:HIS:HD2	23:3:862:TRP:CZ2	2.24	0.56
23:3:1028:THR:HG22	23:3:1088:LYS:HD3	1.86	0.56
1:A:251:ASP:CA	1:A:337:VAL:CG2	2.84	0.55
1:A:319:LEU:HD13	3:C:637:LEU:HB3	1.86	0.55
1:A:434:HIS:HB3	3:C:892:GLN:OE1	2.07	0.55
1:A:783:TYR:CD1	31:P:228:ILE:HG12	2.41	0.55
14:G:16:G:H4'	14:G:17:U:O5'	2.04	0.55
15:H:154:C:O2'	15:H:155:C:H5'	2.04	0.55
21:1:570:TYR:HD1	21:1:573:LYS:HD2	1.71	0.55
1:A:89:LEU:O	1:A:89:LEU:HD23	2.06	0.55
1:A:331:TRP:C	1:A:331:TRP:HE3	2.14	0.55
1:A:361:HIS:HD1	1:A:361:HIS:H	1.54	0.55
1:A:387:PHE:HE1	3:C:327:TYR:CA	2.05	0.55
1:A:744:LYS:HZ1	31:P:212:ASN:C	2.14	0.55
1:A:2113:LYS:CE	4:D:1229:ASP:CA	2.84	0.55
15:H:141:C:H2'	15:H:142:C:H6	1.71	0.55
15:H:149:A:C4	15:H:150:U:C5	2.95	0.55
15:H:180:G:C2	15:H:181:G:C5	2.94	0.55
33:T:351:ASP:C	33:T:352:THR:OG1	2.48	0.55
1:A:530:LEU:CA	30:M:198:GLN:NE2	2.27	0.55
1:A:1321:GLU:O	1:A:1503:TRP:NE1	2.39	0.55
1:A:1418:ARG:HE	1:A:1464:LEU:HD23	1.72	0.55
1:A:2325:VAL:CG1	4:D:788:GLY:O	2.33	0.55
3:C:674:CYS:HG	3:C:822:MET:CE	2.16	0.55
5:E:250:LEU:HD22	5:E:262:TRP:HB2	1.88	0.55
21:1:1137:ARG:HH21	22:2:524:LEU:HD13	1.72	0.55
1:A:89:LEU:HD13	1:A:660:PHE:HZ	1.71	0.55
1:A:280:GLU:HB2	2:B:48:A:C4'	2.36	0.55
3:C:706:GLN:NE2	3:C:708:THR:H	2.02	0.55
22:2:650:ILE:HG12	22:2:688:GLY:HA3	1.89	0.55
28:J:270:ASP:CG	32:R:222:PRO:CB	2.77	0.55
28:J:406:PHE:CD1	28:J:411:MET:HE2	2.41	0.55
1:A:151:MET:SD	1:A:628:GLY:O	2.65	0.55
1:A:305:ARG:CG	3:C:878:ILE:CG2	2.85	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:PRO:O	1:A:465:LYS:HB3	2.05	0.55
1:A:1035:GLN:HA	1:A:1446:GLN:NE2	2.21	0.55
1:A:1690:ASP:OD1	1:A:1691:ASN:N	2.39	0.55
1:A:1757:GLU:CD	32:R:451:ILE:HD11	2.30	0.55
2:B:94:U:H2'	2:B:95:G:H5''	1.89	0.55
3:C:185:PRO:HG3	3:C:482:TYR:CZ	2.41	0.55
3:C:439:PRO:HB2	3:C:443:VAL:HB	1.88	0.55
3:C:674:CYS:SG	3:C:822:MET:HE1	2.45	0.55
21:1:1166:ILE:O	21:1:1170:THR:HG23	2.07	0.55
23:3:526:HIS:HB3	23:3:534:ASN:HB2	1.88	0.55
24:4:29:LEU:HD22	24:4:33:PHE:HE2	1.72	0.55
34:V:641:ASP:O	34:V:644:ARG:N	2.39	0.55
37:Z:566:TYR:CD2	37:Z:580:PRO:HG2	2.36	0.55
1:A:356:ILE:HG22	1:A:357:ASN:H	1.72	0.55
1:A:1607:GLU:N	1:A:1632:PHE:O	2.38	0.55
1:A:1930:TYR:O	1:A:1933:PHE:HB3	2.06	0.55
1:A:2073:TRP:HD1	1:A:2074:ARG:N	2.04	0.55
3:C:702:ASN:O	3:C:703:GLU:HB2	2.07	0.55
5:E:162:ARG:CZ	5:E:203:ASP:O	2.55	0.55
15:H:165:A:H2'	15:H:166:G:H5'	1.88	0.55
18:w:478:GLU:CA	23:3:978:LEU:HD11	2.36	0.55
23:3:996:ILE:HG23	23:3:999:ARG:H	1.72	0.55
32:R:422:MET:C	32:R:424:SER:H	2.12	0.55
1:A:319:LEU:HB2	3:C:638:ASP:HA	1.89	0.55
1:A:596:TYR:O	1:A:597:LYS:C	2.50	0.55
1:A:1233:ASP:O	1:A:1236:SER:OG	2.23	0.55
1:A:1899:VAL:HB	1:A:1902:PHE:HD2	1.71	0.55
3:C:78:GLU:OE1	33:T:198:ARG:NE	2.36	0.55
3:C:79:THR:CG2	33:T:199:VAL:CG1	2.84	0.55
3:C:567:GLU:OE1	3:C:572:GLU:HB3	2.06	0.55
5:E:260:ARG:NH1	5:E:276:ILE:HD11	2.22	0.55
14:G:23:U:O2	14:G:23:U:H2'	2.07	0.55
18:w:485:ASN:ND2	23:3:976:LYS:O	2.39	0.55
21:1:1255:PHE:CD2	22:2:487:LEU:HD22	2.42	0.55
31:P:33:ARG:HG3	31:P:33:ARG:HH11	1.72	0.55
33:T:233:LEU:HD23	33:T:233:LEU:C	2.32	0.55
36:Y:22:VAL:HG22	36:Y:26:VAL:HG13	1.88	0.55
37:Z:600:ARG:HB3	37:Z:600:ARG:NH1	2.08	0.55
38:z:123:LEU:HD22	38:z:127:HIS:CD2	2.42	0.55
1:A:283:VAL:HG13	1:A:284:ARG:N	2.22	0.55
1:A:312:TYR:CD2	3:C:882:GLY:CA	2.86	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:848:GLU:CD	32:R:424:SER:OG	2.50	0.55
1:A:1099:PHE:HE2	1:A:1153:VAL:HG13	1.72	0.55
1:A:1457:HIS:HE1	1:A:1459:ARG:HG3	1.68	0.55
1:A:1757:GLU:CD	32:R:451:ILE:CD1	2.80	0.55
1:A:1971:LEU:HB2	1:A:1976:TRP:CE2	2.42	0.55
2:B:63:A:O2'	5:E:106:LYS:NZ	2.39	0.55
21:1:1017:LEU:HD13	21:1:1050:VAL:HG21	1.89	0.55
21:1:1076:ALA:O	21:1:1080:THR:HG23	2.07	0.55
23:3:441:GLY:O	23:3:775:ASN:CB	2.55	0.55
32:R:74:LEU:HD23	32:R:75:ASP:OD1	2.06	0.55
32:R:436:VAL:CG2	32:R:437:TYR:CE1	2.89	0.55
34:V:484:SER:C	34:V:486:THR:H	2.15	0.55
36:Y:85:GLU:O	37:Z:502:ALA:CB	2.55	0.55
3:C:149:LEU:HA	3:C:427:PHE:CD2	2.41	0.55
14:G:142:U:H2'	14:G:143:U:C6	2.42	0.55
15:H:150:U:H2'	15:H:151:C:H6	1.71	0.55
16:o:46:ALA:CB	16:o:68:THR:CB	2.85	0.55
25:5:17:VAL:HG23	25:5:67:ILE:HD11	1.89	0.55
36:Y:37:TRP:HZ3	37:Z:498:GLY:HA3	1.66	0.55
1:A:1457:HIS:HE2	32:R:425:GLY:H	1.46	0.55
1:A:1645:LEU:HB2	1:A:1714:ALA:HB3	1.88	0.55
1:A:2306:HIS:HD2	1:A:2308:VAL:H	1.54	0.55
3:C:220:ARG:HG2	3:C:479:THR:HG21	1.89	0.55
15:H:168:A:C6	12:n:54:GLN:CB	2.90	0.55
21:1:1174:GLU:OE2	21:1:1210:HIS:NE2	2.35	0.55
23:3:452:LEU:HB3	23:3:478:PHE:CE1	2.42	0.55
27:7:60:SER:HG	27:7:63:ARG:H	1.54	0.55
29:L:224:PHE:CD1	32:R:86:LEU:O	2.59	0.55
37:Z:574:ASN:O	37:Z:577:ASN:N	2.33	0.55
1:A:311:GLU:HB3	3:C:885:THR:HG21	1.89	0.54
4:D:1048:VAL:O	4:D:1050:GLU:N	2.40	0.54
23:3:309:ASP:HA	23:3:332:THR:HG22	1.88	0.54
23:3:848:PRO:HB2	23:3:851:ILE:HG22	1.89	0.54
24:4:14:THR:CA	24:4:59:VAL:O	2.28	0.54
26:6:39:PRO:HB3	26:6:70:TYR:HB2	1.88	0.54
28:J:294:HIS:HE1	29:L:227:THR:HB	1.70	0.54
31:P:224:MET:HE2	31:P:228:ILE:CD1	2.36	0.54
32:R:86:LEU:HD12	32:R:86:LEU:O	2.06	0.54
1:A:350:PHE:CE2	1:A:398:THR:HG21	2.43	0.54
5:E:119:THR:HG21	5:E:161:ARG:HB2	1.87	0.54
15:H:153:A:C3'	15:H:154:C:C5'	2.86	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1179:ASP:HB3	22:2:511:LEU:CD1	2.37	0.54
21:1:1279:ALA:HA	23:3:1167:TYR:HE1	1.70	0.54
35:X:312:GLU:O	35:X:327:TYR:HB2	2.07	0.54
1:A:148:TRP:CH2	1:A:616:PHE:HB2	2.42	0.54
1:A:420:ARG:CZ	2:B:56:C:O2'	2.55	0.54
1:A:738:MET:HE3	1:A:739:ILE:HG13	1.89	0.54
1:A:1127:GLY:O	1:A:1128:TYR:C	2.48	0.54
3:C:140:HIS:CD2	3:C:233:GLU:HG3	2.41	0.54
3:C:144:CYS:C	3:C:312:SER:HB2	2.33	0.54
3:C:510:LEU:HB3	3:C:576:ILE:HD11	1.89	0.54
3:C:559:ILE:C	3:C:559:ILE:HD12	2.31	0.54
13:F:36:A:H2'	13:F:37:C:H4'	1.89	0.54
13:F:38:G:H2'	13:F:39:A:C8	2.42	0.54
13:F:56:A:C2	15:H:20:G:C2	2.96	0.54
23:3:553:GLN:HA	23:3:566:PHE:O	2.07	0.54
23:3:1014:TYR:OH	23:3:1019:ASN:OD1	2.24	0.54
28:J:218:GLU:HG3	28:J:219:GLU:OE2	2.07	0.54
37:Z:612:TYR:C	37:Z:614:TRP:N	2.63	0.54
37:Z:614:TRP:CD1	37:Z:614:TRP:C	2.85	0.54
1:A:529:THR:HB	30:M:199:PRO:HD3	1.88	0.54
1:A:676:ARG:HG3	13:F:56:A:P	2.48	0.54
1:A:1820:LYS:HD3	1:A:1914:MET:HE2	1.88	0.54
1:A:2298:LEU:C	4:D:1283:PRO:CB	2.78	0.54
3:C:749:THR:HG1	3:C:752:SER:HB2	1.72	0.54
28:J:220:LEU:HD13	28:J:220:LEU:C	2.32	0.54
32:R:241:MET:SD	32:R:245:GLU:CD	2.91	0.54
32:R:402:ASN:HB3	35:X:191:GLN:HB2	1.90	0.54
36:Y:10:ILE:HD13	36:Y:98:ASN:HD21	1.73	0.54
1:A:387:PHE:CD1	3:C:327:TYR:CD1	2.95	0.54
1:A:699:GLU:O	1:A:701:ILE:HD12	2.07	0.54
1:A:1306:LYS:HB2	14:G:-6:C:H4'	1.89	0.54
1:A:1459:ARG:HG3	32:R:424:SER:N	2.22	0.54
3:C:145:PHE:CZ	3:C:427:PHE:HE1	2.21	0.54
5:E:161:ARG:NH1	5:E:203:ASP:OD1	2.40	0.54
18:w:145:CYS:HA	18:w:155:SER:O	2.08	0.54
23:3:913:LEU:HD23	23:3:920:VAL:HG12	1.89	0.54
28:J:262:ARG:HD3	29:L:220:PRO:CG	2.38	0.54
29:L:224:PHE:HD1	32:R:86:LEU:O	1.91	0.54
33:T:455:GLN:NE2	33:T:456:PRO:HD2	2.22	0.54
1:A:705:LYS:HG2	32:R:251:ILE:CG1	2.38	0.54
1:A:1333:VAL:HG11	1:A:1367:ASN:HD22	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2095:ASP:OD1	1:A:2095:ASP:N	2.41	0.54
5:E:108:HIS:ND1	5:E:128:SER:CB	2.70	0.54
5:E:310:TYR:CZ	5:E:322:LYS:HD2	2.42	0.54
23:3:138:GLN:HG2	23:3:161:HIS:CE1	2.43	0.54
23:3:336:ALA:HB2	23:3:349:VAL:HG13	1.90	0.54
32:R:131:ASP:OD2	32:R:132:LEU:HD23	2.07	0.54
1:A:592:TYR:HA	1:A:595:LYS:O	2.08	0.54
1:A:978:GLU:OE2	1:A:1187:PHE:HB2	2.07	0.54
1:A:1328:LEU:HD22	1:A:1368:LEU:HD21	1.89	0.54
1:A:1930:TYR:C	1:A:1930:TYR:CD2	2.85	0.54
1:A:2325:VAL:O	4:D:788:GLY:CA	2.56	0.54
3:C:259:LYS:CE	3:C:262:ARG:HD2	2.36	0.54
3:C:482:TYR:CD2	3:C:493:PHE:HB2	2.42	0.54
3:C:700:ILE:CG2	3:C:735:PHE:CD2	2.83	0.54
21:1:470:ASP:OD1	21:1:471:ASP:N	2.41	0.54
21:1:632:PHE:HA	21:1:635:VAL:HG22	1.90	0.54
23:3:144:LEU:HB3	23:3:152:LEU:HD11	1.89	0.54
23:3:253:GLU:OE2	23:3:254:ASN:ND2	2.41	0.54
28:J:408:ASP:OD1	28:J:443:ILE:HG22	2.07	0.54
1:A:119:LEU:HD11	1:A:477:LYS:HG3	1.88	0.54
1:A:173:GLU:O	1:A:520:TYR:CD2	2.61	0.54
1:A:436:PRO:O	1:A:437:ALA:HB3	2.07	0.54
15:H:183:G:C4	15:H:184:C:C5	2.95	0.54
17:p:194:PHE:CB	17:p:200:ALA:HB2	2.38	0.54
21:1:331:ALA:O	21:1:335:LYS:N	2.34	0.54
31:P:228:ILE:HD12	31:P:228:ILE:N	2.23	0.54
33:T:356:LEU:N	33:T:356:LEU:CD1	2.70	0.54
37:Z:612:TYR:O	37:Z:615:SER:N	2.29	0.54
1:A:120:TYR:N	1:A:483:GLN:O	2.33	0.54
1:A:122:ILE:HD13	1:A:483:GLN:HG3	1.90	0.54
1:A:254:TYR:O	1:A:434:HIS:HD2	1.91	0.54
1:A:278:LYS:O	1:A:452:LYS:HD2	2.08	0.54
1:A:384:VAL:CG2	3:C:334:ILE:HG23	2.35	0.54
1:A:384:VAL:HG21	3:C:334:ILE:CG1	2.38	0.54
1:A:465:LYS:HG3	1:A:465:LYS:O	2.08	0.54
1:A:1778:TRP:CE2	1:A:1858:PRO:HG3	2.42	0.54
1:A:2067:PHE:CE2	1:A:2069:SER:HA	2.43	0.54
3:C:135:CYS:SG	3:C:227:LEU:HB2	2.47	0.54
15:H:45:C:N3	18:w:395:TRP:CG	2.76	0.54
21:1:893:ILE:HG13	21:1:928:TYR:CD2	2.43	0.54
22:2:476:GLU:N	22:2:479:ASP:OD2	2.41	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:7:15:GLN:O	27:7:21:THR:OG1	2.22	0.54
28:J:255:LEU:HD22	29:L:235:LEU:CD1	2.35	0.54
31:P:30:TYR:OH	32:R:162:ALA:C	2.50	0.54
32:R:232:MET:O	32:R:232:MET:HG2	2.07	0.54
1:A:256:TYR:CZ	3:C:888:ARG:CZ	2.91	0.54
1:A:264:PHE:CE1	1:A:455:VAL:CG1	2.75	0.54
1:A:1838:LYS:HG3	1:A:1868:MET:SD	2.49	0.54
1:A:2113:LYS:HE3	4:D:1229:ASP:CA	2.38	0.54
1:A:2325:VAL:HG13	4:D:789:MET:HA	1.88	0.54
3:C:79:THR:HA	33:T:199:VAL:H	1.73	0.54
14:G:137:C:H2'	14:G:138:A:O4'	2.07	0.54
15:H:3:C:H2'	15:H:4:G:H8	1.73	0.54
21:1:826:ASP:OD1	21:1:827:ARG:N	2.39	0.54
21:1:1010:THR:O	21:1:1012:PRO:HD3	2.08	0.54
31:P:188:TRP:O	31:P:190:ASP:N	2.39	0.54
32:R:135:PRO:HD2	33:T:341:ALA:HB1	1.90	0.54
32:R:442:ARG:CD	32:R:443:GLY:CA	2.70	0.54
38:z:61:PHE:CD2	38:z:62:ILE:HG12	2.42	0.54
1:A:335:PRO:HG3	3:C:139:HIS:CB	2.36	0.53
1:A:2117:ILE:O	1:A:2304:PHE:HB2	2.07	0.53
3:C:700:ILE:HA	3:C:705:VAL:HG12	1.89	0.53
3:C:742:PRO:HB2	3:C:786:ASN:H	1.72	0.53
5:E:178:LEU:CD1	5:E:222:LEU:HD22	2.37	0.53
32:R:442:ARG:NH1	32:R:444:GLY:N	2.41	0.53
33:T:287:HIS:CE1	33:T:313:ARG:HG3	2.43	0.53
37:Z:485:GLU:O	37:Z:489:GLU:CB	2.56	0.53
1:A:705:LYS:HG2	32:R:251:ILE:CG2	2.38	0.53
1:A:1403:LEU:O	32:R:412:ASP:HB2	2.08	0.53
1:A:1930:TYR:CD2	1:A:1931:THR:N	2.76	0.53
1:A:2129:TYR:HB3	1:A:2172:MET:HE3	1.90	0.53
14:G:135:G:H1	15:H:41:U:H3	1.56	0.53
15:H:84:C:O2	15:H:84:C:H2'	2.09	0.53
23:3:166:LEU:O	23:3:186:GLU:HA	2.08	0.53
33:T:454:VAL:HG12	33:T:455:GLN:N	2.24	0.53
34:V:525:PHE:O	34:V:528:ILE:N	2.41	0.53
1:A:151:MET:HE1	1:A:629:PHE:HA	1.91	0.53
1:A:386:PRO:HB3	3:C:372:PHE:CD1	2.43	0.53
1:A:628:GLY:O	1:A:629:PHE:HB2	2.09	0.53
1:A:1118:PRO:CD	1:A:1119:ASP:H	2.19	0.53
1:A:1605:GLU:OE2	1:A:2286:VAL:HG21	2.07	0.53
1:A:1962:THR:CG2	37:Z:524:ARG:CG	2.86	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:87:ASP:O	5:E:88:ARG:HB2	2.07	0.53
13:F:53:A:H2'	13:F:54:G:O4'	2.09	0.53
21:1:626:ASN:ND2	21:1:630:ARG:HH12	2.06	0.53
21:1:1299:GLU:HA	21:1:1302:TYR:CE2	2.44	0.53
33:T:384:HIS:O	33:T:385:TYR:CB	2.55	0.53
35:X:181:PHE:HA	36:Y:50:GLY:H	1.73	0.53
36:Y:32:TYR:C	36:Y:34:ASP:H	2.15	0.53
1:A:664:HIS:CE1	1:A:666:LYS:CB	2.85	0.53
1:A:1957:ASP:O	1:A:1960:THR:OG1	2.19	0.53
3:C:78:GLU:C	33:T:198:ARG:HA	2.25	0.53
3:C:449:ILE:CD1	3:C:466:SER:N	2.71	0.53
15:H:82:G:HO2'	15:H:83:A:H5'	1.71	0.53
21:1:822:ARG:HH11	36:Y:31:GLU:HG2	1.74	0.53
21:1:1077:THR:O	21:1:1080:THR:OG1	2.22	0.53
21:1:1127:THR:HA	22:2:571:LEU:HB3	1.88	0.53
23:3:3:LEU:HD12	23:3:1093:MET:SD	2.48	0.53
28:J:218:GLU:HG3	28:J:219:GLU:N	2.23	0.53
32:R:103:ARG:HH11	32:R:103:ARG:CG	2.21	0.53
1:A:2073:TRP:CH2	1:A:2310:ARG:HG2	2.44	0.53
1:A:2298:LEU:HD13	4:D:1265:GLN:CB	2.39	0.53
3:C:481:MET:SD	3:C:559:ILE:HD11	2.48	0.53
18:w:445:HIS:CG	18:w:446:PHE:CE2	2.97	0.53
23:3:712:VAL:HG23	23:3:722:SER:HB3	1.91	0.53
32:R:171:LEU:HD11	32:R:201:GLU:CD	2.32	0.53
36:Y:24:ASP:CG	36:Y:25:LYS:H	2.14	0.53
1:A:115:ASP:HB3	1:A:486:LYS:HE2	1.91	0.53
1:A:665:SER:HB3	32:R:215:ASN:HB2	1.90	0.53
1:A:881:ILE:HG23	1:A:918:THR:HG23	1.88	0.53
1:A:1457:HIS:HE2	32:R:425:GLY:N	2.04	0.53
1:A:2310:ARG:HH12	1:A:2314:PHE:HE1	1.56	0.53
2:B:18:C:C2'	2:B:19:A:O5'	2.56	0.53
3:C:220:ARG:O	3:C:448:LYS:HE2	2.08	0.53
3:C:360:ALA:N	3:C:361:PRO:CD	2.71	0.53
15:H:147:G:C2	15:H:148:C:C2	2.97	0.53
15:H:153:A:H3'	15:H:154:C:C5'	2.38	0.53
21:1:1157:TYR:O	26:6:38:ARG:NH2	2.40	0.53
23:3:195:ASP:OD1	23:3:197:THR:OG1	2.23	0.53
23:3:250:ILE:HD13	23:3:259:LYS:HB3	1.91	0.53
23:3:547:CYS:HB3	23:3:556:ILE:HG22	1.90	0.53
23:3:667:ILE:HB	23:3:675:LEU:HB2	1.91	0.53
31:P:41:ILE:HD11	33:T:318:ARG:HB2	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:z:61:PHE:HD2	38:z:62:ILE:HG12	1.74	0.53
1:A:393:LEU:HD13	3:C:375:GLU:O	2.08	0.53
1:A:586:GLY:O	1:A:1549:VAL:HG12	2.08	0.53
3:C:449:ILE:HG22	3:C:457:VAL:HG13	1.88	0.53
5:E:108:HIS:ND1	5:E:128:SER:HB2	2.24	0.53
5:E:178:LEU:CD2	5:E:208:ILE:CD1	2.87	0.53
15:H:68:G:C2'	15:H:69:U:H5'	2.37	0.53
23:3:141:VAL:HG11	23:3:213:LEU:HD12	1.89	0.53
23:3:440:HIS:CD2	23:3:733:PRO:CG	2.92	0.53
1:A:203:VAL:HG23	1:A:237:THR:CG2	2.35	0.53
1:A:299:ILE:CD1	3:C:920:PRO:C	2.82	0.53
1:A:308:ILE:HG22	1:A:308:ILE:O	2.09	0.53
1:A:384:VAL:HG21	3:C:334:ILE:HG23	1.80	0.53
3:C:82:GLN:CG	33:T:237:LYS:HA	2.38	0.53
15:H:79:G:C2	15:H:80:A:C5	2.97	0.53
21:1:642:PRO:HB3	21:1:682:HIS:HE2	1.74	0.53
21:1:944:SER:HA	21:1:948:ARG:NE	2.23	0.53
28:J:359:VAL:O	28:J:363:ARG:HG2	2.08	0.53
33:T:318:ARG:HH11	33:T:318:ARG:CG	2.22	0.53
37:Z:571:PRO:HD3	37:Z:579:TRP:CH2	2.43	0.53
1:A:299:ILE:HD11	3:C:920:PRO:O	2.09	0.53
1:A:417:ARG:HH12	2:B:58:U:C5'	2.21	0.53
3:C:259:LYS:HG2	3:C:262:ARG:HG3	1.90	0.53
5:E:232:ARG:O	5:E:262:TRP:HH2	1.91	0.53
21:1:516:LEU:O	21:1:520:THR:HG23	2.08	0.53
24:4:47:ASP:HB3	24:4:52:GLN:O	2.08	0.53
33:T:387:PHE:CD1	33:T:387:PHE:C	2.87	0.53
1:A:148:TRP:CZ2	1:A:616:PHE:HA	2.44	0.53
1:A:264:PHE:CE1	1:A:459:LEU:CD1	2.81	0.53
1:A:405:LEU:CD1	3:C:265:LEU:HD22	2.39	0.53
1:A:723:ASN:ND2	1:A:788:GLN:OE1	2.41	0.53
1:A:748:ASP:HA	31:P:214:THR:CG2	2.34	0.53
1:A:1275:ARG:HD2	1:A:1375:TRP:CD1	2.44	0.53
1:A:1425:LYS:CG	32:R:417:ASN:OD1	2.56	0.53
1:A:1781:ASP:HB3	1:A:1808:PHE:HB3	1.90	0.53
3:C:250:ARG:NE	3:C:451:HIS:CD2	2.76	0.53
3:C:516:LEU:HB2	3:C:575:GLN:HE22	1.73	0.53
13:F:50:A:H2'	13:F:51:U:C6	2.44	0.53
13:F:56:A:C6	15:H:20:G:C6	2.96	0.53
22:2:614:ARG:HH11	22:2:614:ARG:CG	2.14	0.53
23:3:211:TYR:HE1	23:3:222:ARG:HG2	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:605:LEU:O	23:3:616:ILE:HA	2.08	0.53
23:3:719:SER:OG	23:3:739:LEU:HD11	2.09	0.53
34:V:530:LYS:O	34:V:532:GLN:N	2.42	0.53
1:A:121:HIS:CD2	1:A:481:PHE:HB3	2.36	0.52
1:A:891:PHE:O	29:L:83:ARG:NH1	2.42	0.52
21:1:599:ASN:O	21:1:603:ALA:CB	2.57	0.52
22:2:504:TRP:C	22:2:506:PHE:H	2.17	0.52
23:3:519:VAL:HG22	23:3:524:ILE:HG12	1.90	0.52
23:3:639:SER:OG	23:3:701:LEU:N	2.42	0.52
23:3:1148:LEU:O	23:3:1152:HIS:N	2.39	0.52
32:R:95:LYS:HD3	32:R:95:LYS:N	2.25	0.52
1:A:356:ILE:CG2	3:C:865:GLY:C	2.82	0.52
1:A:1701:VAL:HA	1:A:1716:GLY:HA3	1.90	0.52
3:C:301:SER:C	3:C:303:LEU:N	2.68	0.52
3:C:943:LEU:HD23	3:C:943:LEU:N	2.24	0.52
13:F:48:A:N3	29:L:33:ARG:NH2	2.57	0.52
13:F:94:C:OP1	28:J:351:ASN:CB	2.57	0.52
14:G:153:C:H4'	14:G:154:U:OP1	2.10	0.52
15:H:81:G:C2	15:H:82:G:C5	2.97	0.52
23:3:550:ASN:HB3	23:3:553:GLN:HB2	1.90	0.52
1:A:171:ASP:CG	1:A:519:ASP:OD2	2.53	0.52
1:A:312:TYR:CZ	3:C:882:GLY:C	2.87	0.52
1:A:406:TRP:CH2	3:C:265:LEU:C	2.87	0.52
3:C:97:VAL:HG12	31:P:47:THR:OG1	2.10	0.52
13:F:34:G:H2'	13:F:35:A:O5'	2.10	0.52
14:G:-4:A:H2'	14:G:-3:A:C8	2.44	0.52
15:H:148:C:C2'	15:H:149:A:H5'	2.39	0.52
21:1:516:LEU:HD11	21:1:558:ARG:HD3	1.91	0.52
21:1:1090:PRO:HG3	21:1:1123:CYS:HB2	1.91	0.52
23:3:128:ARG:HH21	23:3:180:PRO:HG3	1.73	0.52
23:3:159:GLU:OE2	26:6:14:GLN:HB2	2.09	0.52
23:3:755:VAL:HG22	23:3:764:ILE:HD12	1.89	0.52
31:P:189:ASP:O	31:P:191:ASP:N	2.43	0.52
32:R:233:HIS:H	32:R:233:HIS:HD2	1.56	0.52
34:V:484:SER:C	34:V:486:THR:N	2.67	0.52
1:A:1214:TRP:CE2	1:A:1230:LEU:HD11	2.45	0.52
1:A:1301:ILE:HD13	1:A:1306:LYS:CE	2.35	0.52
5:E:178:LEU:N	5:E:178:LEU:HD23	2.25	0.52
14:G:-12:G:H4'	14:G:-11:G:OP1	2.09	0.52
21:1:1108:ASN:OD1	21:1:1109:ARG:N	2.43	0.52
23:3:114:ARG:NE	23:3:136:GLU:OE1	2.32	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:52:PRO:O	32:R:53:ARG:HB2	2.09	0.52
32:R:81:LYS:HA	32:R:81:LYS:HE3	1.87	0.52
1:A:204:LEU:HD23	1:A:205:ASP:OD1	2.09	0.52
1:A:267:LYS:HZ1	2:B:49:A:P	2.24	0.52
1:A:338:VAL:O	3:C:266:GLU:HG2	2.10	0.52
1:A:384:VAL:HG22	3:C:334:ILE:CG2	2.33	0.52
1:A:387:PHE:CE1	3:C:326:ILE:HG22	2.45	0.52
1:A:664:HIS:NE2	1:A:666:LYS:CG	2.73	0.52
1:A:666:LYS:HB2	1:A:668:VAL:HG23	1.83	0.52
1:A:1275:ARG:NH1	1:A:1378:GLU:OE1	2.43	0.52
3:C:80:ILE:CD1	3:C:80:ILE:N	2.73	0.52
3:C:143:THR:HB	41:C:1500:GTP:O1A	2.09	0.52
3:C:700:ILE:CG2	3:C:741:GLY:O	2.57	0.52
13:F:36:A:C8	13:F:36:A:C4'	2.93	0.52
13:F:57:U:H2'	13:F:58:G:C8	2.45	0.52
21:1:717:THR:HG22	21:1:718:PRO:CD	2.39	0.52
21:1:762:ALA:O	21:1:766:THR:OG1	2.19	0.52
23:3:159:GLU:HB3	23:3:161:HIS:CD2	2.44	0.52
37:Z:524:ARG:HD2	37:Z:525:TYR:HB3	1.92	0.52
1:A:128:PHE:CD1	1:A:473:PHE:CZ	2.98	0.52
1:A:665:SER:OG	1:A:666:LYS:HD3	2.10	0.52
1:A:1631:LEU:HD12	1:A:1660:TYR:HD2	1.74	0.52
1:A:2133:PRO:HD2	1:A:2139:VAL:HG13	1.92	0.52
3:C:78:GLU:CG	3:C:80:ILE:CD1	2.54	0.52
3:C:139:HIS:O	3:C:259:LYS:NZ	2.36	0.52
3:C:449:ILE:HD11	3:C:466:SER:HA	1.91	0.52
3:C:508:LYS:HB3	3:C:566:THR:CG2	2.39	0.52
3:C:710:ASN:O	3:C:712:LYS:N	2.42	0.52
18:w:478:GLU:CA	23:3:978:LEU:CD1	2.87	0.52
21:1:1254:LEU:O	21:1:1262:ARG:HG2	2.09	0.52
23:3:1059:PRO:O	23:3:1062:THR:HG23	2.08	0.52
33:T:267:ASP:O	33:T:268:LYS:CG	2.56	0.52
37:Z:597:ARG:NH1	37:Z:601:LEU:HD13	2.24	0.52
1:A:203:VAL:CG2	1:A:237:THR:CB	2.88	0.52
1:A:433:GLU:OE1	1:A:436:PRO:CB	2.54	0.52
1:A:661:GLU:CG	32:R:210:PRO:CB	2.88	0.52
1:A:1162:PRO:HG3	31:P:194:PHE:CG	2.44	0.52
1:A:1459:ARG:HD2	32:R:422:MET:O	2.09	0.52
2:B:27:U:O2'	2:B:28:A:O5'	2.23	0.52
14:G:11:A:N1	14:G:12:G:C8	2.77	0.52
23:3:285:MET:SD	23:3:305:THR:HB	2.49	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:304:GLN:HE22	23:3:335:VAL:HA	1.73	0.52
24:4:41:ASN:HB2	24:4:60:GLU:HB3	1.92	0.52
33:T:318:ARG:HH11	33:T:319:THR:HG23	1.74	0.52
1:A:47:GLU:OE1	1:A:47:GLU:N	2.35	0.52
3:C:710:ASN:O	3:C:711:ARG:C	2.53	0.52
3:C:711:ARG:CZ	3:C:730:ARG:O	2.57	0.52
3:C:902:HIS:ND1	3:C:903:HIS:HB2	2.25	0.52
21:1:1289:ASN:HB3	21:1:1295:TYR:H	1.75	0.52
23:3:108:GLY:O	26:6:82:ARG:HD3	2.09	0.52
23:3:232:GLY:HA2	23:3:252:SER:HA	1.90	0.52
24:4:34:LEU:HA	24:4:37:GLY:O	2.10	0.52
32:R:135:PRO:O	32:R:136:ASP:CB	2.58	0.52
1:A:191:ILE:HG23	1:A:572:PHE:CZ	2.44	0.52
3:C:259:LYS:HG2	3:C:262:ARG:CG	2.39	0.52
3:C:510:LEU:HD22	3:C:514:TYR:HE2	1.75	0.52
15:H:45:C:H41	18:w:395:TRP:NE1	2.02	0.52
21:1:901:GLN:HA	21:1:939:ARG:HH22	1.72	0.52
28:J:406:PHE:CD2	28:J:411:MET:HE2	2.45	0.52
31:P:193:VAL:HG23	31:P:194:PHE:N	2.25	0.52
33:T:347:THR:O	33:T:354:ILE:HG23	2.10	0.52
1:A:676:ARG:HG3	13:F:55:C:O3'	2.09	0.52
2:B:42:U:H3	14:G:-3:A:N1	1.47	0.52
3:C:449:ILE:CD1	3:C:466:SER:CA	2.88	0.52
3:C:600:LEU:N	3:C:601:PRO:HD2	2.25	0.52
15:H:45:C:C2	18:w:395:TRP:HB3	2.45	0.52
21:1:661:ARG:NH1	21:1:696:ASP:OD2	2.39	0.52
21:1:1070:LYS:HB3	21:1:1073:ILE:HD12	1.91	0.52
21:1:1096:THR:HA	21:1:1099:ASN:ND2	2.25	0.52
23:3:259:LYS:HG3	23:3:266:ASP:OD1	2.09	0.52
23:3:1048:ASP:HB3	23:3:1052:ASN:H	1.75	0.52
31:P:189:ASP:OD2	31:P:192:VAL:CG2	2.59	0.52
36:Y:69:ARG:NH2	36:Y:74:GLY:O	2.34	0.52
1:A:312:TYR:N	1:A:312:TYR:CD1	2.78	0.51
1:A:941:LYS:HG3	1:A:1071:PHE:CE1	2.46	0.51
1:A:1275:ARG:HD2	1:A:1375:TRP:NE1	2.25	0.51
3:C:64:LYS:NZ	31:P:206:LYS:HG3	2.22	0.51
3:C:89:LEU:O	3:C:91:GLU:N	2.43	0.51
21:1:1256:HIS:ND1	21:1:1261:VAL:HG11	2.24	0.51
23:3:460:TRP:CZ2	23:3:507:SER:HA	2.46	0.51
23:3:476:VAL:HG22	23:3:762:LEU:HD22	1.91	0.51
23:3:1134:SER:HB2	23:3:1136:GLU:OE1	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:P:32:SER:O	31:P:35:LEU:HD12	2.09	0.51
1:A:245:LEU:HD22	1:A:430:TRP:CH2	2.44	0.51
1:A:664:HIS:NE2	1:A:666:LYS:CB	2.73	0.51
1:A:672:VAL:HG21	33:T:267:ASP:OD1	2.10	0.51
1:A:805:GLU:CB	31:P:194:PHE:CZ	2.89	0.51
3:C:77:VAL:HG13	33:T:196:LEU:HB3	1.91	0.51
13:F:36:A:H3'	13:F:37:C:C5'	2.26	0.51
21:1:1185:ARG:HD2	21:1:1218:ASN:CG	2.35	0.51
21:1:1253:GLY:HA3	21:1:1265:TYR:CG	2.45	0.51
26:6:54:TYR:HA	26:6:57:ARG:HB2	1.92	0.51
29:L:224:PHE:CE1	32:R:86:LEU:HD13	2.44	0.51
33:T:392:PRO:HA	33:T:414:ALA:O	2.09	0.51
1:A:296:PHE:HB3	3:C:656:ALA:HB2	1.92	0.51
1:A:366:LYS:N	1:A:366:LYS:CD	2.73	0.51
1:A:519:ASP:C	1:A:519:ASP:OD1	2.54	0.51
1:A:589:THR:OG1	1:A:590:GLY:N	2.44	0.51
1:A:642:ARG:NH2	2:B:56:C:C2	2.78	0.51
1:A:750:TRP:CZ2	1:A:778:ARG:HG2	2.45	0.51
1:A:1179:SER:O	1:A:1182:ASN:N	2.44	0.51
1:A:1784:ASN:ND2	1:A:1897:LEU:HD12	2.22	0.51
3:C:674:CYS:SG	3:C:822:MET:CE	2.99	0.51
13:F:45:A:N1	22:2:554:ARG:NH2	2.53	0.51
21:1:1179:ASP:HB2	21:1:1185:ARG:HD3	1.93	0.51
23:3:331:ASP:OD2	23:3:394:ASN:HB2	2.11	0.51
33:T:267:ASP:O	33:T:268:LYS:HB2	2.09	0.51
33:T:454:VAL:CG2	33:T:463:SER:OG	2.58	0.51
38:z:97:GLY:HA2	38:z:141:MET:HE1	1.93	0.51
1:A:221:ASN:ND2	2:B:12:U:OP1	2.43	0.51
1:A:232:LEU:HB2	1:A:233:PRO:HD3	1.93	0.51
1:A:782:LEU:HB3	31:P:224:MET:SD	2.50	0.51
3:C:65:TYR:C	3:C:66:TYR:CG	2.86	0.51
3:C:300:LEU:HD13	3:C:300:LEU:N	2.25	0.51
3:C:449:ILE:HD11	3:C:465:MET:C	2.35	0.51
15:H:55:U:H1'	15:H:58:U:H5	1.74	0.51
15:H:107:A:C6	15:H:108:G:C5	2.99	0.51
37:Z:593:PHE:O	37:Z:597:ARG:CB	2.57	0.51
1:A:152:ARG:CG	1:A:152:ARG:NH1	2.73	0.51
1:A:227:ARG:H	1:A:417:ARG:HA	1.75	0.51
1:A:830:LEU:HA	1:A:882:LYS:HZ2	1.75	0.51
1:A:1667:ARG:HD2	1:A:1679:TYR:CE2	2.46	0.51
1:A:2147:MET:O	1:A:2274:PRO:HD3	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:678:THR:HG23	3:C:683:ASN:H	1.75	0.51
5:E:231:MET:SD	5:E:262:TRP:CE3	3.04	0.51
13:F:68:C:N4	31:P:33:ARG:CB	2.45	0.51
21:1:1054:GLU:OE1	21:1:1057:ARG:NH1	2.36	0.51
23:3:854:ALA:HB1	23:3:856:LYS:HD2	1.93	0.51
23:3:1002:VAL:HB	23:3:1010:ILE:HB	1.93	0.51
38:z:37:CYS:SG	38:z:130:PHE:HB2	2.50	0.51
1:A:1447:VAL:HG12	1:A:1449:LYS:HG2	1.92	0.51
13:F:43:A:O2'	13:F:44:G:H5'	2.11	0.51
7:i:89:ASP:CB	18:w:171:PHE:CB	2.89	0.51
18:w:411:CYS:O	18:w:414:TYR:N	2.37	0.51
21:1:231:ARG:HA	21:1:607:ALA:HB2	1.92	0.51
23:3:264:GLN:HE22	23:3:322:VAL:H	1.58	0.51
23:3:745:PHE:CZ	23:3:747:SER:HB3	2.46	0.51
33:T:318:ARG:HG3	33:T:318:ARG:HH11	1.76	0.51
36:Y:37:TRP:CZ3	37:Z:498:GLY:C	2.86	0.51
1:A:349:ALA:HB2	1:A:399:ALA:CB	2.19	0.51
1:A:468:LYS:HD3	1:A:468:LYS:C	2.35	0.51
1:A:1320:LYS:NZ	32:R:434:TYR:CD1	2.77	0.51
1:A:1962:THR:HG23	37:Z:524:ARG:CB	2.28	0.51
1:A:2090:ILE:HA	1:A:2223:CYS:O	2.10	0.51
3:C:220:ARG:O	3:C:448:LYS:CE	2.58	0.51
13:F:34:G:N3	13:F:34:G:C3'	2.72	0.51
13:F:94:C:H5''	28:J:347:HIS:HB3	1.92	0.51
22:2:469:VAL:HG12	22:2:471:ARG:H	1.76	0.51
23:3:113:ARG:HB2	23:3:116:VAL:HB	1.91	0.51
23:3:971:ASP:OD1	23:3:972:LEU:N	2.43	0.51
33:T:459:LEU:HD12	33:T:460:ASP:N	2.25	0.51
36:Y:37:TRP:CH2	37:Z:498:GLY:N	2.74	0.51
1:A:95:MET:N	1:A:96:PRO:HD2	2.26	0.51
1:A:1629:ILE:HB	1:A:1662:ILE:HB	1.92	0.51
1:A:1923:TRP:HB3	1:A:1927:ILE:HD11	1.93	0.51
1:A:2081:ALA:HB1	4:D:1010:SER:CB	2.40	0.51
2:B:94:U:H5	9:d:104:ASP:O	1.94	0.51
3:C:133:THR:O	3:C:226:VAL:O	2.29	0.51
13:F:34:G:N3	13:F:34:G:C5'	2.73	0.51
13:F:35:A:N3	13:F:35:A:C5'	2.73	0.51
18:w:485:ASN:ND2	23:3:976:LYS:CG	2.62	0.51
23:3:354:GLY:HA3	23:3:432:ARG:HH12	1.76	0.51
24:4:16:TYR:HA	24:4:57:GLY:O	2.10	0.51
24:4:16:TYR:HD1	24:4:58:PHE:CE2	2.28	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:257:GLU:HA	29:L:232:TYR:CE2	2.46	0.51
28:J:273:TYR:CD2	32:R:228:PRO:CG	2.94	0.51
32:R:134:ARG:O	32:R:135:PRO:C	2.54	0.51
1:A:206:TRP:CD1	1:A:213:LEU:HD21	2.45	0.51
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.93	0.51
1:A:1373:GLN:HB3	1:A:1378:GLU:OE2	2.11	0.51
1:A:1502:PHE:CZ	1:A:1505:LYS:HB3	2.45	0.51
3:C:131:ASN:ND2	3:C:223:ASP:OD2	2.44	0.51
3:C:388:VAL:O	3:C:388:VAL:HG22	2.10	0.51
14:G:11:A:N3	14:G:11:A:C5'	2.73	0.51
14:G:11:A:N1	14:G:12:G:N7	2.59	0.51
18:w:478:GLU:HA	23:3:978:LEU:HD11	1.91	0.51
21:1:669:GLN:O	21:1:672:ALA:N	2.44	0.51
23:3:246:SER:O	23:3:260:ASN:ND2	2.44	0.51
23:3:404:LEU:HD23	23:3:407:ILE:HD11	1.92	0.51
23:3:488:GLY:C	23:3:490:THR:H	2.19	0.51
23:3:520:TYR:CE1	23:3:522:ASP:HB2	2.46	0.51
23:3:896:PHE:HB2	23:3:899:THR:HG22	1.93	0.51
28:J:273:TYR:CD1	32:R:228:PRO:HG2	2.46	0.51
33:T:300:ILE:O	33:T:301:ASP:HB2	2.11	0.51
1:A:331:TRP:CE2	3:C:635:LEU:HD22	2.46	0.51
1:A:823:SER:OG	1:A:933:ARG:NH1	2.44	0.51
1:A:1276:GLU:O	1:A:1279:VAL:HG12	2.11	0.51
3:C:93:ILE:CD1	33:T:230:ILE:CD1	2.89	0.51
5:E:276:ILE:C	5:E:277:PHE:HD1	2.19	0.51
15:H:111:G:O3'	15:H:112:G:O4'	2.29	0.51
21:1:475:PHE:CE1	21:1:502:LEU:HB2	2.46	0.51
21:1:582:LEU:HD23	21:1:630:ARG:HB3	1.93	0.51
23:3:556:ILE:HD11	23:3:564:VAL:HB	1.93	0.51
23:3:1144:VAL:O	23:3:1148:LEU:HB2	2.11	0.51
33:T:385:TYR:CE2	33:T:400:PHE:HB3	2.46	0.51
34:V:576:THR:O	34:V:580:ARG:N	2.36	0.51
1:A:434:HIS:C	1:A:434:HIS:HD1	2.19	0.50
1:A:1435:GLY:O	1:A:1438:VAL:HG22	2.10	0.50
3:C:215:VAL:HG11	3:C:242:LEU:HD22	1.93	0.50
23:3:28:GLN:HE22	23:3:343:LYS:HG2	1.77	0.50
23:3:80:VAL:HB	23:3:88:VAL:HG23	1.93	0.50
23:3:110:SER:HB3	26:6:82:ARG:HH12	1.75	0.50
28:J:252:GLU:OE1	28:J:260:ARG:HB3	2.12	0.50
28:J:360:ASP:HA	28:J:363:ARG:HD2	1.91	0.50
32:R:185:GLY:C	32:R:186:VAL:HG13	2.35	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:220:ARG:CB	32:R:220:ARG:HH11	2.24	0.50
1:A:251:ASP:N	1:A:337:VAL:HG21	2.26	0.50
1:A:863:GLU:OE2	1:A:916:LYS:NZ	2.36	0.50
1:A:1930:TYR:HD2	1:A:1931:THR:N	2.09	0.50
1:A:2298:LEU:CD1	4:D:1285:SER:CA	2.89	0.50
3:C:452:THR:O	3:C:578:ARG:N	2.43	0.50
3:C:457:VAL:HG12	3:C:462:GLY:CA	2.41	0.50
3:C:619:THR:O	3:C:620:LYS:HG3	2.11	0.50
3:C:753:GLU:C	3:C:755:ASP:H	2.19	0.50
5:E:229:TYR:CE2	5:E:272:ARG:NH1	2.77	0.50
5:E:276:ILE:C	5:E:277:PHE:CD1	2.89	0.50
15:H:51:A:N6	15:H:63:G:O6	2.44	0.50
23:3:506:LEU:HB3	23:3:547:CYS:SG	2.52	0.50
23:3:669:LEU:HD22	23:3:673:VAL:HG21	1.93	0.50
37:Z:574:ASN:O	37:Z:576:PHE:N	2.44	0.50
3:C:94:ILE:HG21	33:T:259:PRO:HB3	1.92	0.50
3:C:387:ASP:O	3:C:389:ASP:OD1	2.30	0.50
14:G:-12:G:O2'	14:G:-11:G:O5'	2.30	0.50
15:H:153:A:C2'	15:H:154:C:C5'	2.86	0.50
15:H:182:U:C2'	15:H:183:G:H5'	2.41	0.50
21:1:1156:GLU:O	26:6:38:ARG:NH1	2.45	0.50
27:7:32:LEU:HA	27:7:35:GLN:HG2	1.93	0.50
32:R:178:ARG:CD	32:R:194:GLN:HE22	2.07	0.50
32:R:434:TYR:CD1	37:Z:616:VAL:CB	2.95	0.50
33:T:329:HIS:CE1	33:T:355:ARG:HG3	2.46	0.50
1:A:89:LEU:CD2	1:A:656:LEU:HD22	2.42	0.50
1:A:232:LEU:CD1	3:C:412:ILE:HD11	2.37	0.50
1:A:329:LEU:HB3	3:C:177:ARG:HE	1.74	0.50
1:A:368:GLN:HA	1:A:369:GLU:OE2	2.10	0.50
1:A:480:LYS:CG	32:R:203:GLN:OE1	2.58	0.50
1:A:661:GLU:OE2	31:P:28:LYS:HB2	2.11	0.50
1:A:1379:PHE:O	1:A:1382:SER:OG	2.17	0.50
1:A:2073:TRP:HH2	1:A:2310:ARG:NH1	2.09	0.50
3:C:134:LEU:HD23	3:C:226:VAL:HB	1.94	0.50
3:C:140:HIS:HB3	3:C:230:ASP:N	2.26	0.50
3:C:456:GLY:O	3:C:457:VAL:HG13	2.11	0.50
3:C:659:VAL:HG12	3:C:660:VAL:N	2.26	0.50
5:E:277:PHE:CE2	5:E:300:ILE:HD12	2.46	0.50
13:F:35:A:C8	14:G:12:G:N1	2.80	0.50
13:F:37:C:N4	14:G:5:G:OP1	2.44	0.50
14:G:-4:A:H2'	14:G:-3:A:H8	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:897:LEU:HD11	21:1:932:ILE:HD13	1.93	0.50
23:3:757:ILE:HG23	23:3:762:LEU:HD13	1.94	0.50
23:3:996:ILE:HD13	23:3:1041:TYR:HD1	1.75	0.50
32:R:125:MET:O	32:R:126:ASN:HB3	2.11	0.50
32:R:434:TYR:CE2	32:R:436:VAL:HG22	2.43	0.50
33:T:306:CYS:SG	33:T:336:VAL:CB	2.97	0.50
36:Y:86:ASP:HB2	37:Z:502:ALA:HB3	1.93	0.50
1:A:76:MET:SD	1:A:88:TYR:CE1	3.05	0.50
1:A:331:TRP:CE3	1:A:331:TRP:C	2.90	0.50
1:A:393:LEU:HD11	3:C:378:TYR:CB	2.41	0.50
1:A:393:LEU:CD1	3:C:379:LYS:HG3	2.36	0.50
1:A:693:ILE:O	1:A:697:MET:N	2.42	0.50
2:B:42:U:C2	14:G:-3:A:C2	2.82	0.50
3:C:93:ILE:HG21	33:T:218:TRP:CE2	2.46	0.50
3:C:499:GLY:C	3:C:500:THR:HG23	2.36	0.50
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.94	0.50
14:G:132:G:H2'	14:G:133:A:C8	2.46	0.50
21:1:822:ARG:HD3	36:Y:32:TYR:OH	2.12	0.50
23:3:550:ASN:OD1	23:3:551:GLN:N	2.41	0.50
23:3:685:ASP:OD1	23:3:686:LEU:N	2.44	0.50
23:3:807:TYR:HE1	23:3:861:GLN:HG3	1.76	0.50
32:R:101:ILE:O	32:R:104:GLN:HG2	2.08	0.50
33:T:297:HIS:HD2	33:T:338:CYS:SG	2.34	0.50
1:A:173:GLU:OE1	38:z:7:GLN:CB	2.60	0.50
1:A:338:VAL:HG21	3:C:867:PRO:CG	2.42	0.50
1:A:2073:TRP:CH2	1:A:2310:ARG:NH1	2.80	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.47	0.50
3:C:336:TYR:CD1	3:C:336:TYR:C	2.89	0.50
13:F:36:A:C3'	13:F:37:C:C5'	2.85	0.50
15:H:25:G:H2'	15:H:26:A:C8	2.45	0.50
15:H:46:U:O2'	15:H:47:U:OP2	2.25	0.50
15:H:70:C:O5'	15:H:70:C:H6	1.94	0.50
15:H:147:G:N2	15:H:148:C:C2	2.80	0.50
21:1:1003:VAL:HG23	21:1:1004:ILE:H	1.77	0.50
21:1:1132:LEU:O	21:1:1135:GLU:N	2.45	0.50
23:3:300:PHE:CG	23:3:312:LYS:HE2	2.46	0.50
31:P:41:ILE:HD11	33:T:318:ARG:HA	1.92	0.50
31:P:210:PHE:CG	33:T:201:SER:OG	2.64	0.50
39:x:443:ASN:HA	39:x:446:MET:O	2.10	0.50
39:x:452:GLN:O	39:x:498:ASP:N	2.44	0.50
1:A:117:PRO:HG2	1:A:131:GLU:HB2	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:HIS:HA	1:A:481:PHE:O	2.12	0.50
1:A:253:ASN:HB3	3:C:893:GLY:O	2.12	0.50
1:A:386:PRO:HB3	3:C:372:PHE:HD1	1.77	0.50
1:A:1209:HIS:CG	1:A:1210:LYS:H	2.30	0.50
3:C:62:ASP:HB3	31:P:206:LYS:HZ3	1.76	0.50
18:w:150:ILE:CB	18:w:154:ALA:HB3	2.41	0.50
1:A:316:PHE:CE1	3:C:635:LEU:CA	2.94	0.50
1:A:948:PRO:O	1:A:951:LEU:HB2	2.12	0.50
1:A:1505:LYS:HE2	37:Z:615:SER:CA	2.40	0.50
3:C:66:TYR:CD2	33:T:457:GLY:CA	2.79	0.50
3:C:244:LYS:CA	3:C:292:TYR:CD2	2.92	0.50
23:3:1050:PHE:HB3	23:3:1167:TYR:HE2	1.75	0.50
23:3:1147:HIS:O	23:3:1151:GLU:HB2	2.10	0.50
33:T:281:ILE:HD12	33:T:282:ARG:HG2	1.92	0.50
1:A:1119:ASP:N	1:A:1120:PRO:CA	2.74	0.50
1:A:1402:ARG:HH21	37:Z:573:PRO:HG3	1.77	0.50
1:A:2303:GLU:CD	1:A:2303:GLU:H	2.19	0.50
3:C:259:LYS:HE2	3:C:262:ARG:HH11	1.77	0.50
5:E:228:THR:HG22	5:E:229:TYR:HD1	1.77	0.50
13:F:41:A:H2'	13:F:42:C:C6	2.47	0.50
15:H:74:U:O5'	15:H:74:U:H6	1.95	0.50
21:1:595:GLU:O	21:1:599:ASN:ND2	2.45	0.50
23:3:12:THR:HA	23:3:34:ARG:NH1	2.27	0.50
23:3:819:MET:O	23:3:823:MET:HG3	2.12	0.50
35:X:282:LEU:HD23	35:X:295:ASP:HA	1.94	0.50
1:A:122:ILE:HD12	1:A:483:GLN:HG3	1.94	0.49
1:A:686:ARG:HH11	1:A:710:LEU:HD13	1.77	0.49
3:C:499:GLY:O	3:C:500:THR:CG2	2.60	0.49
14:G:132:G:O4'	18:w:399:LEU:CD1	2.57	0.49
21:1:1040:GLY:HA2	21:1:1080:THR:HG22	1.94	0.49
23:3:4:TYR:HB2	23:3:1132:PHE:CZ	2.47	0.49
23:3:458:ALA:HB3	23:3:477:SER:HB3	1.94	0.49
23:3:550:ASN:HD21	23:3:595:VAL:N	2.10	0.49
23:3:1188:ASN:O	23:3:1192:ASN:ND2	2.31	0.49
31:P:66:ARG:HH11	31:P:66:ARG:CG	2.24	0.49
1:A:259:ASP:C	1:A:259:ASP:OD1	2.55	0.49
1:A:348:PRO:O	1:A:350:PHE:N	2.45	0.49
1:A:965:VAL:HG13	1:A:966:TRP:CD1	2.47	0.49
1:A:1403:LEU:O	32:R:412:ASP:CB	2.60	0.49
1:A:1700:GLY:H	1:A:1717:ASN:HD22	1.60	0.49
3:C:116:MET:O	3:C:119:LEU:HB3	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:854:ARG:NH1	3:C:879:ASP:OD2	2.45	0.49
5:E:265:ARG:N	5:E:272:ARG:HH21	2.10	0.49
15:H:181:G:N2	15:H:182:U:C2	2.80	0.49
21:1:717:THR:HG22	21:1:718:PRO:HD3	1.93	0.49
23:3:274:ARG:HG2	23:3:387:PHE:CE1	2.47	0.49
23:3:755:VAL:HG13	23:3:762:LEU:HD11	1.93	0.49
36:Y:48:THR:OG1	36:Y:49:GLU:OE1	2.30	0.49
1:A:387:PHE:CZ	3:C:330:THR:CB	2.96	0.49
1:A:1120:PRO:HG2	1:A:1121:ASN:H	1.78	0.49
2:B:20:G:HI'	2:B:21:A:OP1	2.12	0.49
3:C:78:GLU:OE1	33:T:198:ARG:NH2	2.45	0.49
3:C:297:ASN:HB3	3:C:298:LEU:HD13	1.95	0.49
3:C:493:PHE:HD2	3:C:551:LEU:HD21	1.76	0.49
3:C:715:GLY:HA2	3:C:729:ALA:HB1	1.93	0.49
5:E:164:PRO:O	5:E:166:LEU:HG	2.13	0.49
21:1:499:LYS:HD3	21:1:534:GLN:NE2	2.27	0.49
21:1:652:CYS:HB3	21:1:692:HIS:CE1	2.46	0.49
21:1:827:ARG:O	21:1:830:TYR:HB3	2.12	0.49
23:3:235:LEU:HG	23:3:250:ILE:HG13	1.93	0.49
23:3:1008:SER:OG	23:3:1009:PHE:N	2.45	0.49
1:A:235:MET:CE	1:A:411:PHE:CA	2.84	0.49
1:A:800:TYR:CB	3:C:59:LEU:HD13	2.43	0.49
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.44	0.49
1:A:1310:ARG:NH2	1:A:1563:HIS:O	2.45	0.49
1:A:1760:GLU:HB2	1:A:1761:PRO:HD2	1.93	0.49
1:A:1807:ILE:HB	1:A:1820:LYS:HB3	1.92	0.49
1:A:2325:VAL:HG11	4:D:789:MET:HA	1.94	0.49
3:C:62:ASP:HB3	31:P:206:LYS:NZ	2.27	0.49
3:C:66:TYR:CE2	31:P:211:VAL:HG11	2.45	0.49
3:C:349:PHE:CD1	3:C:356:PHE:HE1	2.22	0.49
15:H:37:U:H2'	15:H:38:A:H8	1.77	0.49
23:3:253:GLU:OE2	23:3:284:GLY:HA3	2.12	0.49
23:3:483:LEU:HD11	23:3:493:GLU:HG3	1.94	0.49
32:R:433:ILE:HG13	32:R:434:TYR:O	2.12	0.49
37:Z:524:ARG:CD	37:Z:524:ARG:C	2.85	0.49
39:x:640:ARG:CB	39:x:667:ALA:CA	2.88	0.49
1:A:115:ASP:CB	1:A:486:LYS:HE2	2.42	0.49
1:A:366:LYS:N	1:A:366:LYS:CE	2.73	0.49
1:A:409:ARG:N	1:A:410:PRO:HD2	2.26	0.49
1:A:1405:LEU:N	32:R:415:LEU:HD21	2.27	0.49
1:A:1818:PHE:CD2	1:A:1848:LEU:HD21	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:133:THR:O	3:C:226:VAL:CB	2.60	0.49
3:C:335:ASN:OD1	3:C:336:TYR:N	2.45	0.49
3:C:709:TRP:N	3:C:709:TRP:CD1	2.79	0.49
11:l:15:VAL:O	12:n:33:GLY:HA3	2.12	0.49
23:3:994:GLN:HE22	23:3:1037:SER:HA	1.78	0.49
32:R:231:VAL:HG23	32:R:232:MET:N	2.26	0.49
32:R:450:SER:OG	32:R:452:TYR:O	2.30	0.49
37:Z:563:ARG:CG	37:Z:563:ARG:NH2	2.73	0.49
1:A:690:MET:HG3	1:A:694:LEU:HD12	1.95	0.49
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.95	0.49
1:A:1809:ILE:HD11	1:A:1845:VAL:HG22	1.93	0.49
3:C:709:TRP:CD1	3:C:709:TRP:H	2.30	0.49
5:E:67:GLY:H	5:E:87:ASP:CG	2.20	0.49
13:F:36:A:C8	13:F:36:A:H5'	2.48	0.49
16:o:46:ALA:HB1	16:o:68:THR:C	2.34	0.49
21:1:805:TYR:CE1	21:1:809:GLU:HG3	2.46	0.49
23:3:23:SER:HA	23:3:94:PRO:HG3	1.95	0.49
23:3:794:SER:HB2	23:3:933:ASN:O	2.12	0.49
23:3:1048:ASP:OD1	23:3:1049:LYS:N	2.45	0.49
28:J:331:GLN:CG	32:R:98:TYR:OH	2.47	0.49
37:Z:526:ILE:N	37:Z:526:ILE:HD12	2.27	0.49
1:A:347:LEU:HD13	1:A:351:TYR:OH	2.12	0.49
1:A:800:TYR:HB3	3:C:59:LEU:HD13	1.95	0.49
1:A:2097:ILE:HD12	1:A:2099:GLU:HB2	1.93	0.49
3:C:140:HIS:O	3:C:258:ASN:HB3	2.13	0.49
3:C:363:SER:O	3:C:364:SER:CB	2.60	0.49
18:w:485:ASN:ND2	23:3:976:LYS:N	2.57	0.49
21:1:1017:LEU:HD21	21:1:1058:ILE:HD11	1.93	0.49
21:1:1273:TYR:OH	21:1:1277:GLN:NE2	2.46	0.49
23:3:31:VAL:HG21	23:3:78:ILE:HD11	1.95	0.49
23:3:440:HIS:ND1	23:3:720:TRP:CH2	2.80	0.49
23:3:527:ILE:HA	23:3:532:ARG:O	2.12	0.49
34:V:525:PHE:O	34:V:526:GLU:C	2.55	0.49
37:Z:597:ARG:HH12	37:Z:601:LEU:CD1	2.22	0.49
1:A:251:ASP:HA	1:A:337:VAL:HG21	1.94	0.49
1:A:1618:LYS:HD2	1:A:1626:CYS:H	1.78	0.49
1:A:1718:TRP:HZ3	1:A:1726:ILE:HD12	1.77	0.49
1:A:2287:ARG:HH22	4:D:1147:ASN:CB	2.15	0.49
3:C:73:TYR:CZ	33:T:487:LYS:CE	2.95	0.49
3:C:137:HIS:NE2	3:C:236:MET:CE	2.75	0.49
3:C:705:VAL:HG21	3:C:718:PHE:CZ	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:74:PHE:HE1	5:E:95:VAL:CG2	2.25	0.49
11:e:15:VAL:O	12:g:33:GLY:HA3	2.12	0.49
13:F:53:A:C6	13:F:54:G:C5	3.00	0.49
14:G:5:G:H2'	14:G:5:G:N3	2.28	0.49
14:G:155:U:H4'	14:G:156:U:OP2	2.13	0.49
15:H:107:A:C2	15:H:108:G:C4	3.01	0.49
15:H:143:A:N3	15:H:143:A:C3'	2.73	0.49
21:1:175:LYS:O	21:1:179:GLY:HA3	2.11	0.49
21:1:1134:ASN:ND2	22:2:534:GLN:HA	2.28	0.49
23:3:47:THR:HG23	23:3:49:LYS:H	1.77	0.49
23:3:785:PRO:HA	23:3:801:GLU:HA	1.95	0.49
24:4:32:LEU:HD21	24:4:79:LEU:HD21	1.94	0.49
31:P:189:ASP:C	31:P:191:ASP:N	2.68	0.49
32:R:55:LEU:CA	32:R:73:PRO:O	2.61	0.49
1:A:87:VAL:HG13	32:R:205:ASP:OD2	2.13	0.49
1:A:1393:ARG:O	1:A:1397:ILE:HG13	2.12	0.49
3:C:301:SER:O	3:C:303:LEU:N	2.44	0.49
3:C:499:GLY:O	3:C:500:THR:HG23	2.13	0.49
5:E:219:VAL:HB	5:E:229:TYR:HB2	1.95	0.49
26:6:43:VAL:HG21	26:6:69:ALA:HB3	1.94	0.49
32:R:131:ASP:OD2	32:R:132:LEU:CD2	2.60	0.49
33:T:442:ARG:HB3	33:T:443:THR:HG23	1.95	0.49
36:Y:38:ILE:HG22	36:Y:90:THR:HG23	1.95	0.49
1:A:91:ALA:O	1:A:94:TYR:N	2.43	0.49
1:A:273:ILE:CG2	1:A:274:PRO:HD2	2.42	0.49
1:A:660:PHE:HB3	32:R:210:PRO:O	2.13	0.49
1:A:2113:LYS:HE2	4:D:1229:ASP:CA	2.41	0.49
3:C:381:LEU:CD2	3:C:416:LEU:HD22	2.42	0.49
5:E:74:PHE:HE1	5:E:95:VAL:HG22	1.77	0.49
15:H:71:C:H2'	15:H:72:U:H6	1.75	0.49
32:R:433:ILE:O	32:R:434:TYR:HB3	2.13	0.49
38:z:11:THR:HG21	38:z:132:LYS:HE2	1.95	0.49
1:A:44:ARG:CG	1:A:45:TYR:CE2	2.95	0.48
1:A:529:THR:HG22	30:M:197:TYR:HB3	1.95	0.48
1:A:1870:ASP:HB2	1:A:1871:PRO:HD3	1.95	0.48
1:A:1998:ASN:O	1:A:2001:SER:OG	2.23	0.48
3:C:82:GLN:HG3	33:T:237:LYS:HA	1.94	0.48
3:C:334:ILE:HD12	3:C:334:ILE:O	2.13	0.48
5:E:153:PHE:N	5:E:153:PHE:CD1	2.78	0.48
13:F:26:U:H3'	13:F:27:A:C5'	2.37	0.48
15:H:45:C:N3	18:w:395:TRP:CB	2.75	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:408:PHE:HB2	25:5:49:ARG:NH1	2.28	0.48
23:3:734:LEU:HD13	23:3:767:LEU:HD21	1.94	0.48
32:R:118:ASP:OD1	32:R:232:MET:HE1	2.13	0.48
33:T:342:GLU:O	33:T:343:PRO:C	2.56	0.48
1:A:794:TYR:CD2	1:A:1028:TYR:HB2	2.47	0.48
1:A:1301:ILE:HD11	2:B:39:C:H5''	1.91	0.48
1:A:1457:HIS:CE1	32:R:424:SER:C	2.90	0.48
3:C:508:LYS:HB3	3:C:566:THR:HG23	1.95	0.48
3:C:855:GLY:O	3:C:856:HIS:CB	2.44	0.48
5:E:162:ARG:HH22	5:E:204:THR:HA	1.74	0.48
13:F:54:G:N2	15:H:22:U:C2	2.81	0.48
14:G:11:A:N3	14:G:11:A:C3'	2.76	0.48
15:H:5:C:H2'	15:H:6:U:H6	1.78	0.48
21:1:483:ASP:OD1	21:1:484:GLU:N	2.46	0.48
23:3:446:GLU:CD	23:3:763:ARG:HD3	2.38	0.48
28:J:360:ASP:HA	28:J:363:ARG:CG	2.44	0.48
38:z:56:ARG:HD3	38:z:64:GLN:OE1	2.13	0.48
1:A:267:LYS:NZ	2:B:49:A:P	2.85	0.48
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.95	0.48
1:A:828:PRO:HG3	1:A:925:TYR:CZ	2.48	0.48
1:A:1214:TRP:CZ2	1:A:1230:LEU:HD11	2.48	0.48
1:A:2298:LEU:HD11	4:D:1285:SER:CA	2.43	0.48
3:C:73:TYR:CE1	33:T:453:ALA:O	2.67	0.48
3:C:230:ASP:CG	3:C:259:LYS:HZ1	2.20	0.48
3:C:297:ASN:HD22	3:C:298:LEU:CD1	2.26	0.48
3:C:333:ASP:OD1	3:C:333:ASP:N	2.42	0.48
3:C:401:ILE:HD11	3:C:423:PHE:HB2	1.96	0.48
13:F:49:G:H2'	13:F:50:A:H8	1.78	0.48
14:G:138:A:H5''	29:L:12:ARG:NE	2.28	0.48
15:H:10:C:H2'	15:H:11:G:C8	2.40	0.48
23:3:157:PRO:HD2	26:6:16:GLY:HA2	1.95	0.48
23:3:870:ASN:ND2	23:3:873:GLN:H	2.10	0.48
33:T:302:VAL:HG23	33:T:315:TRP:O	2.14	0.48
37:Z:604:LYS:HA	37:Z:607:VAL:HG23	1.94	0.48
1:A:412:ASN:OD1	1:A:413:LEU:HD23	2.13	0.48
1:A:2149:PRO:O	1:A:2160:PRO:HD3	2.13	0.48
3:C:291:MET:CG	3:C:292:TYR:CE1	2.96	0.48
3:C:443:VAL:O	3:C:447:PRO:CD	2.62	0.48
3:C:452:THR:O	3:C:577:PHE:CA	2.60	0.48
13:F:8:C:H6	13:F:8:C:C5'	2.15	0.48
13:F:66:C:H2'	13:F:67:G:O4'	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:-8:U:H2'	14:G:-7:C:O4'	2.13	0.48
14:G:9:C:H2'	14:G:10:U:C6	2.48	0.48
15:H:25:G:N3	15:H:26:A:C8	2.82	0.48
23:3:886:GLU:OE1	23:3:926:TYR:OH	2.24	0.48
23:3:1149:ARG:HH12	23:3:1161:LEU:HD13	1.79	0.48
28:J:339:TRP:C	32:R:116:TYR:CE2	2.92	0.48
28:J:406:PHE:HB3	28:J:411:MET:HG2	1.96	0.48
32:R:433:ILE:HG13	32:R:434:TYR:N	2.27	0.48
35:X:212:ASN:H	35:X:307:GLN:HE22	1.60	0.48
1:A:210:HIS:CD2	1:A:210:HIS:C	2.92	0.48
1:A:258:PHE:HZ	1:A:275:GLY:O	1.96	0.48
1:A:387:PHE:HD1	3:C:327:TYR:CD1	2.31	0.48
1:A:774:LYS:HG2	15:H:23:A:C8	2.48	0.48
1:A:1214:TRP:NE1	1:A:1276:GLU:OE1	2.23	0.48
3:C:911:PRO:HB2	3:C:934:MET:HE3	1.95	0.48
13:F:45:A:H4'	13:F:46:G:OP2	2.14	0.48
13:F:53:A:C6	15:H:25:G:C4	3.02	0.48
21:1:1167:TYR:O	21:1:1170:THR:OG1	2.25	0.48
23:3:457:ASN:HD21	23:3:504:PRO:HB3	1.79	0.48
23:3:458:ALA:C	23:3:757:ILE:HG12	2.39	0.48
23:3:624:CYS:SG	23:3:625:LEU:HD13	2.54	0.48
23:3:930:LEU:HA	23:3:937:LEU:HD23	1.95	0.48
27:7:40:TYR:HA	27:7:43:TYR:CD2	2.49	0.48
32:R:103:ARG:CG	32:R:103:ARG:NH1	2.75	0.48
32:R:419:SER:C	32:R:420:LYS:O	2.55	0.48
33:T:185:MET:CB	33:T:186:PRO:CD	2.90	0.48
33:T:213:GLU:HB2	33:T:218:TRP:O	2.14	0.48
34:V:549:LYS:O	34:V:552:ALA:CB	2.60	0.48
38:z:72:GLY:C	38:z:112:GLN:HE22	2.22	0.48
1:A:323:LEU:N	1:A:324:PRO:CD	2.77	0.48
1:A:366:LYS:N	1:A:366:LYS:HD3	2.27	0.48
1:A:595:LYS:CE	1:A:644:ILE:HD11	2.38	0.48
1:A:718:ARG:HH21	32:R:259:LYS:CE	2.25	0.48
1:A:1370:ARG:NH1	34:V:468:ASP:H	2.09	0.48
3:C:350:ASN:HB3	3:C:353:THR:HG23	1.94	0.48
3:C:445:ALA:O	3:C:449:ILE:HG13	2.12	0.48
3:C:678:THR:HG23	3:C:683:ASN:CA	2.43	0.48
3:C:736:GLY:N	3:C:770:PHE:HE2	2.10	0.48
21:1:1212:LEU:HD13	21:1:1237:LEU:HD13	1.96	0.48
23:3:142:TYR:CE1	23:3:157:PRO:HB3	2.48	0.48
23:3:565:TYR:CG	23:3:619:LEU:HD13	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1055:VAL:HG23	23:3:1093:MET:HE2	1.95	0.48
32:R:215:ASN:HD22	32:R:216:LYS:N	2.11	0.48
1:A:338:VAL:HG21	3:C:867:PRO:HD2	1.96	0.48
1:A:1295:ILE:HG13	1:A:1296:GLN:N	2.29	0.48
3:C:135:CYS:SG	3:C:227:LEU:HA	2.54	0.48
3:C:149:LEU:CA	3:C:427:PHE:CE2	2.97	0.48
3:C:349:PHE:HB2	3:C:356:PHE:CE1	2.48	0.48
3:C:514:TYR:CD1	3:C:515:THR:N	2.82	0.48
15:H:83:A:C2	15:H:84:C:N3	2.82	0.48
17:p:152:ILE:O	17:p:222:TYR:HA	2.13	0.48
21:1:634:VAL:O	21:1:637:SER:OG	2.27	0.48
23:3:842:PHE:HD2	23:3:843:LEU:HD12	1.78	0.48
23:3:926:TYR:HE1	23:3:942:LYS:HG3	1.77	0.48
28:J:273:TYR:CZ	32:R:228:PRO:CB	2.82	0.48
32:R:55:LEU:C	32:R:73:PRO:O	2.56	0.48
38:z:25:ASP:HB2	38:z:134:THR:OG1	2.13	0.48
1:A:549:GLU:CD	1:A:552:ARG:NH1	2.72	0.48
1:A:1332:HIS:HB3	1:A:1359:HIS:HE1	1.78	0.48
1:A:2298:LEU:HD11	4:D:1265:GLN:CB	2.44	0.48
3:C:82:GLN:O	33:T:202:GLY:HA3	2.13	0.48
3:C:457:VAL:HG12	3:C:462:GLY:HA3	1.96	0.48
3:C:477:HIS:HD1	3:C:478:THR:N	2.12	0.48
5:E:243:LEU:HD11	5:E:247:GLY:CA	2.41	0.48
14:G:17:U:H2'	14:G:18:A:C8	2.49	0.48
15:H:83:A:C2	15:H:84:C:C4	3.01	0.48
18:w:444:ALA:O	18:w:446:PHE:N	2.47	0.48
21:1:1297:ARG:NH1	27:7:39:SER:OG	2.46	0.48
33:T:384:HIS:O	33:T:385:TYR:HB3	2.13	0.48
1:A:253:ASN:CG	1:A:334:THR:O	2.57	0.48
1:A:405:LEU:HD11	3:C:265:LEU:HD22	1.96	0.48
1:A:630:TRP:CD1	1:A:630:TRP:H	2.30	0.48
1:A:1892:PRO:HD3	1:A:1941:ARG:HH21	1.79	0.48
3:C:128:LEU:O	3:C:199:LEU:N	2.37	0.48
3:C:690:GLU:HB2	3:C:691:PRO:HD2	1.95	0.48
13:F:44:G:H2'	22:2:554:ARG:HG2	1.96	0.48
15:H:37:U:H2'	15:H:38:A:C8	2.49	0.48
15:H:73:C:HO2'	15:H:74:U:H5'	1.77	0.48
18:w:479:TYR:H	18:w:484:GLY:HA3	1.79	0.48
22:2:636:MET:HE1	24:4:35:GLN:O	2.14	0.48
22:2:652:GLY:N	22:2:655:SER:O	2.45	0.48
23:3:21:ASN:HD21	23:3:28:GLN:HG2	1.77	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:58:VAL:HG12	23:3:1155:LEU:HB3	1.95	0.48
23:3:539:PRO:HD2	23:3:558:LEU:HD21	1.95	0.48
23:3:891:VAL:HA	23:3:906:LEU:O	2.13	0.48
23:3:1057:ARG:HG2	23:3:1058:LEU:O	2.13	0.48
32:R:184:GLN:O	32:R:188:PHE:HB2	2.13	0.48
34:V:576:THR:O	34:V:579:SER:N	2.47	0.48
36:Y:110:ASP:OD1	36:Y:111:HIS:N	2.43	0.48
1:A:417:ARG:NH1	2:B:58:U:C5'	2.77	0.48
1:A:529:THR:HB	30:M:199:PRO:CD	2.44	0.48
1:A:546:LEU:HD11	1:A:595:LYS:CG	2.43	0.48
1:A:731:LEU:HD23	1:A:736:GLU:HB2	1.94	0.48
1:A:2073:TRP:CD1	1:A:2073:TRP:C	2.91	0.48
1:A:2310:ARG:HH11	1:A:2310:ARG:CG	2.27	0.48
1:A:2328:ALA:HB3	4:D:787:ALA:C	2.38	0.48
2:B:42:U:H2'	2:B:43:U:O4'	2.13	0.48
3:C:93:ILE:O	3:C:94:ILE:CB	2.62	0.48
3:C:145:PHE:HB2	3:C:312:SER:CB	2.32	0.48
16:o:46:ALA:CA	16:o:68:THR:O	2.61	0.48
21:1:208:PRO:N	21:1:656:LYS:HE3	2.29	0.48
23:3:476:VAL:O	23:3:482:THR:HA	2.14	0.48
23:3:981:CYS:SG	23:3:1021:LEU:HG	2.54	0.48
32:R:402:ASN:HB2	35:X:192:ARG:CG	2.43	0.48
32:R:415:LEU:C	32:R:417:ASN:N	2.67	0.48
34:V:527:GLY:O	34:V:530:LYS:N	2.47	0.48
1:A:238:LEU:HB3	1:A:411:PHE:HE2	1.79	0.47
1:A:356:ILE:HG23	3:C:865:GLY:C	2.39	0.47
1:A:409:ARG:HD2	1:A:409:ARG:O	2.14	0.47
1:A:758:ARG:HD2	1:A:775:ASN:ND2	2.28	0.47
1:A:1183:PRO:HA	1:A:1201:ARG:HE	1.78	0.47
1:A:1754:TYR:CD1	21:1:948:ARG:NH1	2.82	0.47
1:A:1768:TYR:HA	1:A:1771:LEU:CB	2.40	0.47
3:C:557:GLN:N	3:C:558:PRO:HD2	2.29	0.47
5:E:263:ASP:OD1	5:E:272:ARG:HB3	2.13	0.47
13:F:44:G:N2	14:G:3:A:C8	2.82	0.47
21:1:209:GLY:HA3	21:1:614:ARG:NH1	2.29	0.47
21:1:823:MET:HE3	21:1:829:ASN:HB3	1.95	0.47
23:3:353:PHE:HB3	23:3:406:PRO:HD3	1.96	0.47
23:3:814:GLN:O	23:3:818:GLN:HB2	2.13	0.47
26:6:19:ILE:HD12	26:6:42:LEU:HD21	1.96	0.47
28:J:273:TYR:CD2	32:R:228:PRO:HG3	2.49	0.47
32:R:120:VAL:CG2	32:R:121:PRO:HD2	2.44	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:X:246:TYR:H	35:X:386:ASP:HA	1.79	0.47
1:A:134:TRP:HB3	1:A:418:THR:HG22	1.95	0.47
1:A:330:THR:O	1:A:331:TRP:CB	2.62	0.47
1:A:666:LYS:HE2	32:R:217:LYS:HG3	1.96	0.47
1:A:1045:GLY:HA3	1:A:1090:ARG:NH2	2.29	0.47
1:A:1270:LEU:HD12	1:A:1274:PHE:CD2	2.49	0.47
1:A:1551:PHE:O	1:A:1553:VAL:HG23	2.14	0.47
3:C:753:GLU:O	3:C:755:ASP:N	2.45	0.47
5:E:269:PRO:O	5:E:270:LYS:CB	2.54	0.47
13:F:12:G:H2'	13:F:13:G:O4'	2.14	0.47
15:H:151:C:C2	15:H:152:G:N7	2.82	0.47
21:1:1124:SER:O	21:1:1127:THR:OG1	2.28	0.47
21:1:1212:LEU:HD22	21:1:1246:MET:HE1	1.96	0.47
23:3:675:LEU:HD23	23:3:686:LEU:HD11	1.96	0.47
23:3:1095:TYR:CZ	23:3:1164:ARG:HD2	2.49	0.47
26:6:23:CYS:HB3	26:6:58:CYS:HB2	1.97	0.47
27:7:69:MET:HA	27:7:72:MET:HG2	1.96	0.47
28:J:436:TYR:OH	28:J:458:PHE:HA	2.14	0.47
33:T:416:ILE:O	33:T:416:ILE:HD13	2.14	0.47
1:A:350:PHE:HE2	1:A:398:THR:HG21	1.79	0.47
1:A:1258:LYS:HE2	32:R:432:GLU:CA	2.44	0.47
1:A:2148:VAL:O	1:A:2150:GLN:HG2	2.14	0.47
1:A:2328:ALA:CB	4:D:787:ALA:C	2.87	0.47
3:C:66:TYR:OH	31:P:216:ARG:HD2	2.13	0.47
3:C:73:TYR:HE1	33:T:453:ALA:O	1.97	0.47
3:C:441:PRO:O	3:C:444:GLY:CA	2.61	0.47
3:C:449:ILE:HD12	3:C:466:SER:OG	2.13	0.47
3:C:673:LYS:HB3	3:C:688:ILE:HG22	1.96	0.47
5:E:178:LEU:CD2	5:E:208:ILE:HD13	2.44	0.47
14:G:138:A:H2'	14:G:139:U:C6	2.49	0.47
21:1:1252:GLN:HG2	22:2:492:LYS:HA	1.96	0.47
23:3:240:GLY:HA3	23:3:246:SER:HB2	1.95	0.47
23:3:867:ARG:HD3	23:3:869:MET:HE3	1.95	0.47
27:7:33:VAL:HG23	27:7:75:PRO:HG2	1.96	0.47
32:R:73:PRO:HG2	32:R:74:LEU:H	1.79	0.47
32:R:189:ASN:HD21	32:R:195:ARG:CZ	2.26	0.47
32:R:250:LYS:HD3	32:R:250:LYS:C	2.39	0.47
34:V:585:ILE:O	34:V:586:PHE:C	2.58	0.47
34:V:625:ARG:O	34:V:629:ASN:CB	2.62	0.47
36:Y:63:VAL:HG23	36:Y:64:ASN:H	1.78	0.47
1:A:121:HIS:O	1:A:123:THR:N	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1192:PHE:HE1	1:A:1274:PHE:CD1	2.32	0.47
1:A:1439:ARG:O	1:A:1443:LYS:HG2	2.15	0.47
1:A:1900:GLU:CD	37:Z:521:PRO:HB2	2.34	0.47
2:B:20:G:OP1	2:B:20:G:H4'	2.12	0.47
3:C:240:GLU:OE2	3:C:292:TYR:OH	2.18	0.47
3:C:438:ILE:CD1	3:C:438:ILE:N	2.76	0.47
14:G:17:U:H2'	14:G:18:A:H8	1.79	0.47
14:G:149:G:N2	14:G:150:U:H2'	2.29	0.47
21:1:464:LEU:HD23	21:1:478:LEU:HD21	1.95	0.47
21:1:781:ASP:HB3	21:1:784:MET:HB2	1.95	0.47
23:3:54:LEU:HD22	23:3:98:MET:HA	1.97	0.47
23:3:120:PHE:HB2	23:3:133:SER:OG	2.15	0.47
26:6:21:ARG:HG3	26:6:56:GLY:HA2	1.96	0.47
26:6:57:ARG:HD2	26:6:62:GLY:C	2.40	0.47
31:P:228:ILE:CD1	31:P:228:ILE:N	2.78	0.47
1:A:203:VAL:HG12	1:A:207:PHE:CD1	2.49	0.47
1:A:2252:LEU:HD23	1:A:2253:PRO:HD2	1.96	0.47
2:B:44:A:H2	14:G:-5:G:O6	1.97	0.47
3:C:73:TYR:OH	33:T:487:LYS:CE	2.62	0.47
3:C:185:PRO:HD3	3:C:482:TYR:CE1	2.50	0.47
5:E:161:ARG:HH11	5:E:161:ARG:CG	2.26	0.47
21:1:869:MET:HE3	21:1:913:GLY:HA3	1.96	0.47
21:1:1172:LEU:HA	22:2:522:PHE:HE1	1.79	0.47
23:3:354:GLY:HA3	23:3:432:ARG:NH1	2.30	0.47
31:P:192:VAL:HG12	31:P:193:VAL:N	2.29	0.47
32:R:103:ARG:NH2	32:R:110:LYS:O	2.40	0.47
32:R:178:ARG:CD	32:R:194:GLN:NE2	2.72	0.47
38:z:29:TRP:HB3	38:z:32:GLU:OE1	2.15	0.47
1:A:393:LEU:HD13	3:C:375:GLU:HG3	1.95	0.47
3:C:507:VAL:HG12	3:C:508:LYS:N	2.29	0.47
14:G:-5:G:O2'	14:G:-4:A:H8	1.98	0.47
15:H:57:A:H2'	15:H:58:U:O4'	2.14	0.47
21:1:404:LEU:HD23	25:5:47:GLN:CD	2.39	0.47
21:1:754:ILE:HA	21:1:757:MET:HE2	1.96	0.47
21:1:1140:GLU:O	21:1:1144:GLN:HG3	2.15	0.47
23:3:459:VAL:HB	23:3:757:ILE:HG23	1.97	0.47
23:3:554:VAL:HB	23:3:566:PHE:HB2	1.97	0.47
28:J:216:ASP:O	28:J:219:GLU:N	2.47	0.47
28:J:375:ASP:O	28:J:376:VAL:C	2.58	0.47
32:R:51:ILE:N	32:R:52:PRO:CD	2.77	0.47
33:T:318:ARG:HH11	33:T:319:THR:CG2	2.28	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:GLU:CD	1:A:36:LYS:HE3	2.39	0.47
1:A:121:HIS:HE2	1:A:481:PHE:CB	2.14	0.47
1:A:340:ILE:HD13	1:A:340:ILE:N	2.29	0.47
1:A:363:HIS:HD2	3:C:283:ASP:O	1.98	0.47
1:A:378:PHE:CD1	1:A:378:PHE:C	2.93	0.47
1:A:639:PHE:O	2:B:28:A:O2'	2.31	0.47
1:A:664:HIS:HE1	1:A:666:LYS:HB2	1.71	0.47
1:A:735:ILE:O	1:A:738:MET:HB3	2.15	0.47
1:A:1241:HIS:ND1	1:A:1287:LEU:HD11	2.29	0.47
2:B:41:U:H2'	2:B:42:U:C6	2.49	0.47
3:C:749:THR:O	3:C:753:GLU:HB2	2.14	0.47
5:E:255:MET:C	5:E:257:ASN:H	2.22	0.47
18:w:485:ASN:HA	23:3:978:LEU:CG	2.44	0.47
21:1:903:GLN:HE22	21:1:910:MET:HG3	1.80	0.47
23:3:18:ILE:HD13	23:3:65:LEU:HG	1.96	0.47
23:3:931:VAL:O	23:3:936:LYS:N	2.40	0.47
23:3:1032:TRP:O	23:3:1048:ASP:HA	2.15	0.47
28:J:273:TYR:CE2	32:R:228:PRO:HB3	2.46	0.47
31:P:227:TYR:N	31:P:227:TYR:CD1	2.81	0.47
32:R:129:ASP:HB3	32:R:131:ASP:CG	2.40	0.47
33:T:257:ARG:HD3	33:T:301:ASP:OD1	2.14	0.47
36:Y:40:LEU:HB2	36:Y:43:LEU:HD11	1.96	0.47
1:A:195:LEU:H	1:A:195:LEU:HD12	1.80	0.47
1:A:592:TYR:O	1:A:595:LYS:O	2.32	0.47
1:A:1455:TRP:CE3	1:A:1456:THR:HB	2.50	0.47
2:B:43:U:H5'	13:F:67:G:H22	1.79	0.47
3:C:115:GLU:O	3:C:118:PHE:CA	2.61	0.47
3:C:457:VAL:CA	3:C:462:GLY:HA3	2.44	0.47
7:i:57:LYS:CA	18:w:316:ARG:O	2.63	0.47
21:1:207:THR:HA	21:1:656:LYS:NZ	2.28	0.47
21:1:699:GLN:HA	21:1:702:ARG:CZ	2.45	0.47
23:3:164:ASN:ND2	23:3:189:TYR:OH	2.34	0.47
23:3:304:GLN:HA	23:3:309:ASP:O	2.15	0.47
23:3:931:VAL:HG12	23:3:932:ASN:N	2.26	0.47
25:5:14:PRO:HB2	25:5:16:GLU:OE1	2.15	0.47
33:T:246:ILE:HB	33:T:267:ASP:OD1	2.15	0.47
38:z:99:VAL:HG12	38:z:130:PHE:CZ	2.50	0.47
1:A:97:HIS:HD2	1:A:473:PHE:HZ	1.59	0.47
1:A:695:ASP:HB3	33:T:374:SER:CB	2.38	0.47
1:A:1608:THR:HG22	1:A:1632:PHE:HB2	1.97	0.47
21:1:535:ILE:O	21:1:538:LEU:N	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:760:GLU:N	21:1:760:GLU:OE1	2.47	0.47
21:1:1132:LEU:HD11	21:1:1150:SER:OG	2.14	0.47
23:3:5:ASN:OD1	23:3:6:LEU:N	2.47	0.47
23:3:212:GLU:OE1	23:3:223:LYS:HD2	2.15	0.47
23:3:498:GLY:HA3	23:3:531:LYS:NZ	2.30	0.47
32:R:67:ILE:HG22	32:R:69:VAL:HG21	1.97	0.47
34:V:467:LEU:O	34:V:468:ASP:CB	2.62	0.47
34:V:547:VAL:O	34:V:548:ALA:C	2.58	0.47
39:x:452:GLN:N	39:x:496:MET:O	2.45	0.47
2:B:12:U:H3	2:B:65:G:H1	1.62	0.47
2:B:41:U:C4	14:G:-1:G:N1	2.83	0.47
3:C:470:PRO:CA	3:C:499:GLY:HA2	2.42	0.47
3:C:490:PHE:CE1	3:C:612:LYS:HD2	2.49	0.47
13:F:49:G:H2'	13:F:50:A:C8	2.50	0.47
14:G:156:U:P	14:G:156:U:H3'	2.54	0.47
15:H:6:U:H2'	15:H:7:U:H6	1.80	0.47
15:H:47:U:H4'	15:H:48:A:OP1	2.15	0.47
15:H:153:A:C8	15:H:154:C:H5'	2.50	0.47
22:2:642:PRO:HG3	22:2:648:LEU:HD22	1.97	0.47
23:3:182:PHE:O	23:3:210:PHE:HA	2.15	0.47
23:3:458:ALA:HA	23:3:741:PHE:CB	2.45	0.47
28:J:255:LEU:CD2	29:L:235:LEU:HD13	2.38	0.47
1:A:67:ARG:HD3	1:A:179:ALA:CB	2.34	0.46
1:A:277:PRO:HA	1:A:448:GLN:HG3	1.96	0.46
1:A:316:PHE:HE1	3:C:635:LEU:CA	2.27	0.46
1:A:437:ALA:O	1:A:439:GLN:HG2	2.15	0.46
1:A:748:ASP:OD2	33:T:484:LYS:NZ	2.43	0.46
1:A:755:HIS:HE1	31:P:223:PHE:CB	2.14	0.46
1:A:1256:PHE:CZ	1:A:1302:GLY:HA3	2.51	0.46
1:A:1364:LEU:HD13	34:V:461:LEU:O	2.15	0.46
1:A:1718:TRP:CZ3	1:A:1723:LYS:HA	2.50	0.46
2:B:43:U:O4	14:G:-4:A:C6	2.68	0.46
3:C:82:GLN:HG3	33:T:238:LEU:N	2.30	0.46
3:C:244:LYS:HG3	3:C:292:TYR:CD2	2.50	0.46
3:C:571:ASN:O	3:C:572:GLU:HB3	2.16	0.46
17:p:179:GLU:CB	17:p:193:GLU:CB	2.93	0.46
21:1:815:PHE:HA	21:1:819:TRP:HD1	1.81	0.46
21:1:1058:ILE:O	21:1:1062:LEU:HG	2.16	0.46
23:3:145:ASN:O	23:3:153:THR:OG1	2.26	0.46
23:3:248:VAL:HG23	23:3:250:ILE:HD11	1.96	0.46
31:P:64:GLU:OE2	31:P:68:ARG:NE	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:GLU:HB2	2:B:48:A:O4'	2.15	0.46
1:A:414:ARG:NH1	3:C:408:LEU:O	2.43	0.46
1:A:1209:HIS:CG	1:A:1210:LYS:N	2.83	0.46
1:A:1212:GLY:HA3	1:A:1280:ASN:ND2	2.31	0.46
1:A:1399:GLN:C	1:A:1401:ARG:H	2.24	0.46
1:A:1824:THR:HA	1:A:1827:TRP:HD1	1.80	0.46
1:A:1892:PRO:HG3	1:A:1941:ARG:HE	1.81	0.46
2:B:42:U:O5'	2:B:42:U:H6	1.97	0.46
2:B:44:A:C2	14:G:-5:G:O6	2.69	0.46
3:C:262:ARG:HG2	41:C:1500:GTP:N2	2.30	0.46
3:C:350:ASN:CB	3:C:353:THR:HG23	2.45	0.46
5:E:274:VAL:C	5:E:275:LYS:HG3	2.40	0.46
13:F:78:A:H8	13:F:78:A:OP2	1.98	0.46
15:H:150:U:H2'	15:H:151:C:C6	2.50	0.46
21:1:732:TRP:HB2	21:1:765:TYR:HE1	1.79	0.46
21:1:738:HIS:CE1	21:1:746:PHE:HE2	2.32	0.46
21:1:1169:VAL:HG12	21:1:1173:LEU:HG	1.97	0.46
23:3:28:GLN:NE2	23:3:343:LYS:HG2	2.31	0.46
23:3:1005:VAL:O	23:3:1032:TRP:HA	2.15	0.46
28:J:239:ARG:C	28:J:239:ARG:HD3	2.40	0.46
31:P:188:TRP:C	31:P:190:ASP:H	2.21	0.46
1:A:388:LEU:HB3	1:A:391:THR:OG1	2.16	0.46
1:A:405:LEU:HD21	3:C:385:VAL:HG12	1.98	0.46
1:A:844:GLU:O	1:A:848:GLU:HG2	2.15	0.46
1:A:982:GLU:HG3	1:A:1169:GLN:HG3	1.97	0.46
1:A:1761:PRO:CB	1:A:1930:TYR:OH	2.55	0.46
1:A:1821:ILE:O	1:A:1912:PRO:HA	2.15	0.46
3:C:221:ILE:HG23	3:C:495:ARG:HB3	1.96	0.46
5:E:87:ASP:O	5:E:88:ARG:CG	2.63	0.46
21:1:728:LEU:O	21:1:731:LEU:N	2.48	0.46
23:3:274:ARG:NH2	23:3:307:GLN:OE1	2.48	0.46
32:R:195:ARG:HB3	32:R:195:ARG:HH11	1.80	0.46
39:x:716:LYS:N	39:x:748:GLU:O	2.47	0.46
1:A:121:HIS:C	1:A:123:THR:H	2.23	0.46
1:A:122:ILE:CD1	1:A:483:GLN:CG	2.89	0.46
1:A:201:ALA:HA	1:A:204:LEU:HB3	1.98	0.46
1:A:1428:HIS:O	1:A:1429:THR:C	2.59	0.46
1:A:1607:GLU:HB2	1:A:1634:SER:HA	1.96	0.46
1:A:1733:ILE:HG23	1:A:1737:ASN:HB2	1.98	0.46
1:A:2070:LYS:HA	1:A:2070:LYS:HD3	1.67	0.46
1:A:2121:ARG:O	1:A:2154:HIS:HA	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2314:PHE:HB3	4:D:1125:SER:N	2.29	0.46
2:B:29:A:O2'	2:B:30:A:H5'	2.15	0.46
3:C:66:TYR:CG	33:T:457:GLY:HA2	2.46	0.46
3:C:80:ILE:HD13	33:T:198:ARG:HG3	1.98	0.46
3:C:89:LEU:C	3:C:89:LEU:CD2	2.82	0.46
3:C:678:THR:HG21	3:C:683:ASN:CB	2.43	0.46
5:E:177:LYS:C	5:E:178:LEU:HD23	2.41	0.46
5:E:260:ARG:CZ	5:E:276:ILE:HD11	2.46	0.46
13:F:37:C:O2	13:F:37:C:H2'	2.15	0.46
14:G:149:G:H2'	14:G:150:U:C6	2.50	0.46
15:H:71:C:O5'	15:H:71:C:H6	1.98	0.46
15:H:79:G:N3	15:H:80:A:C8	2.83	0.46
15:H:142:C:H2'	15:H:143:A:H5'	1.98	0.46
21:1:572:HIS:HB2	21:1:612:THR:HG23	1.96	0.46
21:1:722:GLU:O	21:1:725:ASP:HB2	2.14	0.46
21:1:819:TRP:CZ3	21:1:867:MET:HE3	2.50	0.46
21:1:842:ASN:HA	21:1:879:LEU:HD11	1.96	0.46
21:1:1210:HIS:CD2	22:2:584:LEU:HD22	2.51	0.46
23:3:30:ILE:HG22	23:3:32:VAL:HG13	1.98	0.46
23:3:228:LEU:HD23	23:3:259:LYS:NZ	2.30	0.46
23:3:238:VAL:HB	23:3:247:GLY:O	2.16	0.46
23:3:718:ARG:HG2	23:3:719:SER:N	2.30	0.46
23:3:801:GLU:O	23:3:864:SER:HA	2.16	0.46
33:T:213:GLU:HG3	33:T:218:TRP:NE1	2.29	0.46
1:A:232:LEU:HD11	3:C:412:ILE:HD13	1.95	0.46
1:A:298:ASP:OD1	1:A:300:ASN:N	2.48	0.46
1:A:1096:HIS:CD2	1:A:1189:MET:HE2	2.51	0.46
1:A:1370:ARG:HH12	34:V:468:ASP:H	1.58	0.46
1:A:1700:GLY:O	1:A:1717:ASN:N	2.41	0.46
1:A:1782:ASP:OD1	1:A:1865:ARG:HD3	2.15	0.46
3:C:385:VAL:CG2	3:C:386:GLY:N	2.78	0.46
15:H:80:A:N3	15:H:81:G:C8	2.84	0.46
21:1:478:LEU:HA	21:1:496:LYS:HE3	1.97	0.46
21:1:579:GLU:HB3	21:1:627:THR:OG1	2.16	0.46
21:1:903:GLN:HG3	21:1:950:GLN:HE22	1.81	0.46
21:1:1186:GLN:HE22	21:1:1225:HIS:HB3	1.79	0.46
21:1:1253:GLY:HA3	21:1:1265:TYR:CD1	2.51	0.46
23:3:195:ASP:OD2	23:3:200:ALA:N	2.43	0.46
23:3:787:LYS:HB3	23:3:800:ILE:HD11	1.96	0.46
23:3:828:GLY:O	23:3:834:LEU:N	2.49	0.46
23:3:851:ILE:HG23	23:3:852:PHE:CD2	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:5:78:SER:HA	25:5:89:VAL:HG21	1.97	0.46
1:A:91:ALA:CA	32:R:207:MET:CE	2.71	0.46
1:A:229:GLN:CB	1:A:415:SER:HB2	2.45	0.46
1:A:592:TYR:O	1:A:593:ARG:C	2.59	0.46
1:A:715:GLU:CD	32:R:258:TRP:HZ3	2.16	0.46
1:A:748:ASP:CB	31:P:214:THR:HG21	2.46	0.46
1:A:1306:LYS:HZ2	2:B:38:C:C2'	2.27	0.46
1:A:1397:ILE:HG12	32:R:408:GLU:CG	2.45	0.46
3:C:145:PHE:CG	3:C:312:SER:HB3	2.49	0.46
3:C:149:LEU:N	3:C:427:PHE:HE2	2.14	0.46
3:C:261:ASP:CG	41:C:1500:GTP:N1	2.61	0.46
21:1:862:GLU:O	21:1:865:ARG:N	2.48	0.46
21:1:972:GLY:O	21:1:976:VAL:HG22	2.15	0.46
23:3:253:GLU:HG3	23:3:254:ASN:HD22	1.81	0.46
25:5:81:ASN:OD1	25:5:82:VAL:N	2.48	0.46
31:P:189:ASP:O	31:P:190:ASP:C	2.58	0.46
33:T:185:MET:HB2	33:T:186:PRO:HD3	1.98	0.46
39:x:640:ARG:CB	39:x:667:ALA:N	2.78	0.46
1:A:132:ILE:CD1	2:B:57:G:OP1	2.64	0.46
1:A:368:GLN:C	1:A:369:GLU:OE2	2.57	0.46
1:A:374:ASP:O	1:A:375:ASP:HB3	2.16	0.46
1:A:384:VAL:HG22	3:C:334:ILE:HG21	1.82	0.46
1:A:1306:LYS:NZ	2:B:38:C:O2'	2.47	0.46
3:C:66:TYR:N	3:C:66:TYR:CD1	2.81	0.46
3:C:507:VAL:HG13	3:C:566:THR:O	2.16	0.46
3:C:559:ILE:HD12	3:C:559:ILE:O	2.15	0.46
3:C:569:ARG:O	3:C:569:ARG:HG2	2.16	0.46
3:C:671:SER:OG	3:C:672:LEU:HD22	2.15	0.46
3:C:853:ARG:O	3:C:854:ARG:CB	2.62	0.46
14:G:135:G:O6	14:G:137:C:N4	2.48	0.46
15:H:30:A:C8	29:L:7:LYS:HD3	2.51	0.46
15:H:107:A:C6	15:H:108:G:C6	3.04	0.46
21:1:859:ASP:OD1	21:1:860:GLU:N	2.47	0.46
23:3:448:ALA:HB3	23:3:764:ILE:HB	1.97	0.46
29:L:78:MET:HB3	29:L:81:GLN:OE1	2.16	0.46
37:Z:604:LYS:HA	37:Z:607:VAL:CG2	2.46	0.46
1:A:362:ARG:C	1:A:362:ARG:CD	2.88	0.46
1:A:780:THR:HG22	1:A:898:PHE:CD2	2.50	0.46
1:A:802:THR:HG22	1:A:803:ALA:H	1.80	0.46
1:A:1237:MET:HG2	1:A:1284:LEU:HD21	1.98	0.46
1:A:1312:PRO:O	1:A:1315:VAL:HG22	2.14	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1399:GLN:HB3	1:A:1401:ARG:HG2	1.98	0.46
1:A:2112:LYS:HE2	1:A:2112:LYS:HB3	1.67	0.46
13:F:56:A:N1	15:H:20:G:C6	2.84	0.46
15:H:78:C:O5'	15:H:78:C:H6	1.98	0.46
21:1:588:TYR:HA	21:1:591:VAL:HG12	1.98	0.46
21:1:759:ALA:O	21:1:763:ASN:HB2	2.16	0.46
23:3:69:ARG:HG2	23:3:70:LEU:O	2.16	0.46
23:3:509:SER:CB	23:3:549:VAL:HG21	2.45	0.46
32:R:88:ILE:HG22	32:R:96:ILE:HG23	1.98	0.46
32:R:220:ARG:NH1	32:R:220:ARG:CB	2.76	0.46
1:A:232:LEU:N	1:A:233:PRO:CD	2.78	0.46
1:A:434:HIS:ND1	1:A:434:HIS:C	2.73	0.46
1:A:841:LEU:HD13	1:A:1433:ASP:HB2	1.98	0.46
1:A:1388:GLU:O	1:A:1392:LYS:HG2	2.16	0.46
1:A:1718:TRP:CZ3	1:A:1726:ILE:HD12	2.50	0.46
3:C:725:ASP:OD1	3:C:727:LEU:CA	2.64	0.46
13:F:43:A:H2	14:G:4:A:H61	1.64	0.46
15:H:45:C:H42	18:w:395:TRP:CG	2.29	0.46
15:H:114:A:H2'	15:H:115:G:H8	1.81	0.46
16:o:61:PRO:O	16:o:86:ALA:HB1	2.16	0.46
17:p:194:PHE:O	17:p:195:GLU:C	2.59	0.46
18:w:394:TYR:HA	18:w:397:TYR:CE2	2.51	0.46
21:1:647:PHE:O	21:1:651:VAL:HG23	2.16	0.46
21:1:1125:PRO:O	21:1:1128:VAL:N	2.49	0.46
21:1:1181:ASP:H	21:1:1184:HIS:HD2	1.64	0.46
23:3:71:THR:HG23	23:3:126:LYS:HD2	1.98	0.46
23:3:482:THR:HG23	23:3:503:THR:O	2.15	0.46
23:3:616:ILE:O	23:3:628:LEU:HB2	2.16	0.46
24:4:29:LEU:HD22	24:4:33:PHE:CE2	2.49	0.46
24:4:32:LEU:CD2	24:4:79:LEU:HD21	2.46	0.46
25:5:46:ARG:HB3	25:5:63:VAL:HG12	1.97	0.46
31:P:54:VAL:HG13	31:P:59:PHE:HZ	1.80	0.46
1:A:34:ALA:HA	5:E:213:ILE:CD1	2.46	0.46
1:A:121:HIS:HD2	1:A:482:PHE:CE1	2.34	0.46
1:A:1328:LEU:HD23	1:A:1470:TYR:CE2	2.51	0.46
1:A:1505:LYS:CD	37:Z:615:SER:CB	2.91	0.46
3:C:678:THR:HG23	3:C:683:ASN:N	2.31	0.46
5:E:248:SER:HB2	5:E:249:TYR:HD1	1.75	0.46
21:1:888:LEU:O	21:1:892:LEU:HG	2.15	0.46
23:3:287:PHE:CD1	23:3:303:ALA:HB1	2.50	0.46
31:P:48:GLN:O	31:P:49:ASP:CB	2.64	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:129:ASP:C	32:R:131:ASP:N	2.73	0.46
32:R:148:ARG:HG3	32:R:148:ARG:NH1	2.31	0.46
37:Z:522:LEU:HD13	37:Z:522:LEU:C	2.41	0.46
1:A:378:PHE:HE2	3:C:335:ASN:HD22	1.62	0.45
1:A:735:ILE:O	1:A:738:MET:HE2	2.16	0.45
1:A:892:LYS:HD2	1:A:912:GLU:OE1	2.16	0.45
1:A:903:SER:OG	1:A:904:HIS:N	2.48	0.45
1:A:1026:ASN:ND2	1:A:1029:GLY:O	2.45	0.45
2:B:22:U:O2	2:B:22:U:H2'	2.15	0.45
5:E:232:ARG:O	5:E:262:TRP:CH2	2.69	0.45
21:1:744:ALA:O	21:1:787:ILE:HG21	2.16	0.45
21:1:1165:TYR:HE1	22:2:575:PHE:CG	2.33	0.45
23:3:58:VAL:HG12	23:3:1155:LEU:HD23	1.98	0.45
23:3:233:ASN:ND2	23:3:286:ILE:HD12	2.31	0.45
23:3:462:VAL:HG21	23:3:508:CYS:HB3	1.98	0.45
23:3:1012:VAL:HA	23:3:1022:ILE:O	2.17	0.45
1:A:121:HIS:C	1:A:123:THR:N	2.74	0.45
1:A:666:LYS:HD3	1:A:666:LYS:N	2.31	0.45
1:A:671:THR:OG1	13:F:69:A:OP1	2.34	0.45
1:A:1084:PRO:HB3	1:A:1101:PHE:CE1	2.51	0.45
3:C:136:GLY:HA3	3:C:228:PHE:O	2.16	0.45
13:F:57:U:C2	13:F:58:G:N7	2.84	0.45
14:G:10:U:O2'	14:G:11:A:OP1	2.28	0.45
21:1:701:VAL:O	21:1:705:SER:HB3	2.16	0.45
23:3:536:TRP:CG	23:3:566:PHE:HZ	2.33	0.45
23:3:700:LYS:NZ	23:3:740:GLU:O	2.41	0.45
23:3:701:LEU:HA	23:3:713:LEU:O	2.16	0.45
1:A:61:MET:HB3	1:A:62:PRO:HD2	1.98	0.45
1:A:305:ARG:NH2	3:C:854:ARG:HD3	2.31	0.45
1:A:907:PRO:CD	31:P:229:LYS:HB2	2.39	0.45
1:A:1957:ASP:HB3	1:A:1960:THR:HG23	1.98	0.45
5:E:146:ARG:NH1	5:E:148:LYS:NZ	2.62	0.45
15:H:60:U:H2'	15:H:61:C:H6	1.81	0.45
21:1:1074:ARG:HD2	21:1:1111:CYS:SG	2.55	0.45
23:3:169:HIS:CD2	23:3:170:VAL:H	2.34	0.45
23:3:526:HIS:HB3	23:3:534:ASN:O	2.17	0.45
23:3:544:ILE:HD11	23:3:556:ILE:HG21	1.98	0.45
23:3:805:ASN:O	23:3:856:LYS:HB3	2.16	0.45
31:P:227:TYR:N	31:P:227:TYR:HD1	2.14	0.45
33:T:306:CYS:SG	33:T:336:VAL:HG12	2.56	0.45
34:V:512:GLY:O	34:V:513:ARG:C	2.60	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:ARG:HH21	3:C:854:ARG:CZ	2.29	0.45
1:A:1434:LYS:O	1:A:1439:ARG:NH1	2.45	0.45
2:B:57:G:H2'	2:B:58:U:H5'	1.99	0.45
3:C:193:THR:HG22	3:C:428:THR:HG21	1.97	0.45
3:C:482:TYR:CE2	3:C:493:PHE:CG	2.89	0.45
4:D:419:GLY:C	4:D:421:HIS:H	2.25	0.45
5:E:119:THR:CG2	5:E:161:ARG:CB	2.73	0.45
5:E:157:CYS:HA	5:E:168:CYS:O	2.16	0.45
15:H:181:G:C2	15:H:182:U:N3	2.84	0.45
21:1:427:PRO:O	21:1:431:LEU:N	2.45	0.45
21:1:834:VAL:O	21:1:838:VAL:HG23	2.16	0.45
21:1:1181:ASP:OD1	21:1:1182:LEU:N	2.46	0.45
23:3:257:THR:OG1	23:3:268:ARG:HG2	2.16	0.45
23:3:482:THR:HG21	23:3:505:THR:OG1	2.17	0.45
23:3:897:SER:HB2	23:3:957:GLY:HA3	1.97	0.45
23:3:905:VAL:HG23	23:3:930:LEU:HB2	1.98	0.45
27:7:73:LEU:HD12	27:7:74:GLN:N	2.32	0.45
31:P:193:VAL:CG2	31:P:194:PHE:N	2.79	0.45
32:R:88:ILE:HD12	32:R:88:ILE:N	2.29	0.45
32:R:181:PRO:O	32:R:182:SER:CB	2.58	0.45
33:T:309:ASP:OD1	33:T:309:ASP:C	2.59	0.45
1:A:966:TRP:HE3	1:A:1178:TYR:CZ	2.35	0.45
1:A:1426:ASP:OD2	32:R:421:GLY:CA	2.64	0.45
1:A:1809:ILE:HB	1:A:1818:PHE:HB2	1.97	0.45
1:A:1900:GLU:OE2	37:Z:521:PRO:CA	2.64	0.45
2:B:47:A:O2'	2:B:48:A:H8	1.98	0.45
3:C:183:SER:OG	3:C:480:LYS:NZ	2.50	0.45
5:E:243:LEU:CD1	5:E:247:GLY:CA	2.84	0.45
15:H:25:G:C2	15:H:26:A:C5	3.04	0.45
15:H:150:U:H3	15:H:181:G:H1	1.62	0.45
15:H:152:G:O2'	15:H:153:A:H1'	2.16	0.45
23:3:259:LYS:HG3	23:3:266:ASP:CG	2.42	0.45
23:3:796:ASN:HA	23:3:871:PRO:HD3	1.98	0.45
28:J:360:ASP:HA	28:J:363:ARG:CD	2.46	0.45
33:T:409:LEU:HD12	33:T:409:LEU:N	2.31	0.45
1:A:75:ASP:HB2	1:A:77:THR:OG1	2.16	0.45
1:A:168:PRO:HG2	1:A:559:ASP:CB	2.36	0.45
1:A:466:ALA:HB3	2:B:54:U:OP2	2.17	0.45
1:A:730:GLY:O	1:A:731:LEU:HB2	2.16	0.45
1:A:1413:ASP:OD1	1:A:1414:ARG:HG3	2.17	0.45
1:A:1604:LEU:HD11	1:A:1725:LEU:HD22	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2169:LEU:HD21	1:A:2272:MET:HG3	1.99	0.45
1:A:2200:MET:HE2	1:A:2200:MET:HB3	1.65	0.45
1:A:2320:LEU:HD21	1:A:2322:GLU:CD	2.41	0.45
3:C:66:TYR:CB	33:T:456:PRO:O	2.51	0.45
3:C:495:ARG:HG3	3:C:495:ARG:O	2.16	0.45
3:C:497:LEU:CD1	3:C:577:PHE:CE1	2.94	0.45
3:C:852:ARG:NH2	14:G:-12:G:OP1	2.50	0.45
4:D:1349:GLY:HA2	4:D:1491:SER:O	2.16	0.45
5:E:260:ARG:CD	5:E:276:ILE:HG12	2.47	0.45
13:F:94:C:H2'	13:F:95:G:H8	1.82	0.45
14:G:-12:G:HO2'	14:G:-11:G:C5'	2.29	0.45
23:3:115:ILE:HD11	27:7:18:TYR:CE1	2.51	0.45
32:R:179:TYR:CE2	32:R:181:PRO:HG3	2.52	0.45
33:T:297:HIS:CD2	33:T:338:CYS:SG	3.09	0.45
37:Z:525:TYR:CE1	37:Z:526:ILE:CG2	2.86	0.45
1:A:193:LEU:HB3	1:A:208:TYR:OH	2.17	0.45
1:A:293:TRP:CE3	1:A:293:TRP:C	2.94	0.45
1:A:648:LEU:HD23	1:A:648:LEU:HA	1.79	0.45
1:A:1457:HIS:NE2	32:R:424:SER:C	2.75	0.45
1:A:1529:ILE:O	1:A:1530:PRO:C	2.59	0.45
1:A:1768:TYR:HE1	1:A:1930:TYR:CE1	2.34	0.45
3:C:926:ALA:N	3:C:927:PRO:HD2	2.32	0.45
5:E:178:LEU:HG	5:E:188:GLN:HB2	1.98	0.45
5:E:277:PHE:CD1	5:E:277:PHE:N	2.83	0.45
15:H:148:C:HO2'	15:H:149:A:H5'	1.76	0.45
21:1:86:ALA:O	21:1:89:ALA:HB3	2.17	0.45
21:1:476:ASP:OD1	21:1:477:LYS:N	2.49	0.45
21:1:1110:VAL:O	21:1:1113:THR:HB	2.17	0.45
21:1:1251:LEU:HD12	22:2:497:SER:OG	2.16	0.45
23:3:223:LYS:HE2	23:3:224:TYR:CZ	2.52	0.45
23:3:429:ARG:HH12	27:7:59:GLU:H	1.65	0.45
23:3:1114:SER:HB2	23:3:1215:TYR:CE1	2.51	0.45
28:J:338:GLU:O	32:R:116:TYR:CE1	2.69	0.45
32:R:128:ASP:OD2	32:R:133:GLN:OE1	2.34	0.45
33:T:393:ASP:O	33:T:413:ASN:ND2	2.49	0.45
37:Z:564:PRO:O	37:Z:582:TYR:CG	2.69	0.45
37:Z:600:ARG:CG	37:Z:600:ARG:NH1	2.73	0.45
39:x:876:GLY:O	39:x:879:LEU:N	2.49	0.45
1:A:586:GLY:O	1:A:592:TYR:CE2	2.69	0.45
1:A:755:HIS:CG	31:P:219:PHE:HE2	2.35	0.45
1:A:833:LYS:HG3	1:A:834:HIS:CD2	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:975:VAL:HG11	1:A:1153:VAL:HG21	1.98	0.45
1:A:1963:GLU:HB2	1:A:1966:HIS:HD2	1.81	0.45
13:F:38:G:OP2	13:F:38:G:C8	2.70	0.45
14:G:6:A:H2'	14:G:7:G:H8	1.82	0.45
21:1:501:LEU:O	21:1:504:ILE:N	2.48	0.45
21:1:592:GLU:O	21:1:596:ILE:HG23	2.16	0.45
21:1:629:ALA:HA	21:1:667:ILE:HG12	1.99	0.45
23:3:383:ASP:OD1	23:3:384:THR:N	2.50	0.45
23:3:1057:ARG:HB2	23:3:1092:ILE:HD13	1.98	0.45
32:R:123:GLU:C	32:R:124:VAL:HG12	2.41	0.45
33:T:316:ASP:C	33:T:316:ASP:OD1	2.58	0.45
36:Y:41:GLY:HA2	36:Y:79:PHE:HB3	1.99	0.45
1:A:305:ARG:HG3	3:C:878:ILE:CB	2.46	0.45
1:A:318:TYR:O	3:C:641:MET:CB	2.65	0.45
1:A:660:PHE:CE2	32:R:209:PRO:CB	3.00	0.45
1:A:733:THR:OG1	1:A:734:PRO:HD3	2.16	0.45
1:A:1013:ASN:OD1	1:A:1030:ILE:HG13	2.16	0.45
1:A:1904:ASP:O	1:A:1908:LYS:HG2	2.16	0.45
1:A:1949:ARG:HA	1:A:1952:VAL:HG23	1.98	0.45
1:A:2074:ARG:O	1:A:2078:ILE:HD13	2.17	0.45
2:B:40:U:O4	14:G:-1:G:O6	2.35	0.45
3:C:137:HIS:HD2	3:C:236:MET:HB2	1.61	0.45
3:C:191:PRO:HG2	3:C:426:GLU:OE1	2.17	0.45
3:C:445:ALA:HB1	3:C:449:ILE:CG1	2.45	0.45
3:C:726:LEU:HD12	3:C:726:LEU:C	2.42	0.45
5:E:162:ARG:HH21	5:E:204:THR:HA	1.78	0.45
13:F:51:U:H2'	13:F:52:U:O4'	2.17	0.45
21:1:552:LEU:HA	21:1:555:VAL:HG12	1.98	0.45
21:1:822:ARG:NH1	36:Y:31:GLU:HG2	2.32	0.45
21:1:897:LEU:O	21:1:901:GLN:HG3	2.17	0.45
21:1:1186:GLN:NE2	21:1:1225:HIS:HB3	2.31	0.45
23:3:643:VAL:HG12	23:3:664:TYR:O	2.17	0.45
25:5:48:ILE:HG12	25:5:62:VAL:HG23	1.99	0.45
28:J:406:PHE:CB	28:J:411:MET:HG2	2.47	0.45
33:T:342:GLU:CB	33:T:343:PRO:HD2	2.47	0.45
33:T:454:VAL:HG22	33:T:463:SER:OG	2.16	0.45
33:T:455:GLN:CG	33:T:456:PRO:CD	2.94	0.45
1:A:44:ARG:CD	1:A:45:TYR:CE2	2.99	0.45
1:A:256:TYR:CG	3:C:888:ARG:NH2	2.85	0.45
1:A:382:GLU:O	1:A:383:PHE:CD2	2.70	0.45
1:A:507:LEU:HD12	1:A:507:LEU:HA	1.79	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661:GLU:CG	32:R:210:PRO:HB3	2.47	0.45
1:A:845:ARG:NH2	1:A:1439:ARG:HE	2.15	0.45
1:A:1258:LYS:HE2	32:R:432:GLU:CB	2.47	0.45
1:A:1780:VAL:HG22	1:A:1809:ILE:HG12	1.99	0.45
3:C:65:TYR:O	3:C:66:TYR:CB	2.65	0.45
3:C:230:ASP:OD2	3:C:233:GLU:CG	2.55	0.45
3:C:502:HIS:ND1	3:C:543:ARG:HB3	2.32	0.45
3:C:926:ALA:HA	3:C:929:LEU:HG	1.98	0.45
13:F:50:A:H2'	13:F:51:U:H6	1.82	0.45
14:G:6:A:H2'	14:G:7:G:C8	2.52	0.45
14:G:12:G:N3	14:G:12:G:C2'	2.79	0.45
14:G:157:U:H5'	21:1:622:GLU:OE1	2.17	0.45
15:H:113:G:H2'	15:H:114:A:H8	1.82	0.45
21:1:942:ASN:CG	21:1:943:LYS:H	2.24	0.45
21:1:1002:ASN:OD1	21:1:1041:ARG:NH2	2.50	0.45
22:2:611:ASP:O	22:2:614:ARG:CB	2.60	0.45
23:3:462:VAL:O	23:3:472:ALA:N	2.46	0.45
23:3:883:GLU:HG3	23:3:884:GLN:N	2.32	0.45
23:3:1051:GLY:HA2	23:3:1100:THR:HA	1.99	0.45
25:5:25:ASN:HD22	25:5:86:TYR:C	2.25	0.45
25:5:26:LEU:HD12	25:5:87:LEU:HD22	1.98	0.45
27:7:31:TRP:HE3	27:7:32:LEU:HD12	1.82	0.45
29:L:226:ASP:OD1	32:R:83:SER:HB2	2.16	0.45
32:R:88:ILE:HG21	32:R:96:ILE:CG2	2.46	0.45
32:R:408:GLU:CG	32:R:409:VAL:N	2.78	0.45
34:V:530:LYS:C	34:V:532:GLN:N	2.74	0.45
34:V:548:ALA:HB1	34:V:585:ILE:C	2.42	0.45
35:X:336:GLY:HA3	35:X:378:GLU:HB2	1.99	0.45
37:Z:524:ARG:HD2	37:Z:525:TYR:CB	2.46	0.45
1:A:76:MET:SD	1:A:88:TYR:CE2	3.10	0.44
1:A:193:LEU:HD12	1:A:194:GLU:N	2.29	0.44
1:A:1147:VAL:HG23	1:A:1148:ASN:N	2.33	0.44
3:C:93:ILE:CG2	33:T:218:TRP:NE1	2.80	0.44
5:E:276:ILE:O	5:E:277:PHE:HD1	2.00	0.44
13:F:68:C:C5	31:P:33:ARG:HG2	2.52	0.44
13:F:94:C:H2'	13:F:95:G:C8	2.52	0.44
15:H:7:U:H2'	15:H:8:C:C6	2.52	0.44
15:H:81:G:N3	15:H:82:G:C8	2.85	0.44
15:H:141:C:H2'	15:H:142:C:C6	2.50	0.44
21:1:810:ILE:O	21:1:813:PRO:HD2	2.17	0.44
23:3:460:TRP:CE2	23:3:507:SER:HA	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:723:TYR:CD1	23:3:725:TYR:HB2	2.53	0.44
23:3:1140:PHE:O	23:3:1144:VAL:HG23	2.17	0.44
28:J:406:PHE:CG	28:J:411:MET:CE	2.97	0.44
32:R:147:THR:HG23	33:T:360:VAL:CG1	2.40	0.44
32:R:416:PHE:O	32:R:416:PHE:CG	2.70	0.44
1:A:89:LEU:CD2	1:A:656:LEU:CD2	2.95	0.44
1:A:1088:PHE:HD1	1:A:1097:ILE:HG12	1.82	0.44
1:A:1430:LEU:HD11	32:R:422:MET:HA	1.98	0.44
1:A:1591:MET:SD	1:A:1611:LYS:NZ	2.75	0.44
1:A:1788:VAL:HA	1:A:1802:PRO:HA	1.98	0.44
1:A:2196:HIS:HB3	1:A:2230:LEU:HD11	1.98	0.44
1:A:2284:MET:HE1	1:A:2311:PRO:HG3	1.99	0.44
1:A:2334:TYR:CE1	4:D:591:GLU:CB	3.00	0.44
2:B:40:U:OP2	2:B:40:U:C6	2.70	0.44
3:C:93:ILE:CG2	33:T:218:TRP:CZ2	3.00	0.44
3:C:388:VAL:HA	3:C:392:LEU:HB2	1.99	0.44
5:E:132:THR:HG21	5:E:146:ARG:HG2	1.98	0.44
5:E:274:VAL:C	5:E:275:LYS:CG	2.91	0.44
13:F:58:G:O2'	13:F:59:G:OP1	2.31	0.44
15:H:143:A:OP2	15:H:143:A:C2	2.71	0.44
15:H:157:G:H5''	15:H:157:G:C8	2.50	0.44
21:1:762:ALA:O	21:1:766:THR:CB	2.64	0.44
21:1:1252:GLN:NE2	22:2:492:LYS:O	2.51	0.44
22:2:613:LEU:HD21	24:4:32:LEU:HD13	1.99	0.44
23:3:404:LEU:HB3	23:3:407:ILE:HD11	1.99	0.44
23:3:536:TRP:CD1	23:3:566:PHE:HZ	2.35	0.44
23:3:607:VAL:HB	23:3:615:ARG:O	2.17	0.44
23:3:1142:GLN:HG2	23:3:1146:MET:HE3	1.98	0.44
23:3:1159:ASP:OD1	23:3:1160:HIS:N	2.49	0.44
28:J:297:ASN:OD1	29:L:223:GLY:O	2.34	0.44
34:V:548:ALA:HB2	34:V:585:ILE:CB	2.42	0.44
38:z:16:LEU:HB3	38:z:165:GLU:HB2	1.99	0.44
1:A:317:PRO:HB2	1:A:327:VAL:HG11	1.98	0.44
1:A:1459:ARG:HD3	1:A:1459:ARG:HA	1.75	0.44
1:A:1785:VAL:O	1:A:1805:GLY:HA3	2.17	0.44
1:A:2328:ALA:CB	4:D:788:GLY:N	2.79	0.44
3:C:140:HIS:HB3	3:C:230:ASP:CB	2.43	0.44
3:C:671:SER:CB	3:C:672:LEU:HD22	2.46	0.44
4:D:721:VAL:HA	4:D:825:THR:O	2.17	0.44
5:E:209:ILE:HG21	5:E:250:LEU:HD11	1.94	0.44
13:F:39:A:H2'	13:F:40:U:C6	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:529:GLY:HA2	21:1:570:TYR:CZ	2.51	0.44
23:3:205:GLN:HB2	23:3:228:LEU:O	2.17	0.44
23:3:747:SER:N	23:3:750:CYS:O	2.51	0.44
25:5:98:PHE:O	25:5:100:LYS:N	2.50	0.44
31:P:188:TRP:N	31:P:188:TRP:CD2	2.86	0.44
32:R:416:PHE:O	32:R:416:PHE:CD1	2.70	0.44
33:T:387:PHE:CZ	33:T:398:TRP:CD1	3.04	0.44
37:Z:500:GLY:O	37:Z:503:GLN:N	2.50	0.44
37:Z:573:PRO:O	37:Z:573:PRO:CD	2.65	0.44
37:Z:597:ARG:CZ	37:Z:601:LEU:HD13	2.47	0.44
1:A:250:VAL:C	1:A:337:VAL:HG21	2.42	0.44
1:A:777:GLY:O	1:A:780:THR:OG1	2.25	0.44
1:A:1074:PHE:HB3	1:A:1079:THR:OG1	2.17	0.44
1:A:1631:LEU:HD12	1:A:1660:TYR:CD2	2.51	0.44
2:B:42:U:O2	14:G:-3:A:H2	2.00	0.44
3:C:334:ILE:HD12	3:C:334:ILE:C	2.42	0.44
13:F:5:U:H5'	13:F:6:C:OP2	2.17	0.44
15:H:159:U:H2'	15:H:160:A:C8	2.52	0.44
15:H:165:A:C6	15:H:166:G:O6	2.71	0.44
18:w:438:LEU:HD22	18:w:440:ILE:HD12	1.99	0.44
21:1:869:MET:HE1	21:1:896:ILE:HG23	2.00	0.44
21:1:937:LEU:O	21:1:940:LEU:HB3	2.18	0.44
22:2:611:ASP:O	22:2:614:ARG:N	2.50	0.44
23:3:1063:ASN:H	23:3:1087:GLN:HE22	1.65	0.44
23:3:1096:HIS:NE2	23:3:1098:GLY:HA2	2.33	0.44
33:T:439:TRP:CE3	33:T:446:ASN:HB2	2.52	0.44
36:Y:36:ALA:CB	37:Z:499:LYS:O	2.54	0.44
39:x:936:TYR:O	39:x:938:ARG:N	2.51	0.44
1:A:359:ILE:O	1:A:360:SER:HB3	2.16	0.44
1:A:373:ASP:OD1	1:A:374:ASP:N	2.51	0.44
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.70	0.44
1:A:1110:ILE:HG22	1:A:1114:LEU:HD12	1.98	0.44
1:A:1402:ARG:HD2	32:R:412:ASP:HA	1.98	0.44
1:A:1533:ARG:HD2	1:A:1751:LEU:O	2.18	0.44
1:A:1553:VAL:O	1:A:1561:PHE:HA	2.18	0.44
1:A:2073:TRP:CZ3	1:A:2313:HIS:CE1	3.05	0.44
1:A:2279:TRP:CD1	1:A:2279:TRP:H	2.35	0.44
3:C:135:CYS:SG	3:C:227:LEU:CB	3.06	0.44
3:C:259:LYS:HD2	41:C:1500:GTP:C5	2.52	0.44
3:C:474:LEU:C	3:C:474:LEU:CD2	2.87	0.44
3:C:673:LYS:HG3	3:C:686:THR:HG23	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:21:A:O3'	14:G:22:C:C6	2.71	0.44
15:H:60:U:H2'	15:H:61:C:C6	2.52	0.44
17:p:172:ASN:C	17:p:174:PHE:N	2.75	0.44
21:1:1211:LEU:O	21:1:1215:VAL:HG23	2.17	0.44
23:3:442:LEU:HD11	23:3:732:THR:OG1	2.17	0.44
23:3:636:GLN:O	23:3:670:GLN:HG2	2.17	0.44
26:6:58:CYS:N	26:6:63:GLY:O	2.46	0.44
36:Y:58:GLN:HB2	37:Z:584:TRP:NE1	2.33	0.44
1:A:121:HIS:CD2	1:A:481:PHE:O	2.70	0.44
1:A:370:PRO:O	1:A:371:LEU:C	2.60	0.44
1:A:381:PRO:HG2	3:C:333:ASP:HB2	2.00	0.44
1:A:707:ARG:O	1:A:711:GLN:HG3	2.17	0.44
1:A:978:GLU:OE2	1:A:1188:ASN:N	2.36	0.44
1:A:1364:LEU:CD1	34:V:461:LEU:O	2.66	0.44
1:A:1667:ARG:HD2	1:A:1679:TYR:CD2	2.52	0.44
1:A:2125:ALA:O	1:A:2150:GLN:NE2	2.50	0.44
1:A:2237:TRP:HZ2	1:A:2248:PRO:HB2	1.81	0.44
3:C:89:LEU:C	3:C:91:GLU:N	2.76	0.44
3:C:301:SER:C	3:C:303:LEU:H	2.25	0.44
3:C:457:VAL:CG1	3:C:462:GLY:HA3	2.46	0.44
15:H:34:U:C4	15:H:35:A:N7	2.85	0.44
15:H:73:C:O5'	15:H:73:C:H6	2.01	0.44
15:H:142:C:O2'	15:H:143:A:H5'	2.18	0.44
15:H:147:G:C6	15:H:148:C:N4	2.86	0.44
20:v:170:LEU:HA	20:v:179:ILE:O	2.18	0.44
20:v:205:GLN:O	20:v:209:GLN:CB	2.65	0.44
21:1:1108:ASN:OD1	21:1:1110:VAL:HG12	2.17	0.44
23:3:812:LYS:O	23:3:816:LYS:CB	2.57	0.44
31:P:193:VAL:HG23	31:P:194:PHE:CB	2.47	0.44
36:Y:63:VAL:HG23	36:Y:64:ASN:N	2.33	0.44
39:x:936:TYR:C	39:x:938:ARG:N	2.73	0.44
1:A:369:GLU:HB2	1:A:370:PRO:HD2	2.00	0.44
1:A:1674:HIS:HB3	1:A:1709:TYR:CE2	2.53	0.44
1:A:2121:ARG:HA	1:A:2121:ARG:HD2	1.55	0.44
3:C:145:PHE:HD1	3:C:312:SER:HB3	1.83	0.44
13:F:9:U:H2'	13:F:10:U:C6	2.52	0.44
13:F:68:C:C5	31:P:33:ARG:CG	2.95	0.44
15:H:26:A:C6	15:H:27:U:C4	3.05	0.44
17:p:155:LEU:CB	17:p:219:LYS:O	2.66	0.44
21:1:1072:ALA:O	21:1:1075:ARG:HB3	2.18	0.44
23:3:929:LYS:HD3	23:3:938:GLU:OE2	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:L:224:PHE:CE1	32:R:86:LEU:HD12	2.43	0.44
37:Z:584:TRP:CZ3	37:Z:586:GLY:HA2	2.53	0.44
1:A:73:HIS:HA	1:A:81:PHE:CE2	2.53	0.44
1:A:81:PHE:O	1:A:82:ARG:C	2.59	0.44
1:A:121:HIS:CA	1:A:481:PHE:O	2.66	0.44
1:A:251:ASP:HA	1:A:337:VAL:CG2	2.48	0.44
1:A:363:HIS:CE1	3:C:287:GLY:CA	3.00	0.44
1:A:1034:LEU:HB2	1:A:1037:ALA:HB2	1.98	0.44
1:A:1555:LEU:HD12	1:A:1560:ILE:HB	2.00	0.44
1:A:1557:LEU:HD13	1:A:1580:HIS:CE1	2.53	0.44
1:A:2280:ASN:HB3	1:A:2309:HIS:CD2	2.53	0.44
18:w:485:ASN:HB2	23:3:976:LYS:HE3	2.00	0.44
21:1:601:ALA:HB2	21:1:635:VAL:HG12	2.00	0.44
21:1:969:LYS:O	21:1:973:HIS:ND1	2.36	0.44
23:3:353:PHE:CD1	23:3:406:PRO:HD3	2.53	0.44
23:3:607:VAL:HG21	23:3:617:ILE:HD12	1.99	0.44
23:3:930:LEU:HG	23:3:934:GLY:HA2	1.98	0.44
24:4:79:LEU:HG	24:4:84:ILE:HG13	2.00	0.44
31:P:66:ARG:HB2	31:P:66:ARG:NH1	2.30	0.44
32:R:124:VAL:HG22	32:R:125:MET:H	1.83	0.44
32:R:132:LEU:HD23	32:R:132:LEU:N	2.31	0.44
32:R:208:GLU:OE2	32:R:211:ARG:NH1	2.51	0.44
32:R:415:LEU:H	32:R:415:LEU:HG	1.56	0.44
33:T:358:ASP:HB2	33:T:365:ARG:HD2	2.00	0.44
1:A:86:ARG:NH2	32:R:211:ARG:CG	2.63	0.44
1:A:94:TYR:CD2	32:R:207:MET:SD	3.11	0.44
1:A:173:GLU:C	1:A:520:TYR:CD2	2.96	0.44
1:A:941:LYS:HE3	1:A:951:LEU:HD21	2.00	0.44
1:A:1038:SER:HA	1:A:1442:PHE:HE2	1.83	0.44
1:A:1900:GLU:CG	37:Z:521:PRO:HG3	2.39	0.44
3:C:439:PRO:O	3:C:440:SER:CB	2.66	0.44
3:C:779:LEU:HD11	3:C:825:PRO:HB2	1.99	0.44
14:G:11:A:C5	14:G:12:G:C8	3.06	0.44
14:G:21:A:O3'	14:G:22:C:H6	2.00	0.44
15:H:6:U:H2'	15:H:7:U:C6	2.53	0.44
21:1:503:LYS:HD2	21:1:515:ALA:HB2	2.00	0.44
21:1:779:SER:HB3	21:1:784:MET:HG2	2.00	0.44
21:1:1131:ALA:O	21:1:1135:GLU:HG2	2.17	0.44
23:3:411:GLN:HA	23:3:1105:GLN:OE1	2.18	0.44
23:3:798:ILE:HA	23:3:867:ARG:O	2.18	0.44
25:5:46:ARG:N	25:5:63:VAL:O	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ARG:HG2	1:A:45:TYR:CD2	2.53	0.43
1:A:79:ARG:HD2	1:A:79:ARG:O	2.18	0.43
1:A:394:TYR:CD1	1:A:394:TYR:N	2.86	0.43
1:A:1118:PRO:O	1:A:1120:PRO:O	2.36	0.43
1:A:1144:LYS:C	1:A:1146:ASP:N	2.75	0.43
1:A:2073:TRP:CH2	1:A:2313:HIS:CG	3.06	0.43
1:A:2222:SER:OG	1:A:2223:CYS:N	2.50	0.43
3:C:229:ILE:CG2	3:C:234:GLY:O	2.66	0.43
5:E:248:SER:HB2	5:E:249:TYR:CE1	2.53	0.43
13:F:35:A:C8	14:G:12:G:O6	2.71	0.43
13:F:68:C:H42	33:T:283:HIS:CE1	2.35	0.43
21:1:903:GLN:HG3	21:1:950:GLN:NE2	2.33	0.43
23:3:176:GLY:O	23:3:178:GLU:HG2	2.17	0.43
23:3:587:VAL:HG11	23:3:590:MET:HE2	1.99	0.43
23:3:745:PHE:HB2	23:3:755:VAL:HG23	2.00	0.43
23:3:998:HIS:HE1	23:3:1064:ASP:OD2	2.00	0.43
23:3:1207:LYS:HA	23:3:1210:ASP:OD2	2.18	0.43
25:5:53:THR:O	25:5:57:ARG:HG3	2.18	0.43
32:R:109:ASP:OD1	32:R:110:LYS:N	2.51	0.43
33:T:454:VAL:CG1	33:T:455:GLN:N	2.81	0.43
1:A:106:MET:HG2	1:A:489:TRP:CZ2	2.53	0.43
1:A:330:THR:O	1:A:331:TRP:HB2	2.17	0.43
1:A:694:LEU:O	1:A:698:PRO:HG3	2.18	0.43
1:A:970:GLU:HB2	1:A:972:GLU:OE2	2.17	0.43
1:A:1301:ILE:HD11	2:B:39:C:OP1	2.18	0.43
1:A:1532:ARG:HG2	1:A:1572:SER:OG	2.18	0.43
1:A:2310:ARG:HH11	1:A:2310:ARG:HB3	1.83	0.43
3:C:135:CYS:N	3:C:226:VAL:O	2.50	0.43
3:C:392:LEU:HD12	3:C:392:LEU:O	2.18	0.43
3:C:508:LYS:O	3:C:566:THR:HG22	2.18	0.43
3:C:674:CYS:HB2	3:C:818:SER:HB3	2.00	0.43
3:C:703:GLU:OE2	3:C:740:THR:CG2	2.50	0.43
5:E:251:LEU:CG	5:E:291:CYS:SG	3.05	0.43
15:H:159:U:H2'	15:H:160:A:H8	1.83	0.43
15:H:182:U:H6	15:H:182:U:O5'	2.01	0.43
21:1:528:ALA:HB2	21:1:563:LEU:HD13	2.00	0.43
21:1:732:TRP:O	21:1:735:ILE:HB	2.19	0.43
22:2:556:LYS:O	22:2:559:PRO:HD3	2.18	0.43
23:3:409:PHE:HD2	23:3:788:PHE:CE2	2.36	0.43
23:3:484:VAL:HG21	23:3:499:PHE:HB2	1.99	0.43
23:3:791:HIS:ND1	23:3:794:SER:HB3	2.33	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:837:GLU:O	23:3:837:GLU:HG2	2.17	0.43
1:A:345:PRO:O	1:A:346:ASP:O	2.35	0.43
1:A:525:LYS:HG2	30:M:194:ARG:CG	2.48	0.43
1:A:908:VAL:HA	1:A:1445:TYR:O	2.18	0.43
1:A:1071:PHE:CD2	1:A:1072:LEU:HG	2.53	0.43
1:A:1544:ARG:HB3	1:A:1672:ASP:OD2	2.19	0.43
1:A:2067:PHE:HB2	1:A:2072:GLU:HG2	2.00	0.43
2:B:12:U:O2'	2:B:13:C:P	2.77	0.43
3:C:131:ASN:HB3	3:C:549:TRP:CZ2	2.52	0.43
3:C:514:TYR:CD1	3:C:514:TYR:C	2.94	0.43
3:C:524:ILE:O	3:C:525:CYS:SG	2.74	0.43
15:H:64:A:H2'	15:H:65:U:C6	2.53	0.43
15:H:153:A:H2'	15:H:154:C:H5''	1.99	0.43
21:1:840:LEU:O	21:1:844:VAL:HG12	2.19	0.43
22:2:482:ALA:O	22:2:485:PRO:HD3	2.18	0.43
23:3:88:VAL:HA	23:3:103:HIS:O	2.18	0.43
23:3:511:LEU:HB2	23:3:517:VAL:HG23	1.99	0.43
23:3:1056:VAL:HG22	23:3:1091:VAL:HG22	2.01	0.43
24:4:67:ALA:HA	24:4:70:ALA:HB3	2.00	0.43
32:R:88:ILE:HG22	32:R:96:ILE:CG2	2.49	0.43
32:R:423:ASP:C	32:R:424:SER:HG	2.03	0.43
33:T:406:ILE:HG22	33:T:407:GLN:N	2.33	0.43
38:z:107:HIS:ND1	38:z:107:HIS:O	2.51	0.43
1:A:232:LEU:HD21	3:C:388:VAL:CG1	2.32	0.43
1:A:298:ASP:OD1	1:A:298:ASP:C	2.62	0.43
1:A:305:ARG:CG	3:C:878:ILE:HG21	2.38	0.43
1:A:318:TYR:O	3:C:641:MET:HB2	2.19	0.43
1:A:459:LEU:HD12	1:A:459:LEU:HA	1.75	0.43
1:A:741:ARG:NH2	33:T:432:ASP:O	2.41	0.43
1:A:1113:TYR:O	1:A:1117:HIS:CB	2.66	0.43
1:A:1263:TRP:CE3	1:A:1295:ILE:HD13	2.53	0.43
2:B:99:C:H2'	2:B:100:C:C6	2.53	0.43
3:C:133:THR:CB	3:C:225:VAL:HG23	2.43	0.43
3:C:297:ASN:HD22	3:C:298:LEU:HD12	1.83	0.43
3:C:350:ASN:HB3	3:C:353:THR:CG2	2.49	0.43
3:C:505:GLN:HG2	3:C:506:PRO:HD2	2.00	0.43
3:C:776:GLU:O	3:C:781:ASP:HA	2.18	0.43
13:F:42:C:H2'	13:F:43:A:C8	2.53	0.43
21:1:885:ASP:OD1	21:1:888:LEU:HB3	2.18	0.43
21:1:1119:VAL:O	21:1:1122:THR:HG22	2.17	0.43
21:1:1120:ALA:HB1	21:1:1125:PRO:HB3	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1179:ASP:HB3	22:2:511:LEU:HD12	2.00	0.43
22:2:630:PRO:HA	22:2:631:PRO:HD3	1.77	0.43
29:L:63:TRP:CH2	29:L:99:HIS:HB2	2.54	0.43
29:L:101:GLU:O	29:L:105:ASP:HB2	2.18	0.43
32:R:54:LEU:HD12	32:R:54:LEU:HA	1.86	0.43
33:T:399:LYS:HG3	33:T:406:ILE:CD1	2.37	0.43
36:Y:36:ALA:HB3	37:Z:498:GLY:O	2.18	0.43
1:A:141:ILE:HG12	1:A:426:LEU:HD23	1.99	0.43
1:A:643:GLY:O	1:A:646:PRO:HD2	2.19	0.43
3:C:145:PHE:N	3:C:312:SER:OG	2.50	0.43
3:C:736:GLY:HA3	3:C:770:PHE:CE2	2.53	0.43
5:E:67:GLY:N	5:E:87:ASP:OD1	2.42	0.43
14:G:-5:G:O2'	14:G:-4:A:H5''	2.18	0.43
15:H:83:A:C4	15:H:84:C:C6	3.07	0.43
15:H:98:G:H5'	15:H:104:U:OP2	2.18	0.43
15:H:154:C:O2'	15:H:155:C:C5'	2.66	0.43
15:H:181:G:C2	15:H:182:U:C4	3.07	0.43
21:1:897:LEU:HD21	21:1:932:ILE:HD13	2.00	0.43
21:1:1235:GLU:O	21:1:1238:ARG:HB3	2.18	0.43
23:3:139:LYS:HB2	23:3:160:ALA:HB3	2.00	0.43
23:3:868:VAL:HG12	23:3:877:LEU:HB2	1.99	0.43
32:R:126:ASN:HD22	32:R:128:ASP:H	1.66	0.43
36:Y:29:HIS:CG	36:Y:91:ILE:HG23	2.53	0.43
1:A:148:TRP:HE3	1:A:629:PHE:CD1	2.35	0.43
1:A:417:ARG:NH1	2:B:58:U:H4'	2.33	0.43
1:A:671:THR:O	1:A:672:VAL:C	2.59	0.43
1:A:1382:SER:HB3	1:A:1416:ILE:HG12	2.00	0.43
1:A:1771:LEU:HD12	1:A:1777:ILE:HD13	2.00	0.43
2:B:95:G:C6	11:e:36:TYR:O	2.72	0.43
3:C:60:HIS:ND1	3:C:60:HIS:O	2.51	0.43
4:D:1583:ASP:C	4:D:1585:GLN:H	2.26	0.43
13:F:36:A:C3'	13:F:36:A:C8	3.01	0.43
15:H:157:G:H2'	15:H:158:G:O4'	2.19	0.43
7:i:85:PRO:CA	18:w:184:ARG:CA	2.94	0.43
21:1:889:GLU:HA	21:1:892:LEU:HD12	2.00	0.43
22:2:613:LEU:HD11	24:4:32:LEU:HD13	1.99	0.43
23:3:32:VAL:HG23	23:3:39:GLU:HB3	1.99	0.43
25:5:114:LYS:HA	25:5:119:ILE:O	2.19	0.43
29:L:73:HIS:CD2	29:L:77:LEU:HD11	2.53	0.43
32:R:52:PRO:HB3	32:R:57:ASP:OD2	2.17	0.43
32:R:119:LEU:HA	32:R:232:MET:CE	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:120:VAL:HG23	32:R:121:PRO:HD2	2.01	0.43
33:T:459:LEU:HG	33:T:461:SER:OG	2.18	0.43
33:T:495:ALA:O	33:T:496:THR:C	2.62	0.43
1:A:661:GLU:HG3	32:R:210:PRO:HB2	2.00	0.43
1:A:790:ARG:HG3	3:C:60:HIS:HD2	1.82	0.43
1:A:1921:ASP:OD2	1:A:1966:HIS:HB3	2.19	0.43
2:B:87:A:H5'	2:B:93:U:OP2	2.19	0.43
3:C:61:GLU:OE1	3:C:62:ASP:N	2.51	0.43
3:C:295:ASP:OD1	3:C:297:ASN:HB2	2.19	0.43
3:C:461:LEU:HD23	3:C:461:LEU:HA	1.78	0.43
4:D:441:GLY:O	4:D:693:THR:N	2.36	0.43
21:1:471:ASP:OD2	21:1:505:LYS:NZ	2.34	0.43
32:R:242:THR:HG22	32:R:244:LYS:H	1.84	0.43
32:R:443:GLY:O	32:R:447:MET:CB	2.67	0.43
1:A:48:LYS:C	1:A:50:LYS:H	2.24	0.43
1:A:781:ARG:NH2	15:H:24:A:H5'	2.34	0.43
1:A:1433:ASP:O	1:A:1434:LYS:HD3	2.19	0.43
1:A:1437:ARG:O	1:A:1440:THR:OG1	2.36	0.43
1:A:1570:LYS:HZ2	30:M:200:ASP:CG	2.26	0.43
1:A:1759:THR:H	21:1:938:TRP:CD1	2.36	0.43
3:C:73:TYR:CE1	33:T:487:LYS:HE2	2.52	0.43
3:C:137:HIS:HD2	3:C:236:MET:CB	2.22	0.43
3:C:275:TYR:OH	3:C:345:GLY:HA2	2.19	0.43
3:C:349:PHE:CG	3:C:356:PHE:HE1	2.36	0.43
3:C:481:MET:HE2	3:C:559:ILE:HD11	2.00	0.43
3:C:941:LYS:HG2	3:C:942:GLY:N	2.34	0.43
13:F:46:G:H2'	13:F:47:A:C8	2.54	0.43
15:H:166:G:N3	15:H:166:G:H2'	2.33	0.43
15:H:180:G:N3	15:H:181:G:C8	2.87	0.43
21:1:892:LEU:HD23	21:1:892:LEU:HA	1.91	0.43
27:7:51:ASN:OD1	27:7:61:LYS:HE2	2.18	0.43
31:P:191:ASP:O	31:P:192:VAL:HG23	2.18	0.43
32:R:116:TYR:CD1	32:R:116:TYR:C	2.97	0.43
33:T:225:ASP:O	33:T:226:ARG:HB2	2.18	0.43
1:A:151:MET:SD	1:A:628:GLY:HA3	2.59	0.43
1:A:175:PRO:CG	1:A:498:ARG:NH2	2.73	0.43
1:A:331:TRP:HZ3	3:C:179:VAL:HG22	1.82	0.43
1:A:412:ASN:OD1	1:A:412:ASN:C	2.62	0.43
1:A:843:LEU:HD22	1:A:867:ILE:HG23	2.01	0.43
1:A:2272:MET:HE3	1:A:2296:LEU:HB3	2.01	0.43
3:C:67:PRO:O	3:C:68:THR:C	2.61	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:70:GLU:C	3:C:70:GLU:CD	2.87	0.43
3:C:289:ILE:CD1	3:C:300:LEU:HD21	2.49	0.43
3:C:381:LEU:HD23	3:C:416:LEU:HD22	1.99	0.43
13:F:39:A:H61	14:G:8:C:N4	2.11	0.43
14:G:12:G:C2	14:G:13:C:O4'	2.71	0.43
18:w:477:GLU:HA	23:3:980:LYS:HZ3	1.84	0.43
21:1:184:VAL:O	21:1:188:ALA:CB	2.66	0.43
23:3:633:LEU:HD12	23:3:637:PRO:HG2	2.00	0.43
28:J:339:TRP:CG	32:R:116:TYR:CD2	3.06	0.43
33:T:347:THR:HG21	33:T:357:TRP:HE1	1.82	0.43
35:X:307:GLN:HB3	35:X:331:LEU:HD13	2.01	0.43
38:z:99:VAL:HG22	38:z:115:PHE:CD1	2.54	0.43
1:A:30:LEU:HB3	5:E:194:TYR:CZ	2.53	0.43
1:A:1735:LYS:NZ	1:A:1765:SER:O	2.50	0.43
1:A:1921:ASP:CG	1:A:1966:HIS:HB3	2.43	0.43
3:C:669:THR:HG22	3:C:690:GLU:CB	2.48	0.43
5:E:178:LEU:CD1	5:E:222:LEU:HD21	2.46	0.43
5:E:321:TYR:OH	5:E:356:ILE:HG23	2.19	0.43
15:H:68:G:C6	15:H:84:C:N4	2.85	0.43
21:1:900:PHE:HA	21:1:903:GLN:HE21	1.83	0.43
21:1:968:GLU:OE1	21:1:968:GLU:N	2.51	0.43
23:3:253:GLU:HA	23:3:286:ILE:HG22	2.01	0.43
23:3:820:ALA:HB2	23:3:843:LEU:HD11	2.00	0.43
23:3:1055:VAL:HB	23:3:1093:MET:HB3	2.00	0.43
26:6:14:GLN:O	26:6:46:CYS:HB3	2.18	0.43
32:R:113:TYR:CG	32:R:118:ASP:OD2	2.72	0.43
33:T:399:LYS:CG	33:T:406:ILE:CD1	2.78	0.43
36:Y:37:TRP:CE2	36:Y:83:CYS:SG	3.11	0.43
36:Y:85:GLU:O	37:Z:502:ALA:CA	2.65	0.43
1:A:120:TYR:CE1	1:A:485:THR:HG22	2.54	0.42
1:A:405:LEU:HD11	3:C:265:LEU:HD13	2.00	0.42
1:A:532:THR:HG21	14:G:2:U:O5'	2.19	0.42
1:A:1373:GLN:NE2	1:A:1381:ASP:OD2	2.52	0.42
1:A:1539:SER:OG	1:A:1540:PRO:HD3	2.19	0.42
1:A:1630:LEU:HA	1:A:1630:LEU:HD23	1.80	0.42
1:A:2302:LYS:HD2	1:A:2306:HIS:CE1	2.54	0.42
3:C:77:VAL:CB	33:T:196:LEU:HG	2.41	0.42
3:C:366:GLN:O	3:C:367:ARG:C	2.58	0.42
3:C:457:VAL:O	3:C:458:ASP:CB	2.67	0.42
13:F:55:C:OP2	13:F:74:U:O2'	2.36	0.42
14:G:132:G:H5'	18:w:399:LEU:HD11	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1108:ASN:CG	21:1:1111:CYS:H	2.26	0.42
23:3:169:HIS:H	23:3:185:LEU:HB2	1.83	0.42
23:3:226:GLU:HG3	23:3:261:PHE:CZ	2.51	0.42
23:3:520:TYR:HE1	23:3:522:ASP:HB2	1.83	0.42
23:3:640:LEU:HD22	23:3:667:ILE:HG12	2.01	0.42
23:3:1188:ASN:OD1	23:3:1189:LYS:N	2.51	0.42
32:R:124:VAL:HG22	32:R:126:ASN:N	2.34	0.42
33:T:284:TYR:N	33:T:284:TYR:CD1	2.87	0.42
36:Y:92:LEU:O	36:Y:96:ASN:CB	2.67	0.42
1:A:250:VAL:HG21	1:A:337:VAL:HG12	2.01	0.42
1:A:284:ARG:HE	1:A:284:ARG:HB3	1.70	0.42
1:A:311:GLU:CB	3:C:885:THR:HG21	2.47	0.42
1:A:349:ALA:CB	1:A:399:ALA:CB	2.74	0.42
1:A:1425:LYS:HG2	32:R:417:ASN:OD1	2.18	0.42
1:A:1427:ARG:O	1:A:1428:HIS:C	2.60	0.42
1:A:2072:GLU:O	1:A:2076:ARG:HG3	2.18	0.42
1:A:2310:ARG:HG2	1:A:2310:ARG:HH11	1.84	0.42
3:C:93:ILE:HG21	33:T:218:TRP:CZ2	2.54	0.42
3:C:115:GLU:C	3:C:117:ASP:N	2.77	0.42
3:C:481:MET:SD	3:C:492:ALA:CB	3.06	0.42
15:H:168:A:N3	15:H:168:A:C2'	2.77	0.42
21:1:460:PRO:C	21:1:464:LEU:HD22	2.44	0.42
21:1:744:ALA:HB2	21:1:784:MET:SD	2.59	0.42
21:1:1289:ASN:HB2	21:1:1294:THR:HA	2.00	0.42
23:3:274:ARG:NH2	23:3:309:ASP:OD2	2.50	0.42
32:R:220:ARG:HB2	32:R:220:ARG:CZ	2.49	0.42
36:Y:37:TRP:NE1	36:Y:83:CYS:CB	2.70	0.42
1:A:32:GLU:OE2	1:A:36:LYS:CE	2.68	0.42
1:A:962:LEU:HB2	1:A:965:VAL:HB	1.99	0.42
1:A:1052:VAL:HG22	1:A:1161:LEU:HD21	2.01	0.42
1:A:1099:PHE:HZ	1:A:1157:ILE:HD11	1.85	0.42
1:A:1457:HIS:HE2	32:R:424:SER:CB	2.32	0.42
1:A:1772:PHE:CD1	1:A:1773:SER:N	2.87	0.42
1:A:1810:PHE:CE1	1:A:1919:LEU:HD12	2.55	0.42
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.84	0.42
3:C:413:ARG:HB2	3:C:414:PRO:HD3	1.99	0.42
3:C:444:GLY:C	3:C:447:PRO:HD2	2.43	0.42
3:C:641:MET:HE2	3:C:655:VAL:HG21	2.01	0.42
15:H:3:C:H2'	15:H:4:G:C8	2.53	0.42
15:H:178:A:N3	15:H:178:A:H2'	2.34	0.42
21:1:707:LEU:O	21:1:710:ALA:HB3	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:811:LEU:HB2	21:1:812:PRO:HD3	2.00	0.42
21:1:1040:GLY:CA	21:1:1080:THR:HG22	2.48	0.42
22:2:613:LEU:HA	22:2:616:SER:OG	2.20	0.42
23:3:310:ILE:O	23:3:330:PHE:HB3	2.19	0.42
23:3:961:ILE:HB	23:3:970:TYR:CD2	2.54	0.42
1:A:94:TYR:HD2	32:R:207:MET:SD	2.43	0.42
1:A:319:LEU:CD1	3:C:637:LEU:HB3	2.48	0.42
1:A:361:HIS:CD2	3:C:279:ARG:CZ	3.03	0.42
2:B:94:U:O2'	2:B:95:G:H3'	2.18	0.42
3:C:323:PHE:CE1	3:C:424:PHE:HE1	2.37	0.42
3:C:706:GLN:HE21	3:C:708:THR:N	2.12	0.42
3:C:863:ILE:HA	3:C:864:PRO:HD3	1.88	0.42
15:H:5:C:H2'	15:H:6:U:C6	2.54	0.42
18:w:403:ASN:N	18:w:417:ARG:O	2.53	0.42
18:w:404:ILE:N	18:w:417:ARG:O	2.47	0.42
21:1:413:LYS:HG3	21:1:415:LEU:HD11	2.01	0.42
21:1:619:ASN:ND2	21:1:624:VAL:HG21	2.34	0.42
21:1:619:ASN:OD1	21:1:620:MET:N	2.52	0.42
21:1:722:GLU:O	21:1:725:ASP:CB	2.67	0.42
21:1:903:GLN:HE22	21:1:910:MET:HE2	1.85	0.42
23:3:185:LEU:HD11	23:3:235:LEU:HD13	2.01	0.42
23:3:287:PHE:HA	23:3:304:GLN:O	2.19	0.42
23:3:1014:TYR:CE2	23:3:1016:ARG:HA	2.55	0.42
23:3:1052:ASN:OD1	23:3:1096:HIS:ND1	2.39	0.42
23:3:1201:PRO:HB2	23:3:1202:PRO:HD3	2.02	0.42
26:6:47:ASP:HA	26:6:50:ASN:O	2.20	0.42
28:J:339:TRP:CD2	32:R:116:TYR:CD2	2.85	0.42
29:L:63:TRP:CZ2	29:L:99:HIS:HB2	2.54	0.42
32:R:183:GLN:HB3	32:R:188:PHE:CD2	2.54	0.42
36:Y:69:ARG:HA	36:Y:76:SER:HA	2.02	0.42
39:x:515:SER:O	39:x:546:LEU:HA	2.19	0.42
1:A:211:GLN:HA	1:A:212:PRO:HD3	1.82	0.42
1:A:258:PHE:CD2	1:A:434:HIS:HA	2.55	0.42
1:A:303:ILE:HG23	3:C:933:PHE:CD1	2.53	0.42
1:A:328:HIS:C	1:A:329:LEU:HD23	2.43	0.42
1:A:380:LEU:H	1:A:380:LEU:HD22	1.84	0.42
1:A:718:ARG:NH2	32:R:259:LYS:CE	2.78	0.42
1:A:1263:TRP:CD2	1:A:1295:ILE:HD13	2.54	0.42
1:A:1363:GLN:O	1:A:1364:LEU:HG	2.18	0.42
1:A:2268:LEU:CD2	4:D:1261:PRO:C	2.82	0.42
3:C:669:THR:HG22	3:C:690:GLU:OE1	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:712:LYS:O	3:C:716:GLU:HG3	2.18	0.42
5:E:277:PHE:CE1	5:E:317:ARG:HG2	2.53	0.42
14:G:5:G:C2	14:G:6:A:C5	3.08	0.42
14:G:136:U:O4	21:1:515:ALA:HA	2.19	0.42
21:1:494:GLU:HA	21:1:497:ILE:HG22	2.01	0.42
21:1:940:LEU:O	21:1:948:ARG:NH2	2.51	0.42
21:1:1255:PHE:HD2	22:2:487:LEU:HD22	1.81	0.42
22:2:536:MET:HE2	22:2:564:ILE:O	2.19	0.42
23:3:456:PRO:HB2	23:3:757:ILE:HD13	2.02	0.42
23:3:508:CYS:SG	23:3:518:GLN:NE2	2.92	0.42
23:3:784:THR:HB	23:3:786:ARG:NH1	2.32	0.42
33:T:318:ARG:CG	33:T:318:ARG:NH1	2.82	0.42
34:V:484:SER:O	34:V:486:THR:N	2.53	0.42
39:x:1004:GLU:CB	39:x:1007:TRP:CB	2.97	0.42
1:A:715:GLU:OE1	32:R:258:TRP:CE3	2.73	0.42
1:A:791:GLN:NE2	1:A:1026:ASN:OD1	2.52	0.42
1:A:1362:ASP:OD1	1:A:1362:ASP:N	2.51	0.42
1:A:1759:THR:N	21:1:938:TRP:CD1	2.88	0.42
1:A:1948:ASP:O	1:A:1951:LYS:HB2	2.20	0.42
1:A:1953:ILE:HD11	1:A:1986:LEU:HD13	2.01	0.42
1:A:2216:CYS:HA	1:A:2225:LEU:HB3	2.01	0.42
3:C:85:ASP:OD2	33:T:240:LEU:HA	2.20	0.42
3:C:90:THR:O	3:C:92:PRO:HD3	2.19	0.42
15:H:107:A:N1	15:H:108:G:C5	2.88	0.42
18:w:410:ILE:HG13	18:w:452:ILE:HG22	2.02	0.42
21:1:1075:ARG:HE	21:1:1075:ARG:HB2	1.64	0.42
23:3:146:ARG:HB2	23:3:150:ALA:HA	2.02	0.42
23:3:353:PHE:O	23:3:432:ARG:NH1	2.44	0.42
23:3:774:PHE:N	23:3:774:PHE:CD2	2.86	0.42
27:7:30:GLU:HA	27:7:33:VAL:HG12	2.02	0.42
30:M:202:CYS:HB2	30:M:219:PHE:HB2	2.02	0.42
32:R:71:GLN:HE21	32:R:71:GLN:HB2	1.61	0.42
33:T:188:PRO:HG3	33:T:443:THR:HG21	2.01	0.42
36:Y:38:ILE:HG12	36:Y:82:LEU:HB3	2.02	0.42
1:A:1116:GLU:C	1:A:1118:PRO:HD3	2.45	0.42
1:A:1560:ILE:HG12	1:A:1668:TRP:CB	2.49	0.42
1:A:1889:LEU:HD11	1:A:2012:LEU:HG	2.02	0.42
1:A:2272:MET:HE3	1:A:2272:MET:HB3	1.74	0.42
3:C:140:HIS:CB	3:C:230:ASP:H	2.33	0.42
3:C:259:LYS:HD2	41:C:1500:GTP:C4	2.55	0.42
3:C:452:THR:HB	3:C:577:PHE:CE2	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:114:GLU:CD	5:E:116:HIS:NE2	2.76	0.42
5:E:152:SER:OG	5:E:153:PHE:HD1	2.03	0.42
13:F:58:G:O2'	13:F:59:G:P	2.78	0.42
14:G:141:C:H2'	14:G:142:U:C6	2.52	0.42
15:H:179:C:C2	15:H:180:G:C8	3.07	0.42
16:o:160:LYS:O	16:o:161:MET:C	2.63	0.42
21:1:401:ASP:HA	21:1:404:LEU:HB2	2.00	0.42
21:1:848:GLU:O	21:1:851:SER:OG	2.32	0.42
21:1:1179:ASP:OD1	21:1:1181:ASP:N	2.52	0.42
23:3:3:LEU:HA	23:3:1130:VAL:O	2.20	0.42
23:3:482:THR:OG1	23:3:501:GLY:HA3	2.19	0.42
23:3:691:THR:HG22	23:3:716:SER:HB3	2.02	0.42
23:3:718:ARG:HG2	23:3:719:SER:H	1.84	0.42
25:5:25:ASN:HB3	25:5:87:LEU:HA	2.02	0.42
28:J:294:HIS:HE1	29:L:227:THR:CB	2.26	0.42
31:P:226:LYS:HD3	31:P:227:TYR:HE1	1.83	0.42
32:R:67:ILE:CG1	32:R:71:GLN:OE1	2.68	0.42
33:T:471:ASP:C	33:T:471:ASP:OD1	2.62	0.42
1:A:371:LEU:HD12	1:A:372:PRO:HD2	2.00	0.42
1:A:380:LEU:HD12	3:C:334:ILE:HA	2.02	0.42
1:A:382:GLU:O	1:A:383:PHE:CG	2.73	0.42
1:A:611:LEU:HA	1:A:611:LEU:HD12	1.85	0.42
1:A:816:TRP:CE2	1:A:820:ARG:HG3	2.55	0.42
1:A:1436:TRP:HA	1:A:1439:ARG:CZ	2.50	0.42
3:C:149:LEU:HA	3:C:427:PHE:HD2	1.82	0.42
3:C:465:MET:HE1	3:C:475:MET:CE	2.50	0.42
14:G:-3:A:H2'	14:G:-2:C:C6	2.55	0.42
15:H:82:G:C2	15:H:83:A:C5	3.08	0.42
17:p:197:ASP:HA	17:p:200:ALA:HB3	2.02	0.42
21:1:527:GLY:O	21:1:531:LEU:HD13	2.20	0.42
22:2:525:PRO:HD2	22:2:528:ILE:HD12	2.00	0.42
23:3:412:ILE:HD12	23:3:1118:VAL:HG11	2.01	0.42
33:T:187:LYS:N	33:T:188:PRO:CD	2.83	0.42
33:T:233:LEU:HD23	33:T:233:LEU:O	2.20	0.42
36:Y:37:TRP:HH2	37:Z:498:GLY:N	2.15	0.42
36:Y:59:TYR:HB3	36:Y:92:LEU:HD23	2.01	0.42
1:A:109:PRO:HD3	1:A:630:TRP:HZ2	1.83	0.42
1:A:312:TYR:HH	3:C:853:ARG:NH2	2.07	0.42
1:A:697:MET:N	1:A:698:PRO:HD3	2.34	0.42
1:A:833:LYS:HE3	1:A:834:HIS:NE2	2.35	0.42
1:A:1301:ILE:CD1	2:B:39:C:OP1	2.67	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1416:ILE:HB	1:A:1417:PRO:HD3	2.01	0.42
1:A:1457:HIS:HE1	32:R:424:SER:HA	1.74	0.42
2:B:41:U:C4	2:B:42:U:O4	2.73	0.42
2:B:92:U:C3'	2:B:93:U:H5'	2.50	0.42
3:C:140:HIS:HB3	3:C:230:ASP:H	1.85	0.42
3:C:149:LEU:HA	3:C:427:PHE:CE2	2.54	0.42
3:C:710:ASN:C	3:C:712:LYS:N	2.77	0.42
4:D:1481:ILE:C	4:D:1483:ARG:H	2.28	0.42
14:G:139:U:H2'	14:G:140:A:C8	2.55	0.42
15:H:26:A:C5	15:H:27:U:C5	3.08	0.42
17:p:209:GLY:O	17:p:211:LYS:N	2.52	0.42
21:1:687:VAL:HA	21:1:690:ILE:HG22	2.01	0.42
21:1:727:VAL:HG12	21:1:731:LEU:HD11	2.02	0.42
21:1:790:LYS:O	21:1:793:LYS:HB3	2.19	0.42
23:3:1039:LEU:HB2	23:3:1043:THR:OG1	2.20	0.42
28:J:240:THR:O	28:J:241:VAL:HB	2.19	0.42
28:J:259:GLN:HE21	29:L:220:PRO:HD3	1.82	0.42
31:P:58:ASP:OD2	31:P:61:ARG:HB2	2.19	0.42
37:Z:564:PRO:C	37:Z:582:TYR:CG	2.98	0.42
1:A:48:LYS:HG2	1:A:49:ARG:N	2.35	0.42
1:A:89:LEU:CD2	1:A:89:LEU:C	2.93	0.42
1:A:428:LYS:HE3	1:A:454:TYR:CE1	2.55	0.42
1:A:479:THR:HG23	32:R:203:GLN:NE2	2.35	0.42
1:A:1188:ASN:ND2	1:A:1233:ASP:OD2	2.47	0.42
1:A:1489:LEU:O	1:A:1492:GLY:N	2.45	0.42
1:A:1503:TRP:CZ2	1:A:1753:LEU:HD21	2.55	0.42
1:A:1555:LEU:HB2	1:A:1558:THR:OG1	2.19	0.42
1:A:1763:LEU:HD23	1:A:1764:SER:O	2.20	0.42
1:A:2117:ILE:H	1:A:2117:ILE:HG12	1.64	0.42
3:C:220:ARG:HD3	3:C:477:HIS:NE2	2.34	0.42
3:C:474:LEU:HD12	3:C:500:THR:O	2.20	0.42
3:C:489:GLN:N	3:C:489:GLN:CD	2.78	0.42
15:H:147:G:C2	15:H:148:C:N3	2.87	0.42
15:H:155:C:H2'	15:H:156:U:H5''	2.02	0.42
15:H:179:C:O2	15:H:180:G:C8	2.72	0.42
21:1:555:VAL:O	21:1:559:ILE:HG12	2.19	0.42
22:2:643:PRO:HG2	24:4:66:ASP:HA	2.01	0.42
23:3:259:LYS:HE3	23:3:266:ASP:OD2	2.20	0.42
23:3:261:PHE:HD1	23:3:261:PHE:HA	1.72	0.42
23:3:288:VAL:HG23	23:3:289:CYS:N	2.33	0.42
23:3:519:VAL:HG22	23:3:524:ILE:HG23	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:673:VAL:HA	23:3:690:ARG:HA	2.02	0.42
23:3:968:ARG:CZ	23:3:979:ARG:HH11	2.33	0.42
23:3:1011:TRP:HB3	23:3:1024:PHE:CZ	2.55	0.42
28:J:216:ASP:O	28:J:218:GLU:N	2.53	0.42
33:T:281:ILE:CD1	33:T:282:ARG:HG2	2.50	0.42
1:A:1320:LYS:NZ	32:R:434:TYR:CE1	2.88	0.41
1:A:1402:ARG:CD	32:R:412:ASP:HA	2.50	0.41
1:A:1942:ALA:CB	1:A:1983:LEU:HD22	2.50	0.41
3:C:291:MET:HG2	3:C:292:TYR:CE1	2.54	0.41
3:C:445:ALA:HB1	3:C:449:ILE:HG13	2.02	0.41
3:C:829:GLU:HG3	3:C:830:PRO:HD2	2.01	0.41
9:d:68:GLU:HA	9:d:97:SER:O	2.19	0.41
13:F:8:C:C6	13:F:8:C:C5'	2.98	0.41
13:F:31:U:H2'	13:F:32:U:C6	2.55	0.41
15:H:68:G:H2'	15:H:69:U:H6	1.82	0.41
9:k:68:GLU:HA	9:k:97:SER:O	2.19	0.41
21:1:699:GLN:O	21:1:700:LYS:C	2.63	0.41
21:1:783:GLU:O	21:1:787:ILE:HG12	2.20	0.41
21:1:1025:LYS:HE2	30:M:210:PHE:CE1	2.55	0.41
23:3:443:GLU:HA	23:3:735:SER:OG	2.20	0.41
23:3:812:LYS:NZ	23:3:855:PRO:HG2	2.35	0.41
28:J:262:ARG:HB3	29:L:220:PRO:HG3	2.02	0.41
28:J:297:ASN:CG	29:L:223:GLY:HA3	2.45	0.41
28:J:368:ARG:O	28:J:372:VAL:HG23	2.20	0.41
32:R:131:ASP:OD2	32:R:132:LEU:N	2.53	0.41
1:A:75:ASP:C	1:A:77:THR:H	2.28	0.41
1:A:120:TYR:HE1	1:A:485:THR:HB	1.84	0.41
1:A:137:GLU:N	1:A:138:PRO:HD2	2.35	0.41
1:A:143:GLN:O	1:A:146:SER:HB3	2.20	0.41
1:A:148:TRP:CZ2	1:A:616:PHE:CA	3.02	0.41
1:A:252:ASP:HB2	1:A:334:THR:CB	2.48	0.41
1:A:344:ASP:OD1	1:A:347:LEU:HD11	2.19	0.41
1:A:470:ARG:CZ	1:A:470:ARG:HB2	2.49	0.41
1:A:615:ARG:HE	1:A:615:ARG:HB2	1.59	0.41
1:A:1051:LEU:HD22	31:P:193:VAL:HG11	2.00	0.41
1:A:1823:HIS:O	1:A:1826:VAL:HG22	2.20	0.41
3:C:73:TYR:HB3	3:C:77:VAL:HG21	2.02	0.41
3:C:259:LYS:HG2	3:C:262:ARG:HD3	1.99	0.41
3:C:449:ILE:CD1	3:C:466:SER:HA	2.50	0.41
15:H:80:A:C2	15:H:81:G:N7	2.88	0.41
15:H:153:A:H62	15:H:177:A:H2	1.67	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1185:ARG:HD2	21:1:1218:ASN:OD1	2.20	0.41
23:3:425:VAL:O	23:3:435:LEU:HD12	2.20	0.41
23:3:436:ARG:HG2	23:3:778:ALA:HA	2.01	0.41
29:L:31:TRP:CH2	29:L:47:LYS:HA	2.55	0.41
32:R:82:MET:HE3	32:R:82:MET:CA	2.48	0.41
32:R:88:ILE:CG2	32:R:96:ILE:HG23	2.48	0.41
32:R:418:GLN:HE21	32:R:418:GLN:HB2	1.64	0.41
32:R:442:ARG:NH1	32:R:443:GLY:CA	2.78	0.41
36:Y:64:ASN:O	36:Y:83:CYS:HB3	2.19	0.41
37:Z:572:PRO:CG	37:Z:588:ASP:OD2	2.67	0.41
1:A:305:ARG:HE	3:C:854:ARG:NH1	2.18	0.41
1:A:629:PHE:CD2	1:A:629:PHE:O	2.73	0.41
1:A:1883:VAL:HG12	1:A:1885:LYS:HG3	2.01	0.41
1:A:2111:LEU:HD21	1:A:2225:LEU:HD21	2.03	0.41
2:B:35:U:OP2	2:B:35:U:C6	2.70	0.41
3:C:148:CYS:SG	3:C:312:SER:O	2.78	0.41
3:C:512:GLU:HG3	3:C:562:THR:O	2.19	0.41
5:E:263:ASP:O	5:E:272:ARG:NE	2.32	0.41
21:1:520:THR:HG21	21:1:558:ARG:HE	1.85	0.41
23:3:8:LEU:HD23	23:3:774:PHE:CZ	2.52	0.41
33:T:225:ASP:O	33:T:226:ARG:CB	2.67	0.41
1:A:206:TRP:CE3	1:A:212:PRO:HB3	2.55	0.41
1:A:346:ASP:O	1:A:347:LEU:C	2.64	0.41
1:A:800:TYR:HB3	3:C:59:LEU:HD11	2.02	0.41
1:A:1554:GLN:NE2	1:A:1620:TYR:O	2.49	0.41
1:A:1730:MET:O	1:A:1734:MET:HG2	2.19	0.41
3:C:70:GLU:CD	3:C:71:GLU:N	2.79	0.41
3:C:445:ALA:CB	3:C:449:ILE:HD11	2.43	0.41
3:C:853:ARG:O	3:C:854:ARG:HB3	2.20	0.41
15:H:152:G:H2'	15:H:152:G:N3	2.36	0.41
15:H:154:C:N3	15:H:176:G:N1	2.61	0.41
18:w:422:PHE:HZ	18:w:450:THR:CG2	2.31	0.41
21:1:1136:TYR:CE1	21:1:1144:GLN:HB3	2.55	0.41
23:3:199:GLU:HB3	23:3:203:ASN:HD21	1.85	0.41
28:J:220:LEU:O	28:J:223:TYR:HB3	2.21	0.41
28:J:412:ASP:O	28:J:413:GLU:C	2.63	0.41
32:R:155:VAL:O	32:R:159:VAL:HG23	2.20	0.41
1:A:280:GLU:CD	1:A:281:PRO:HD2	2.46	0.41
1:A:363:HIS:HD2	3:C:283:ASP:C	2.28	0.41
1:A:387:PHE:HD1	3:C:327:TYR:CE1	2.38	0.41
1:A:2332:ASP:C	1:A:2334:TYR:H	2.28	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:589:LYS:HB3	3:C:659:VAL:O	2.20	0.41
3:C:704:VAL:O	3:C:709:TRP:CZ2	2.74	0.41
3:C:707:ILE:HD11	3:C:735:PHE:HB2	2.01	0.41
5:E:348:ASP:OD1	5:E:348:ASP:C	2.62	0.41
13:F:40:U:O4	13:F:41:A:N6	2.54	0.41
15:H:103:U:C3'	15:H:104:U:H5'	2.51	0.41
21:1:621:ASP:OD2	21:1:623:TYR:HB3	2.19	0.41
21:1:719:TYR:CD1	23:3:218:ASN:HB2	2.56	0.41
23:3:116:VAL:HA	23:3:117:PRO:HD3	1.95	0.41
23:3:896:PHE:CZ	23:3:972:LEU:HB2	2.55	0.41
24:4:69:TYR:OH	24:4:73:ILE:HG13	2.20	0.41
28:J:340:GLN:N	28:J:341:PRO:HD3	2.35	0.41
28:J:360:ASP:C	28:J:363:ARG:HG3	2.45	0.41
31:P:192:VAL:CG1	31:P:193:VAL:N	2.83	0.41
33:T:223:SER:OG	33:T:224:ALA:N	2.53	0.41
35:X:173:GLN:NE2	35:X:176:GLU:HA	2.36	0.41
1:A:151:MET:SD	1:A:628:GLY:CA	3.09	0.41
1:A:280:GLU:HB2	2:B:48:A:H4'	2.01	0.41
1:A:335:PRO:HG3	3:C:139:HIS:CG	2.56	0.41
1:A:398:THR:CG2	3:C:382:ALA:CB	2.96	0.41
1:A:1325:LEU:HD23	1:A:1325:LEU:HA	1.86	0.41
1:A:1948:ASP:HA	1:A:1951:LYS:HD2	2.01	0.41
1:A:2073:TRP:CZ3	1:A:2313:HIS:CG	3.09	0.41
1:A:2117:ILE:HG21	1:A:2301:PRO:HB2	2.02	0.41
1:A:2120:LEU:HD12	1:A:2120:LEU:N	2.35	0.41
3:C:97:VAL:HG21	31:P:45:GLN:CG	2.46	0.41
3:C:137:HIS:NE2	3:C:236:MET:SD	2.93	0.41
13:F:39:A:H2'	13:F:40:U:O4'	2.21	0.41
14:G:-2:C:H2'	14:G:-1:G:H8	1.82	0.41
15:H:72:U:H6	15:H:72:U:O5'	2.03	0.41
15:H:171:U:H2'	15:H:172:C:O4'	2.21	0.41
18:w:34:ARG:O	18:w:35:ASP:C	2.62	0.41
21:1:815:PHE:HA	21:1:819:TRP:CD1	2.56	0.41
22:2:487:LEU:HD23	22:2:487:LEU:C	2.46	0.41
23:3:168:TYR:CE1	27:7:69:MET:HB3	2.55	0.41
23:3:442:LEU:HD13	23:3:734:LEU:HD23	1.99	0.41
23:3:587:VAL:CG1	23:3:590:MET:HG3	2.49	0.41
33:T:297:HIS:CE1	33:T:300:ILE:HD12	2.56	0.41
33:T:455:GLN:CG	33:T:456:PRO:HD2	2.51	0.41
36:Y:24:ASP:O	36:Y:26:VAL:N	2.54	0.41
38:z:67:ASP:HB2	38:z:112:GLN:HE21	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:x:936:TYR:O	39:x:937:ILE:C	2.63	0.41
1:A:228:TRP:CD1	1:A:228:TRP:H	2.38	0.41
1:A:296:PHE:CZ	3:C:593:GLU:HB2	2.56	0.41
1:A:530:LEU:CB	30:M:198:GLN:HE21	2.17	0.41
1:A:866:LEU:O	1:A:869:GLN:HB3	2.21	0.41
1:A:984:MET:SD	1:A:1048:MET:HE1	2.60	0.41
1:A:1035:GLN:HA	1:A:1446:GLN:HE22	1.84	0.41
1:A:1099:PHE:CE2	1:A:1153:VAL:HG13	2.53	0.41
1:A:1221:THR:O	1:A:1223:GLU:HG3	2.20	0.41
1:A:1430:LEU:HD21	32:R:422:MET:HA	2.03	0.41
1:A:1458:GLN:HE21	1:A:1463:LYS:HG3	1.86	0.41
3:C:230:ASP:OD1	3:C:259:LYS:HB2	2.17	0.41
3:C:270:PRO:HA	3:C:271:PRO:HD3	1.87	0.41
3:C:457:VAL:C	3:C:458:ASP:CG	2.88	0.41
4:D:577:LYS:O	4:D:581:SER:N	2.54	0.41
14:G:155:U:C4'	14:G:156:U:H5'	2.49	0.41
15:H:4:G:H2'	15:H:5:C:C6	2.55	0.41
15:H:83:A:H2'	15:H:84:C:H1'	2.00	0.41
21:1:1127:THR:O	22:2:571:LEU:HD13	2.21	0.41
23:3:314:THR:HG22	23:3:315:LEU:N	2.36	0.41
23:3:521:PRO:HA	23:3:544:ILE:CG2	2.49	0.41
23:3:524:ILE:CD1	23:3:556:ILE:HD13	2.49	0.41
24:4:67:ALA:O	24:4:70:ALA:HB3	2.21	0.41
28:J:273:TYR:CD1	32:R:228:PRO:CB	3.04	0.41
29:L:214:ILE:O	29:L:215:PRO:C	2.63	0.41
31:P:189:ASP:C	31:P:191:ASP:H	2.29	0.41
31:P:189:ASP:CG	31:P:192:VAL:CG2	2.94	0.41
32:R:103:ARG:O	32:R:104:GLN:C	2.64	0.41
1:A:61:MET:HB3	1:A:62:PRO:CD	2.50	0.41
1:A:1891:LEU:HB2	1:A:1893:PHE:CE2	2.55	0.41
1:A:2090:ILE:H	1:A:2090:ILE:HD13	1.86	0.41
1:A:2259:VAL:HG22	1:A:2260:GLN:H	1.86	0.41
2:B:20:G:C1'	2:B:21:A:OP1	2.69	0.41
3:C:300:LEU:N	3:C:300:LEU:CD1	2.84	0.41
13:F:60:C:H5''	32:R:219:PRO:HB3	2.01	0.41
15:H:160:A:H2'	15:H:161:U:C6	2.55	0.41
9:k:62:HIS:O	9:k:103:GLY:HA3	2.21	0.41
17:p:184:PRO:C	17:p:186:ARG:N	2.75	0.41
21:1:719:TYR:HB3	23:3:216:GLY:O	2.20	0.41
21:1:1016:LEU:O	21:1:1019:ARG:HB3	2.20	0.41
21:1:1055:TRP:O	21:1:1058:ILE:HB	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1092:ASP:OD1	21:1:1092:ASP:N	2.53	0.41
23:3:86:ARG:CD	23:3:104:GLN:HE21	2.33	0.41
23:3:205:GLN:HE21	23:3:227:PRO:HB3	1.85	0.41
23:3:554:VAL:HG12	23:3:556:ILE:HG23	2.01	0.41
26:6:90:ASN:OD1	26:6:91:LEU:N	2.54	0.41
30:M:208:THR:HG22	30:M:210:PHE:HD2	1.85	0.41
31:P:73:GLU:C	31:P:73:GLU:CD	2.88	0.41
37:Z:525:TYR:HD1	37:Z:526:ILE:CG2	2.29	0.41
38:z:141:MET:O	38:z:144:LEU:HB2	2.20	0.41
1:A:128:PHE:CD1	1:A:473:PHE:CE1	3.09	0.41
1:A:155:LYS:CE	1:A:624:GLY:O	2.68	0.41
1:A:173:GLU:O	1:A:520:TYR:HD2	2.02	0.41
1:A:292:ASP:O	1:A:294:ASN:ND2	2.54	0.41
1:A:331:TRP:CD1	3:C:635:LEU:HD13	2.55	0.41
1:A:440:PRO:O	1:A:441:VAL:C	2.64	0.41
1:A:596:TYR:O	1:A:598:LEU:N	2.54	0.41
1:A:965:VAL:O	1:A:1100:ARG:NH1	2.54	0.41
1:A:1052:VAL:CG2	1:A:1161:LEU:HD21	2.51	0.41
1:A:1407:ASP:OD1	1:A:1407:ASP:N	2.51	0.41
1:A:1661:TRP:NE1	1:A:1697:SER:O	2.53	0.41
1:A:1757:GLU:CG	32:R:451:ILE:HG13	2.51	0.41
1:A:1776:ILE:O	1:A:1859:LYS:N	2.48	0.41
1:A:1788:VAL:HG21	1:A:1800:THR:HB	2.03	0.41
1:A:2117:ILE:HG22	1:A:2303:GLU:HA	2.03	0.41
2:B:27:U:HO2'	2:B:28:A:P	2.42	0.41
3:C:64:LYS:HE2	3:C:64:LYS:HA	2.02	0.41
3:C:65:TYR:O	3:C:66:TYR:CG	2.73	0.41
3:C:79:THR:HA	33:T:199:VAL:O	2.20	0.41
3:C:132:VAL:HG11	3:C:226:VAL:CG2	2.49	0.41
3:C:133:THR:HB	3:C:225:VAL:HA	2.02	0.41
3:C:513:ASN:O	3:C:513:ASN:ND2	2.54	0.41
3:C:518:ASP:N	3:C:519:GLU:OE2	2.54	0.41
5:E:115:LEU:O	5:E:116:HIS:CD2	2.74	0.41
5:E:243:LEU:HD22	5:E:243:LEU:HA	1.80	0.41
14:G:132:G:C4'	18:w:399:LEU:HD13	2.51	0.41
15:H:152:G:H2'	15:H:153:A:C1'	2.51	0.41
17:p:156:ASN:O	17:p:219:LYS:O	2.39	0.41
21:1:184:VAL:O	21:1:188:ALA:HB2	2.21	0.41
21:1:642:PRO:HB3	21:1:682:HIS:NE2	2.36	0.41
21:1:664:GLY:O	21:1:667:ILE:HB	2.21	0.41
21:1:770:MET:O	21:1:774:ILE:HG12	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:963:LYS:HG2	21:1:1003:VAL:HB	2.02	0.41
21:1:1080:THR:HA	21:1:1083:TYR:CD2	2.56	0.41
21:1:1092:ASP:OD1	21:1:1093:VAL:N	2.54	0.41
21:1:1227:ILE:O	21:1:1231:MET:HG2	2.20	0.41
21:1:1252:GLN:OE1	22:2:499:PRO:HA	2.20	0.41
23:3:65:LEU:HD12	23:3:79:VAL:O	2.21	0.41
23:3:509:SER:OG	23:3:517:VAL:O	2.20	0.41
23:3:631:GLN:HG2	23:3:632:ALA:O	2.21	0.41
23:3:910:ALA:HB2	23:3:948:VAL:HG23	2.02	0.41
28:J:376:VAL:HB	28:J:411:MET:HE1	2.01	0.41
31:P:188:TRP:C	31:P:188:TRP:HE3	2.29	0.41
32:R:69:VAL:HG12	32:R:70:ALA:N	2.36	0.41
32:R:106:GLN:N	32:R:106:GLN:CD	2.79	0.41
32:R:132:LEU:HD13	33:T:399:LYS:HE3	2.02	0.41
32:R:414:ARG:NH2	32:R:414:ARG:CB	2.73	0.41
33:T:209:CYS:O	33:T:221:THR:HA	2.21	0.41
33:T:210:ILE:HG12	33:T:221:THR:HG22	2.03	0.41
33:T:294:LEU:N	33:T:294:LEU:HD23	2.36	0.41
33:T:400:PHE:HD1	33:T:401:PRO:HA	1.86	0.41
36:Y:10:ILE:O	36:Y:13:LEU:N	2.53	0.41
36:Y:67:LEU:HA	36:Y:80:CYS:HA	2.02	0.41
37:Z:566:TYR:CE2	37:Z:584:TRP:HE3	2.29	0.41
38:z:135:GLY:HA2	38:z:138:VAL:CG2	2.50	0.41
1:A:76:MET:HE2	1:A:88:TYR:CE2	2.55	0.41
1:A:107:PRO:O	1:A:108:MET:HB2	2.21	0.41
1:A:118:VAL:HG12	1:A:119:LEU:N	2.36	0.41
1:A:247:THR:OG1	1:A:429:ASN:CB	2.60	0.41
1:A:347:LEU:O	1:A:348:PRO:C	2.63	0.41
1:A:384:VAL:O	1:A:385:GLU:HG2	2.21	0.41
1:A:395:THR:HG23	3:C:383:GLN:NE2	2.24	0.41
1:A:842:ALA:HB1	1:A:920:ALA:HB1	2.03	0.41
1:A:1425:LYS:CB	32:R:417:ASN:OD1	2.69	0.41
1:A:1771:LEU:O	1:A:1777:ILE:HD12	2.20	0.41
1:A:1776:ILE:HD13	1:A:1813:ARG:HD3	2.03	0.41
2:B:19:A:HO2'	2:B:20:G:P	2.38	0.41
3:C:149:LEU:HD11	3:C:427:PHE:CB	2.51	0.41
3:C:354:ARG:CG	3:C:354:ARG:HH11	2.34	0.41
3:C:513:ASN:ND2	3:C:513:ASN:C	2.78	0.41
13:F:42:C:C2	13:F:43:A:C8	3.09	0.41
15:H:24:A:O2'	15:H:26:A:OP2	2.38	0.41
21:1:1286:ARG:N	23:3:1006:GLN:HE22	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:274:ARG:HD2	23:3:389:PRO:HD3	2.02	0.41
25:5:14:PRO:O	25:5:17:VAL:HG22	2.21	0.41
28:J:423:GLU:OE1	28:J:423:GLU:HA	2.21	0.41
29:L:49:ARG:NH1	29:L:53:TRP:HB3	2.36	0.41
33:T:399:LYS:HB2	33:T:404:SER:HB3	2.03	0.41
33:T:434:GLY:HA2	33:T:464:GLY:N	2.36	0.41
34:V:530:LYS:O	34:V:531:GLU:C	2.64	0.41
1:A:265:THR:HG22	1:A:314:ILE:HG12	2.03	0.40
1:A:393:LEU:N	3:C:379:LYS:HE3	2.13	0.40
1:A:1528:GLN:HG3	1:A:1530:PRO:CD	2.51	0.40
1:A:1957:ASP:OD2	1:A:1959:THR:OG1	2.37	0.40
2:B:19:A:H2'	2:B:20:G:C5'	2.49	0.40
3:C:221:ILE:HG13	3:C:479:THR:OG1	2.21	0.40
3:C:235:VAL:HG13	3:C:239:THR:OG1	2.22	0.40
3:C:392:LEU:N	3:C:393:PRO:CD	2.84	0.40
5:E:178:LEU:CD2	5:E:208:ILE:HD11	2.51	0.40
14:G:146:C:C4	14:G:147:C:N4	2.89	0.40
15:H:112:G:O5'	15:H:112:G:H8	2.04	0.40
21:1:765:TYR:O	21:1:769:VAL:HG23	2.20	0.40
21:1:806:ILE:HG12	21:1:810:ILE:HD12	2.03	0.40
21:1:997:LEU:O	21:1:1001:VAL:HG23	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CZ	2.56	0.40
23:3:6:LEU:HD12	23:3:1128:ILE:HD11	2.03	0.40
23:3:194:ASN:O	23:3:196:PRO:HD3	2.21	0.40
25:5:27:PRO:HG3	25:5:85:ARG:NH1	2.36	0.40
31:P:63:LEU:C	31:P:63:LEU:CD2	2.93	0.40
34:V:585:ILE:O	34:V:588:GLN:N	2.54	0.40
35:X:263:PRO:CG	35:X:265:LYS:H	2.34	0.40
37:Z:563:ARG:HH21	37:Z:563:ARG:HG3	1.83	0.40
1:A:76:MET:SD	1:A:88:TYR:CZ	3.15	0.40
1:A:212:PRO:HD2	1:A:225:TYR:OH	2.21	0.40
1:A:225:TYR:O	1:A:418:THR:CB	2.68	0.40
1:A:363:HIS:NE2	3:C:287:GLY:CA	2.74	0.40
1:A:393:LEU:C	3:C:379:LYS:HG2	2.45	0.40
1:A:1251:SER:O	1:A:1298:ARG:NH2	2.55	0.40
1:A:1263:TRP:CZ2	1:A:1292:GLU:HG2	2.56	0.40
1:A:1451:ASN:HB2	32:R:428:GLY:O	2.21	0.40
1:A:1529:ILE:HG13	1:A:1530:PRO:HD3	2.03	0.40
3:C:64:LYS:NZ	31:P:209:ARG:NH1	2.70	0.40
3:C:85:ASP:HA	33:T:238:LEU:HB3	2.03	0.40
3:C:534:VAL:HG12	3:C:535:ALA:N	2.31	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:856:HIS:ND1	3:C:856:HIS:C	2.79	0.40
13:F:42:C:H2'	13:F:43:A:O4'	2.21	0.40
15:H:2:U:H2'	15:H:3:C:C6	2.55	0.40
15:H:149:A:N3	15:H:150:U:C6	2.89	0.40
17:p:172:ASN:O	17:p:173:GLN:C	2.64	0.40
21:1:658:TRP:CZ3	21:1:700:LYS:HD2	2.55	0.40
21:1:935:THR:O	21:1:939:ARG:HG2	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CE2	2.56	0.40
22:2:614:ARG:O	22:2:618:GLY:N	2.51	0.40
22:2:648:LEU:O	22:2:649:LYS:HD3	2.21	0.40
23:3:983:ASN:HB2	23:3:1021:LEU:HB2	2.03	0.40
24:4:17:VAL:HG13	24:4:84:ILE:CG2	2.48	0.40
28:J:338:GLU:O	32:R:116:TYR:CD2	2.75	0.40
28:J:376:VAL:HG13	28:J:377:LYS:N	2.36	0.40
31:P:44:ARG:HG3	33:T:258:SER:CA	2.51	0.40
35:X:238:THR:O	35:X:393:VAL:HG23	2.21	0.40
39:x:558:ALA:O	39:x:561:SER:N	2.54	0.40
1:A:82:ARG:HB3	1:A:83:HIS:HD1	1.86	0.40
1:A:247:THR:HG23	1:A:249:LEU:HD12	2.03	0.40
1:A:378:PHE:CE2	3:C:335:ASN:HB2	2.56	0.40
1:A:652:LEU:HD23	1:A:652:LEU:HA	1.84	0.40
1:A:1057:ARG:O	1:A:1060:GLU:HB2	2.22	0.40
1:A:1273:TYR:HD2	1:A:1274:PHE:CD2	2.39	0.40
1:A:1581:LEU:HD22	1:A:1746:ARG:NH1	2.36	0.40
1:A:2144:CYS:HB2	1:A:2270:PHE:CE1	2.57	0.40
3:C:375:GLU:N	3:C:376:PRO:HD2	2.37	0.40
5:E:255:MET:O	5:E:257:ASN:N	2.54	0.40
17:p:156:ASN:N	17:p:219:LYS:O	2.54	0.40
21:1:922:GLY:O	21:1:925:VAL:HG12	2.22	0.40
21:1:933:CYS:HA	21:1:936:VAL:HB	2.02	0.40
21:1:1130:PRO:HB3	22:2:528:ILE:HG23	2.04	0.40
23:3:63:ARG:HD2	23:3:83:ASP:HA	2.03	0.40
23:3:379:LEU:HB2	23:3:383:ASP:HB3	2.04	0.40
23:3:388:GLN:NE2	23:3:389:PRO:HD2	2.36	0.40
23:3:606:ALA:HA	23:3:616:ILE:HD13	2.04	0.40
28:J:275:ASN:OD1	28:J:275:ASN:C	2.65	0.40
32:R:424:SER:O	32:R:425:GLY:C	2.65	0.40
33:T:339:GLN:CG	33:T:340:ALA:N	2.84	0.40
36:Y:37:TRP:HH2	37:Z:498:GLY:HA3	1.59	0.40
37:Z:491:ASP:O	37:Z:495:ALA:HB3	2.21	0.40
1:A:91:ALA:HB2	32:R:207:MET:HE3	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:ASN:ND2	2:B:27:U:H3'	2.36	0.40
1:A:938:PRO:O	1:A:941:LYS:HD3	2.22	0.40
1:A:1118:PRO:CD	1:A:1119:ASP:N	2.82	0.40
1:A:2120:LEU:HD12	1:A:2120:LEU:H	1.86	0.40
3:C:71:GLU:C	3:C:71:GLU:CD	2.88	0.40
3:C:229:ILE:HG12	3:C:239:THR:HG21	2.04	0.40
3:C:567:GLU:O	3:C:567:GLU:HG3	2.20	0.40
13:F:96:U:H2'	13:F:97:U:C6	2.56	0.40
21:1:1052:ALA:HA	21:1:1055:TRP:CD1	2.51	0.40
21:1:1248:GLN:NE2	23:3:1030:PRO:HD3	2.36	0.40
23:3:179:ASN:HB3	23:3:213:LEU:O	2.22	0.40
23:3:192:ALA:HA	23:3:200:ALA:HB3	2.02	0.40
23:3:464:ARG:NH1	23:3:473:TYR:OH	2.53	0.40
23:3:535:GLU:HG2	23:3:536:TRP:N	2.36	0.40
25:5:42:TYR:CZ	25:5:73:ALA:HA	2.56	0.40
28:J:322:MET:HA	28:J:322:MET:HE2	2.03	0.40
31:P:210:PHE:CD2	33:T:455:GLN:CD	2.90	0.40
33:T:220:VAL:HG12	33:T:221:THR:N	2.37	0.40
1:A:148:TRP:CZ3	1:A:612:ILE:HG23	2.56	0.40
1:A:283:VAL:O	1:A:284:ARG:CZ	2.67	0.40
1:A:692:ASP:HA	33:T:376:ARG:HH21	1.72	0.40
1:A:718:ARG:NH2	32:R:259:LYS:HG3	2.36	0.40
1:A:787:GLU:OE1	1:A:790:ARG:NH2	2.53	0.40
1:A:923:ASP:OD2	1:A:1439:ARG:HD3	2.22	0.40
1:A:1161:LEU:HD23	1:A:1161:LEU:HA	1.85	0.40
1:A:2195:THR:O	1:A:2199:ILE:HG12	2.21	0.40
1:A:2332:ASP:O	1:A:2334:TYR:N	2.54	0.40
3:C:144:CYS:SG	3:C:148:CYS:SG	3.15	0.40
3:C:259:LYS:HG3	41:C:1500:GTP:C5	2.57	0.40
3:C:592:VAL:HG12	3:C:603:MET:SD	2.62	0.40
3:C:673:LYS:HD3	3:C:673:LYS:H	1.86	0.40
3:C:926:ALA:N	3:C:927:PRO:CD	2.84	0.40
10:f:5:LEU:O	11:e:49:GLY:HA3	2.22	0.40
18:w:420:LYS:O	18:w:424:ARG:HG3	2.20	0.40
21:1:570:TYR:O	21:1:574:ILE:HG12	2.22	0.40
21:1:839:GLU:O	21:1:842:ASN:HB2	2.22	0.40
21:1:1023:ILE:O	21:1:1026:ASN:HB2	2.21	0.40
23:3:561:GLY:O	23:3:582:GLU:HA	2.22	0.40
23:3:999:ARG:NE	23:3:1041:TYR:OH	2.54	0.40
28:J:216:ASP:O	28:J:217:GLU:C	2.64	0.40
32:R:422:MET:C	32:R:424:SER:N	2.73	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:T:218:TRP:HZ3	33:T:220:VAL:CG2	2.35	0.40
35:X:231:ALA:O	35:X:236:THR:OG1	2.39	0.40
36:Y:32:TYR:C	36:Y:34:ASP:N	2.80	0.40
37:Z:612:TYR:C	37:Z:614:TRP:H	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2186/2335 (94%)	2036 (93%)	117 (5%)	33 (2%)	8	38
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	5	28
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	43	77
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3	22
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100	100
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	41
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1	10
18	w	419/501 (84%)	379 (90%)	37 (9%)	3 (1%)	18	55
19	u	93/793 (12%)	87 (94%)	4 (4%)	2 (2%)	5	28
20	v	90/464 (19%)	67 (74%)	16 (18%)	7 (8%)	1	10
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	21	58
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100
23	3	1165/1217 (96%)	1086 (93%)	78 (7%)	1 (0%)	48	83
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	9	41
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	87/110 (79%)	80 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	9	39
29	L	128/802 (16%)	119 (93%)	8 (6%)	1 (1%)	16	52
30	M	34/343 (10%)	30 (88%)	3 (9%)	1 (3%)	3	23
31	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	5	28
32	R	295/540 (55%)	249 (84%)	31 (10%)	15 (5%)	1	15
33	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	2	18
34	V	443/908 (49%)	412 (93%)	26 (6%)	5 (1%)	11	45
35	X	142/396 (36%)	131 (92%)	11 (8%)	0	100	100
36	Y	102/322 (32%)	91 (89%)	11 (11%)	0	100	100
37	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	1	15
38	z	176/472 (37%)	170 (97%)	6 (3%)	0	100	100
39	x	561/1041 (54%)	536 (96%)	20 (4%)	5 (1%)	14	49
All	All	12632/20929 (60%)	11667 (92%)	812 (6%)	153 (1%)	13	42

All (153) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP
1	A	346	ASP
1	A	383	PHE
1	A	570	ASP
1	A	629	PHE
1	A	701	ILE
1	A	1119	ASP
3	C	388	VAL
3	C	427	PHE
3	C	444	GLY
3	C	457	VAL
3	C	458	ASP
3	C	516	LEU
3	C	824	THR
4	D	957	VAL
4	D	1584	ILE
5	E	193	THR
17	p	157	ASN
17	p	183	VAL
17	p	195	GLU
18	w	284	ARG
20	v	139	PRO
20	v	165	ARG
20	v	218	PRO
28	J	413	GLU
31	P	49	ASP
32	R	71	GLN
32	R	135	PRO
32	R	136	ASP
32	R	186	VAL
32	R	412	ASP
32	R	416	PHE
32	R	420	LYS
32	R	425	GLY
33	T	186	PRO
33	T	268	LYS
33	T	341	ALA
33	T	343	PRO
33	T	495	ALA
34	V	596	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	V	597	PRO
37	Z	499	LYS
37	Z	531	LEU
37	Z	536	ARG
37	Z	569	PRO
39	x	937	ILE
1	A	122	ILE
1	A	308	ILE
1	A	349	ALA
1	A	367	SER
1	A	370	PRO
1	A	374	ASP
1	A	631	ALA
1	A	1141	ARG
3	C	90	THR
3	C	364	SER
3	C	572	GLU
3	C	711	ARG
16	o	160	LYS
17	p	159	PRO
17	p	160	GLU
17	p	177	PHE
17	p	186	ARG
19	u	280	VAL
20	v	115	PRO
21	l	112	ILE
28	J	217	GLU
28	J	341	PRO
28	J	376	VAL
28	J	709	VAL
31	P	190	ASP
32	R	191	GLY
32	R	422	MET
33	T	301	ASP
34	V	485	GLN
37	Z	613	LYS
1	A	51	PHE
1	A	212	PRO
1	A	378	PHE
1	A	699	GLU
1	A	1118	PRO
1	A	1140	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	E	60	MET
5	E	88	ARG
5	E	256	ASP
17	p	222	TYR
18	w	177	ARG
30	M	197	TYR
32	R	104	GLN
32	R	173	PRO
33	T	406	ILE
34	V	578	SER
39	x	1005	SER
1	A	363	HIS
1	A	480	LYS
1	A	698	PRO
1	A	1092	ILE
1	A	1114	LEU
1	A	1828	ALA
3	C	63	LYS
3	C	754	VAL
3	C	856	HIS
5	E	162	ARG
16	o	32	PRO
17	p	208	GLN
17	p	209	GLY
21	1	417	PRO
21	1	456	VAL
28	J	604	PRO
32	R	124	VAL
33	T	401	PRO
39	x	935	ASP
1	A	359	ILE
3	C	361	PRO
3	C	615	PRO
5	E	159	PRO
20	v	217	PRO
32	R	126	ASN
32	R	423	ASP
33	T	185	MET
33	T	189	GLN
33	T	226	ARG
39	x	980	GLN
39	x	981	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	94	ILE
3	C	360	ALA
3	C	623	GLU
5	E	270	LYS
17	p	173	GLN
20	v	141	ILE
20	v	220	PRO
21	1	944	SER
29	L	215	PRO
34	V	609	GLN
3	C	66	TYR
5	E	149	GLY
37	Z	571	PRO
1	A	186	GLU
19	u	221	PRO
18	w	229	TRP
21	1	418	PRO
24	4	27	PRO
28	J	241	VAL
33	T	411	GLY
4	D	585	ILE
5	E	324	PRO
17	p	184	PRO
21	1	932	ILE
23	3	491	VAL

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	38 (41%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	21 (25%)	10 (12%)
All	All	379/686 (55%)	140 (36%)	35 (9%)

All (140) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G
2	B	25	C
2	B	26	A
2	B	28	A
2	B	35	U
2	B	36	C
2	B	38	C
2	B	40	U
2	B	41	U
2	B	45	C
2	B	47	A
2	B	57	G
2	B	70	A
2	B	71	C
13	F	5	U
13	F	6	C
13	F	7	G
13	F	8	C
13	F	10	U
13	F	12	G
13	F	25	C
13	F	26	U
13	F	27	A
13	F	28	A
13	F	29	A
13	F	33	G
13	F	34	G
13	F	36	A
13	F	37	C
13	F	38	G
13	F	44	G
13	F	45	A
13	F	46	G
13	F	47	A
13	F	48	A
13	F	49	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	F	51	U
13	F	54	G
13	F	55	C
13	F	56	A
13	F	58	G
13	F	59	G
13	F	60	C
13	F	61	C
13	F	62	C
13	F	68	C
13	F	74	U
13	F	78	A
13	F	79	C
13	F	85	U
13	F	86	U
13	F	87	C
14	G	-11	G
14	G	-6	C
14	G	-4	A
14	G	-3	A
14	G	1	G
14	G	2	U
14	G	3	A
14	G	4	A
14	G	5	G
14	G	7	G
14	G	8	C
14	G	10	U
14	G	11	A
14	G	12	G
14	G	13	C
14	G	17	U
14	G	21	A
14	G	22	C
14	G	23	U
14	G	24	G
14	G	25	G
14	G	26	U
14	G	27	U
14	G	28	A
14	G	29	C
14	G	30	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	G	31	U
14	G	131	U
14	G	132	G
14	G	135	G
14	G	136	U
14	G	137	C
14	G	143	U
14	G	144	A
14	G	145	U
14	G	146	C
14	G	147	C
14	G	148	U
14	G	149	G
14	G	150	U
14	G	151	C
14	G	152	C
14	G	154	U
14	G	156	U
14	G	159	U
14	G	161	U
14	G	162	C
14	G	163	C
15	H	14	C
15	H	20	G
15	H	23	A
15	H	24	A
15	H	25	G
15	H	29	A
15	H	30	A
15	H	31	G
15	H	44	U
15	H	45	C
15	H	46	U
15	H	47	U
15	H	48	A
15	H	65	U
15	H	112	G
15	H	143	A
15	H	147	G
15	H	149	A
15	H	152	G
15	H	153	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	H	154	C
15	H	156	U
15	H	157	G
15	H	160	A
15	H	163	G
15	H	164	C
15	H	166	G
15	H	167	U
15	H	169	C
15	H	177	A
15	H	178	A
15	H	179	C
15	H	183	G

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	18	C
2	B	19	A
2	B	20	G
2	B	23	C
2	B	24	G
2	B	25	C
2	B	27	U
2	B	39	C
2	B	40	U
13	F	5	U
13	F	7	G
13	F	25	C
13	F	33	G
13	F	35	A
13	F	36	A
13	F	37	C
13	F	47	A
13	F	48	A
13	F	50	A
13	F	58	G
13	F	59	G
14	G	-12	G
14	G	16	G
14	G	21	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	G	22	C
14	G	136	U
14	G	148	U
14	G	151	C
14	G	153	C
14	G	155	U
15	H	29	A
15	H	46	U
15	H	47	U
15	H	156	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
41	GTP	C	1500	42	33,34,34	1.45	5 (15%)	50,54,54	2.04	10 (20%)
40	IHP	A	3000	-	36,36,36	1.04	2 (5%)	60,60,60	1.74	15 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	GTP	C	1500	42	-	8/22/38/38	0/3/3/3
40	IHP	A	3000	-	-	6/30/54/54	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	C	1500	GTP	C5-N7	-3.76	1.31	1.39
41	C	1500	GTP	C6-N1	-3.32	1.32	1.38
41	C	1500	GTP	PA-O3A	3.16	1.62	1.59
40	A	3000	IHP	P5-O45	-2.95	1.43	1.54
40	A	3000	IHP	P2-O12	2.73	1.64	1.59
41	C	1500	GTP	C8-N9	-2.57	1.31	1.37
41	C	1500	GTP	C4-N9	-2.56	1.31	1.38

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	C	1500	GTP	C5-C4-N3	-7.07	117.14	128.39
41	C	1500	GTP	C2-N3-C4	5.94	122.54	112.30
41	C	1500	GTP	N9-C4-N3	5.74	137.44	125.95
40	A	3000	IHP	O35-P5-O15	-4.53	88.19	105.85
40	A	3000	IHP	O45-P5-O35	4.13	123.30	107.80
40	A	3000	IHP	P3-O13-C3	-3.69	113.57	123.43
40	A	3000	IHP	O16-C6-C1	3.64	116.50	108.76
41	C	1500	GTP	O6-C6-C5	-3.58	117.08	126.53
40	A	3000	IHP	C6-C1-C2	-3.22	103.37	110.43
41	C	1500	GTP	C2-N1-C6	-3.08	119.53	125.11
41	C	1500	GTP	C5-C6-N1	2.90	120.64	113.25
41	C	1500	GTP	O2G-PG-O3B	2.89	114.34	104.64
41	C	1500	GTP	O2A-PA-O3A	2.81	114.87	107.27
40	A	3000	IHP	O44-P4-O34	2.74	118.06	107.80
40	A	3000	IHP	C5-C6-C1	-2.65	104.62	110.43
40	A	3000	IHP	O15-C5-C4	-2.40	103.66	108.76
40	A	3000	IHP	O31-P1-O11	-2.37	96.62	105.85
40	A	3000	IHP	O12-C2-C3	2.34	113.74	108.76
40	A	3000	IHP	P6-O16-C6	-2.34	117.18	123.43
41	C	1500	GTP	O4'-C4'-C3'	2.27	109.66	105.15
40	A	3000	IHP	O45-P5-O15	-2.25	97.08	105.85
40	A	3000	IHP	O35-P5-O25	2.22	119.48	110.83
41	C	1500	GTP	C6-C5-N7	2.12	134.15	130.29
40	A	3000	IHP	O42-P2-O22	2.07	118.91	110.83
40	A	3000	IHP	C4-C3-C2	2.07	114.96	110.43

There are no chirality outliers.

All (14) torsion outliers are listed below:

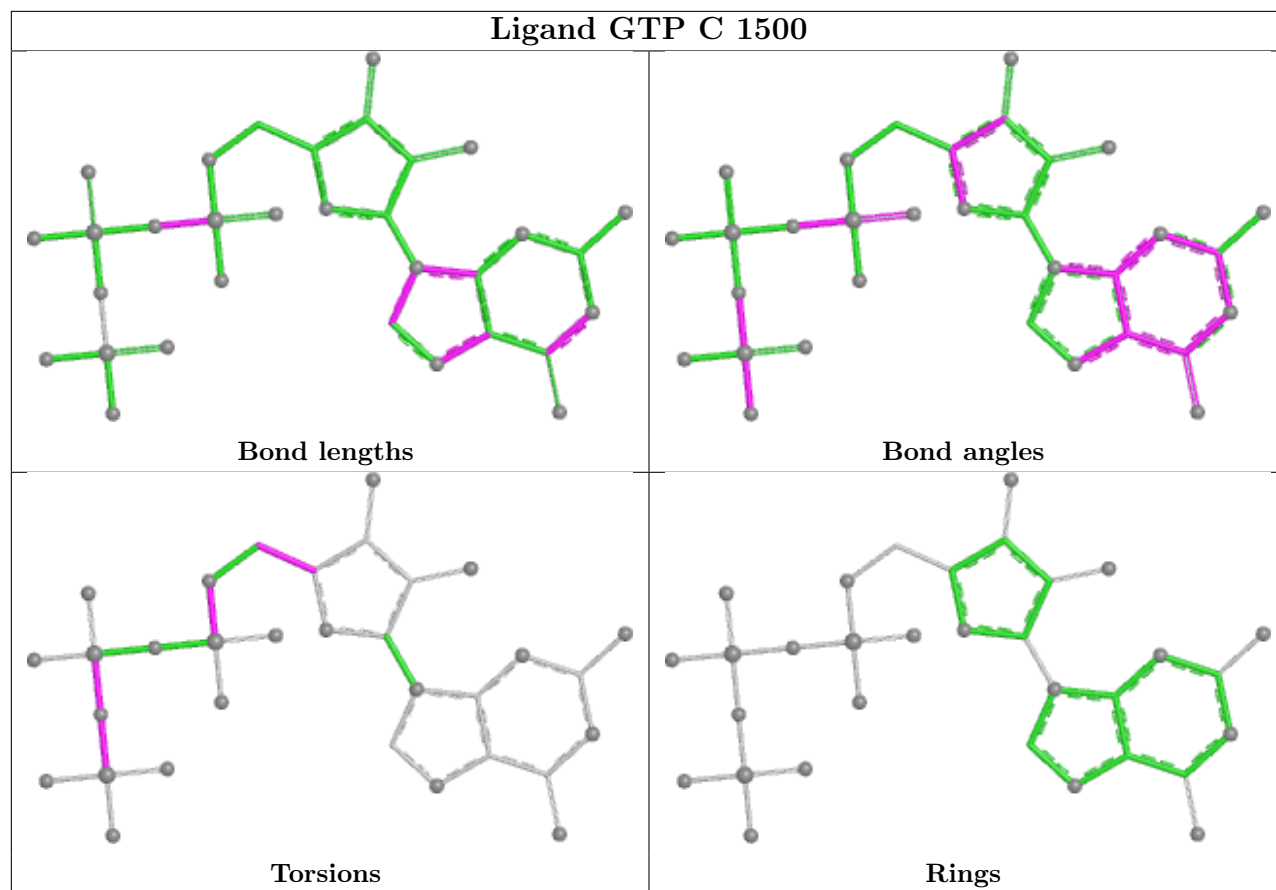
Mol	Chain	Res	Type	Atoms
40	A	3000	IHP	C4-C5-O15-P5
40	A	3000	IHP	C6-C5-O15-P5
41	C	1500	GTP	PB-O3B-PG-O3G
41	C	1500	GTP	C5'-O5'-PA-O1A
41	C	1500	GTP	C5'-O5'-PA-O2A
41	C	1500	GTP	O4'-C4'-C5'-O5'
41	C	1500	GTP	C3'-C4'-C5'-O5'
41	C	1500	GTP	C5'-O5'-PA-O3A
40	A	3000	IHP	C1-O11-P1-O21
40	A	3000	IHP	C2-O12-P2-O22
40	A	3000	IHP	C5-O15-P5-O25
41	C	1500	GTP	PG-O3B-PB-O2B
40	A	3000	IHP	C1-O11-P1-O31
41	C	1500	GTP	PG-O3B-PB-O1B

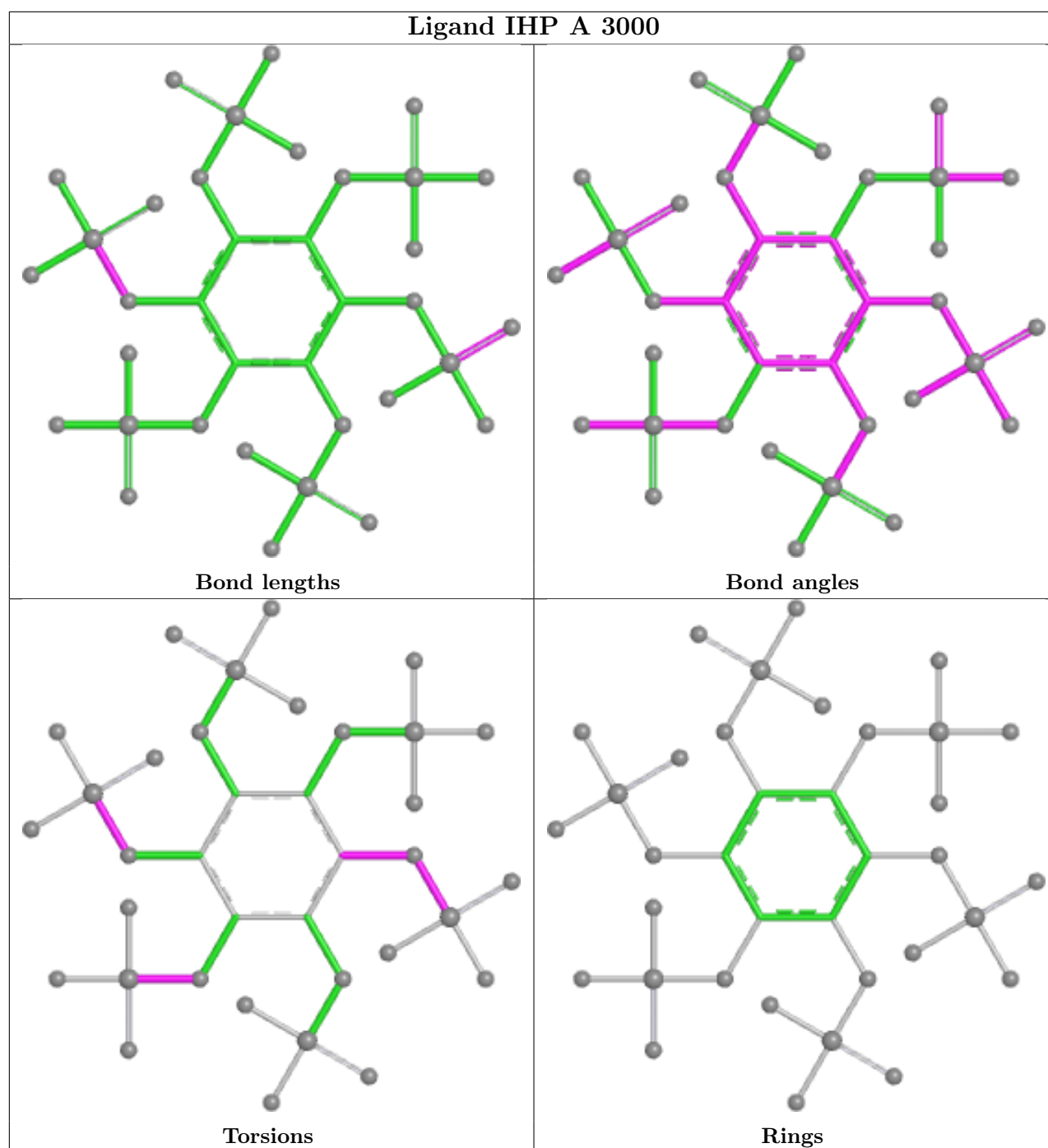
There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	C	1500	GTP	11	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

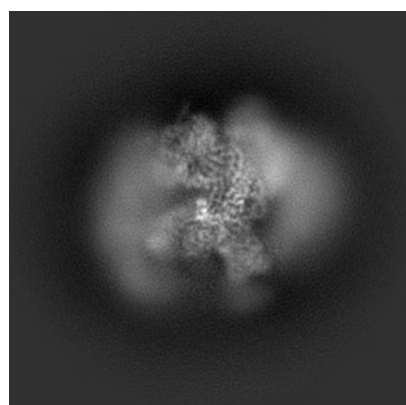
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6891. These allow visual inspection of the internal detail of the map and identification of artifacts.

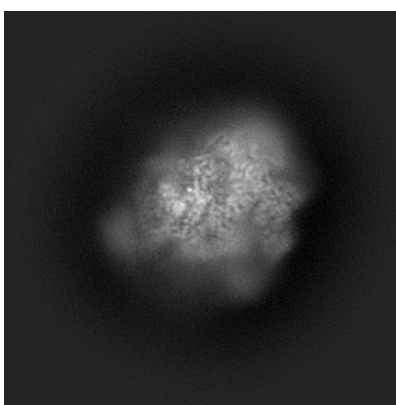
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

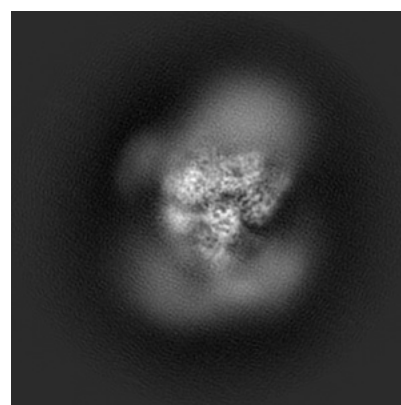
6.1.1 Primary map



X



Y

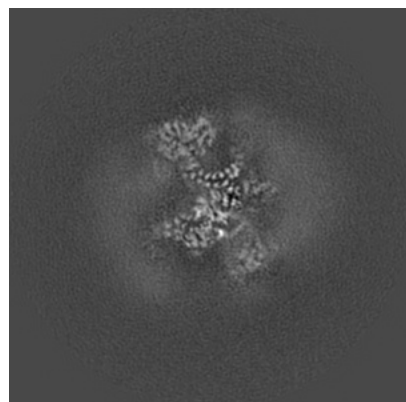


Z

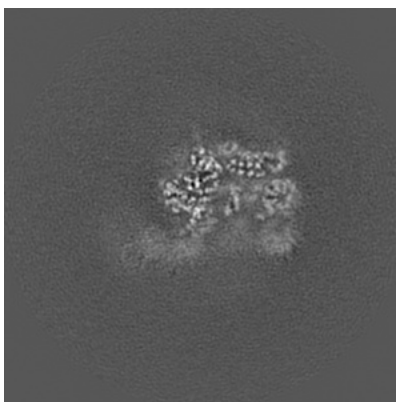
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

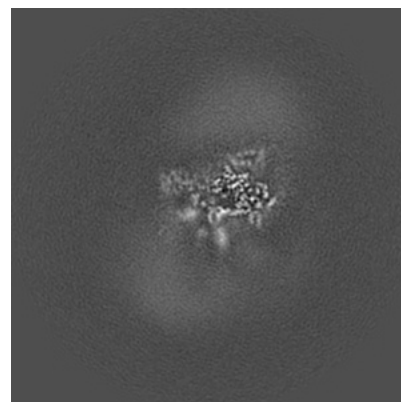
6.2.1 Primary map



X Index: 200



Y Index: 200

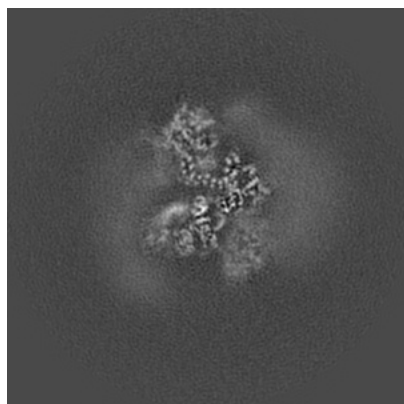


Z Index: 200

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

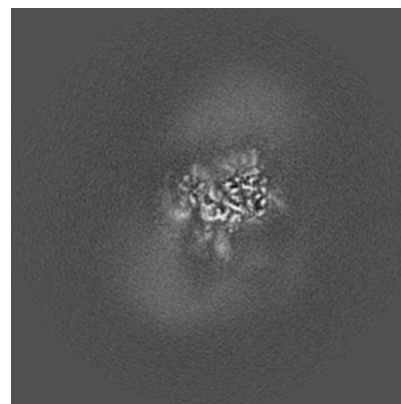
6.3.1 Primary map



X Index: 210



Y Index: 195

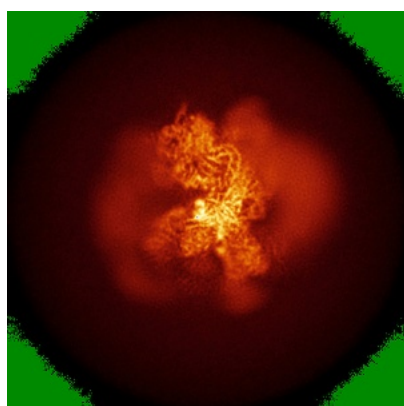


Z Index: 193

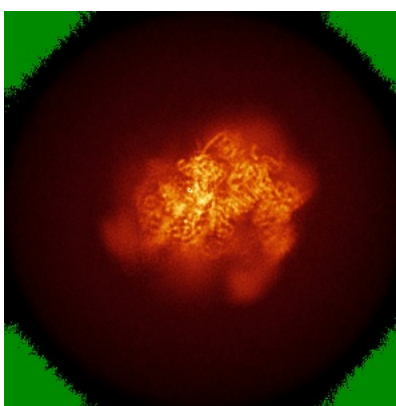
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

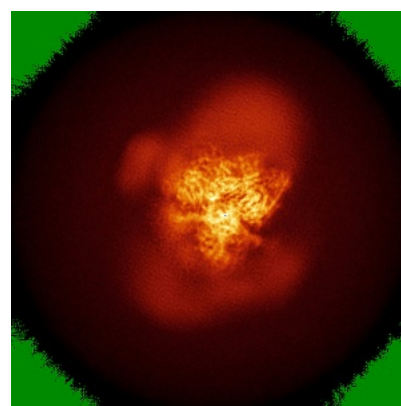
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0346. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

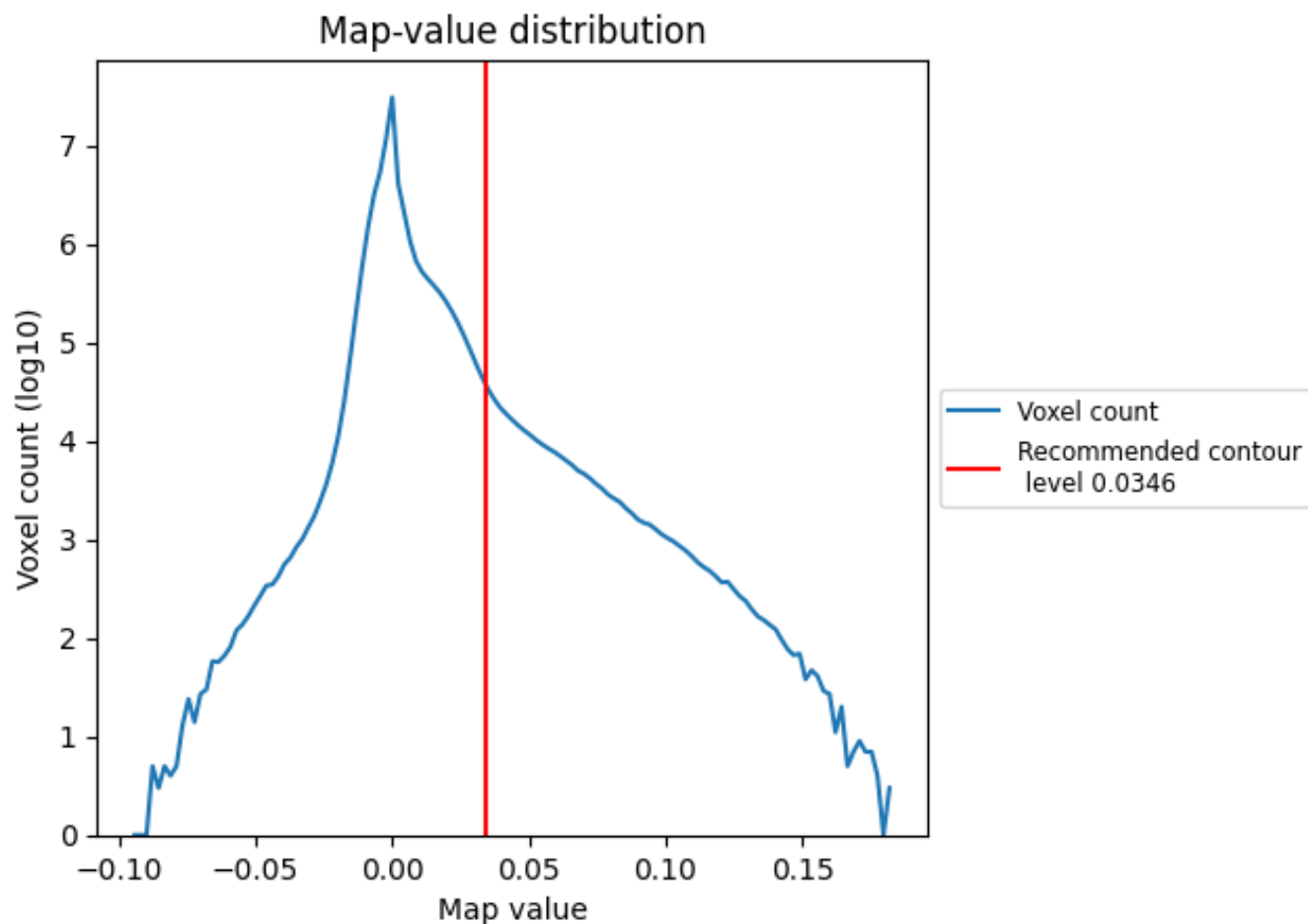
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

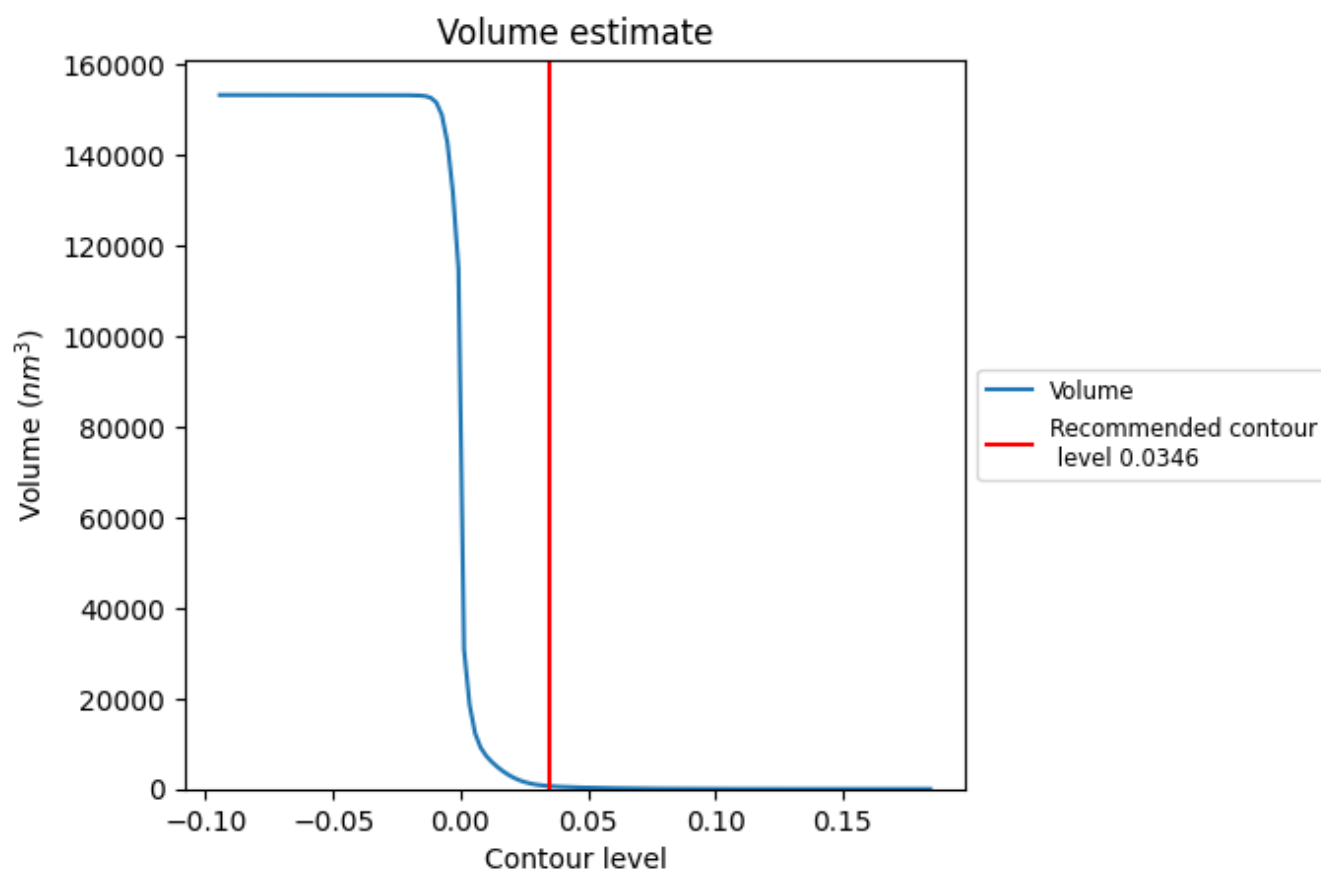
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

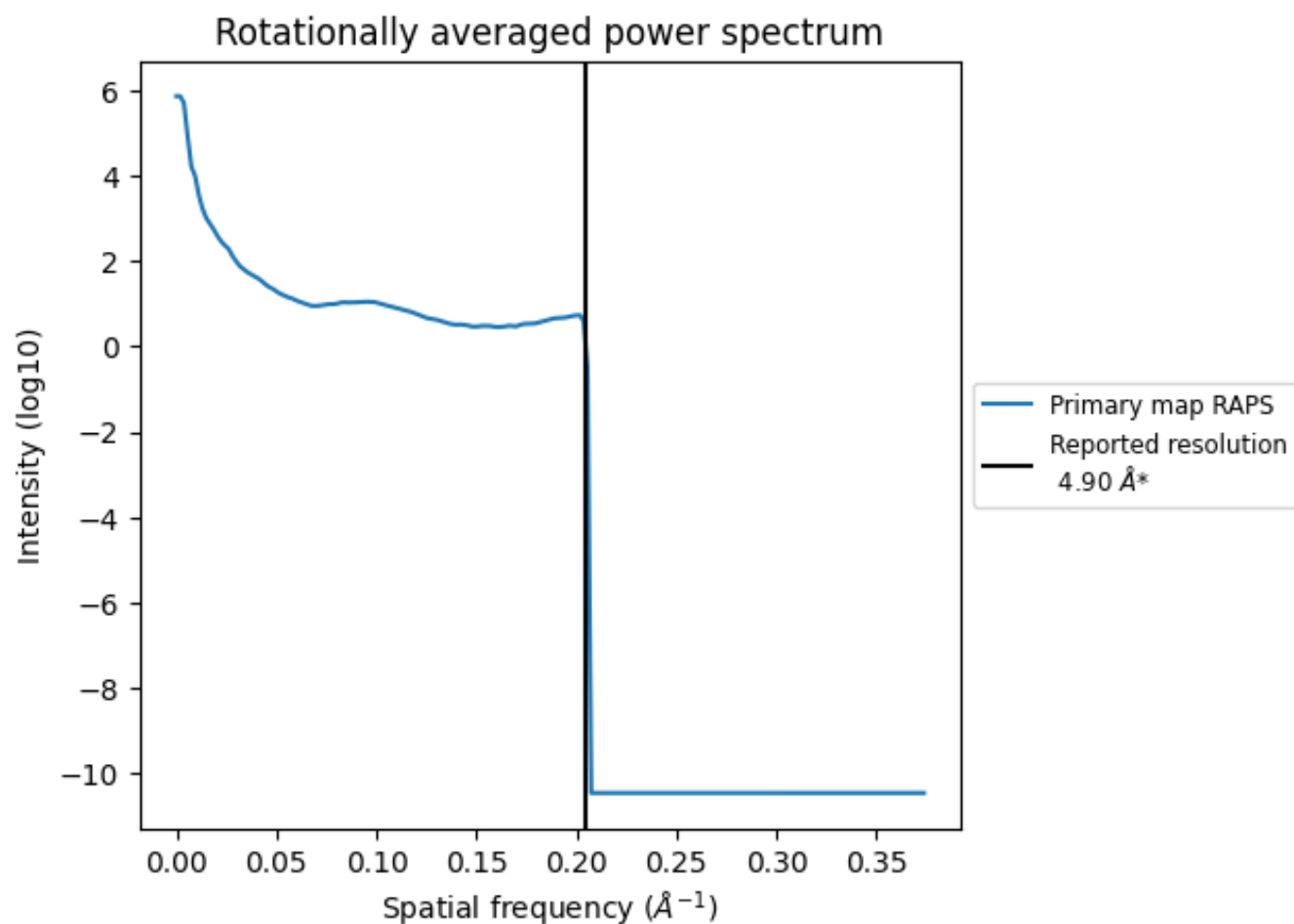
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 642 nm³; this corresponds to an approximate mass of 580 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

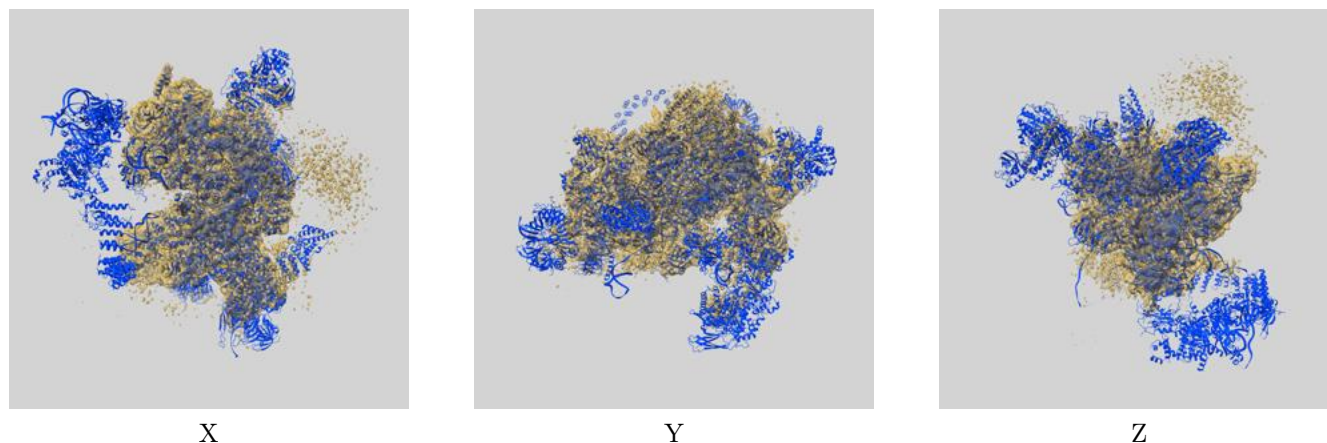
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

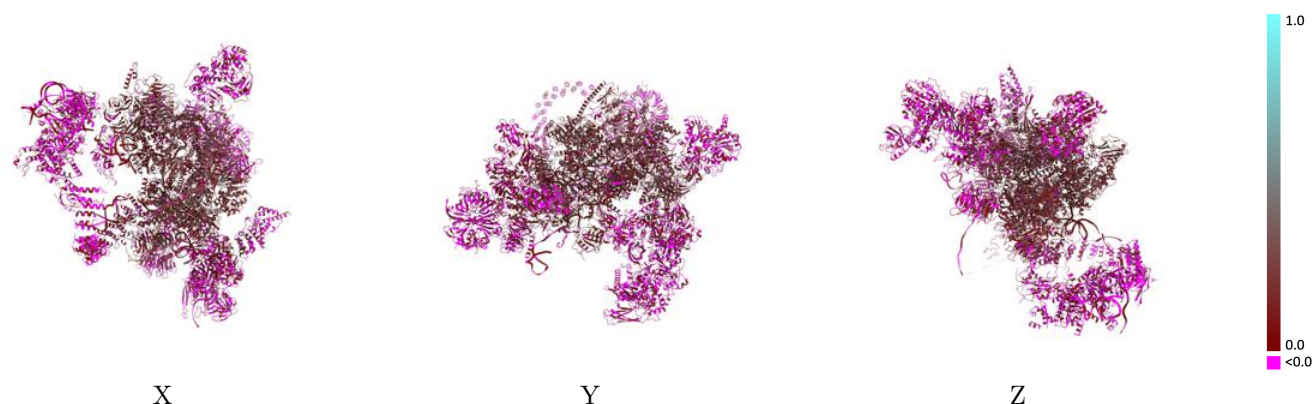
This section contains information regarding the fit between EMDB map EMD-6891 and PDB model 5Z58. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0346 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)

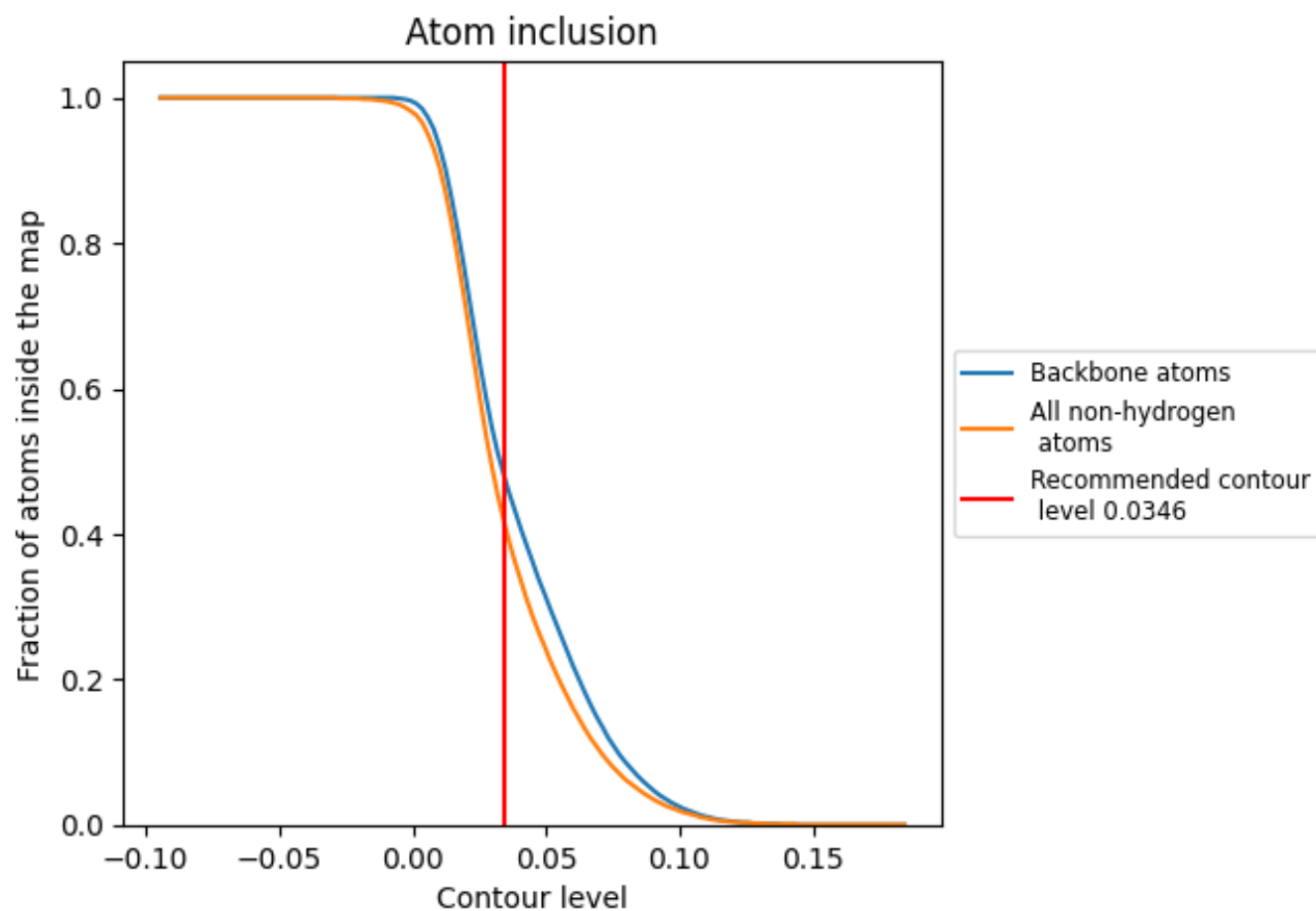


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 41% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0346) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4120	 0.1310
1	 0.6670	 0.2300
2	 0.2970	 0.1480
3	 0.6080	 0.1670
4	 0.0730	 0.0080
5	 0.7300	 0.2390
6	 0.5060	 0.1590
7	 0.6800	 0.2240
A	 0.5570	 0.1970
B	 0.5980	 0.1040
C	 0.4530	 0.0950
D	 0.1160	 0.0400
E	 0.0260	 0.0260
F	 0.5990	 0.1470
G	 0.6230	 0.1490
H	 0.3420	 0.0880
J	 0.2790	 0.0660
L	 0.4750	 0.2070
M	 0.7170	 0.2530
P	 0.3090	 0.1160
R	 0.4080	 0.1660
T	 0.7530	 0.2280
V	 0.3420	 0.1200
X	 0.7090	 0.2160
Y	 0.6250	 0.2470
Z	 0.5950	 0.2670
a	 0.0000	 0.0170
b	 0.0050	 0.0410
c	 0.0220	 0.0060
d	 0.0940	 -0.0040
e	 0.0050	 0.0020
f	 0.0170	 -0.0230
g	 0.0000	 0.0030
h	 0.0000	 0.0340
i	 0.0000	 0.0210



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
j	 0.0000	 -0.0440
k	 0.0000	 0.0110
l	 0.0000	 0.0140
m	 0.0000	 -0.0500
n	 0.0000	 0.0110
o	 0.0000	 0.0280
p	 0.0000	 0.0160
u	 0.0000	 0.0040
v	 0.0000	 0.0460
w	 0.1150	 0.0420
x	 0.0290	 0.0110
z	 0.4980	 0.1870