



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:54 AM UTC

PDB ID : 8KAI / pdb_00008kai
Title : Crystal structure of SpyCas9-crRNA-tracrRNA complex bound to 17nt target DNA
Authors : Chen, Y.; Chen, J.; Liu, L.
Deposited on : 2023-08-03
Resolution : 3.49 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

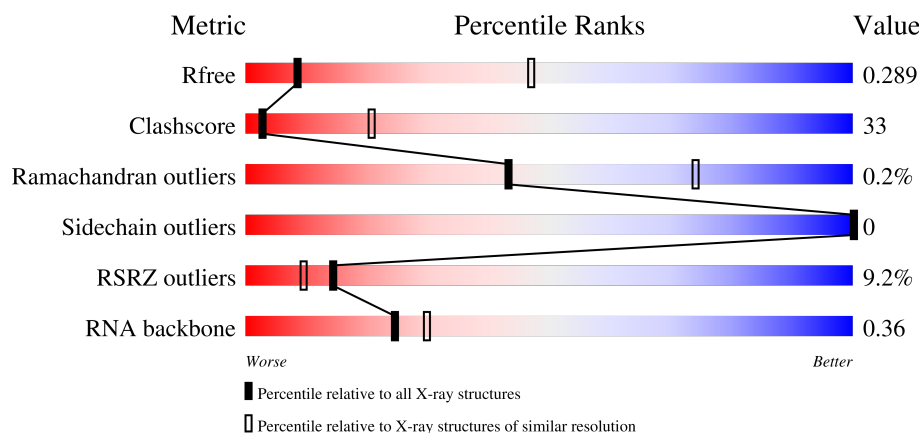
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.49 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)
RNA backbone	3983	1010 (3.98-3.02)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	34	3% 26% 47% 18% 9%
1	E	34	6% 26% 53% 12% 9%
2	B	1368	7% 47% 49% ..
2	F	1368	13% 45% 51% ..

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Mol	Chain	Length	Quality of chain
3	C	25	52% 48%
3	G	25	40% 60%
4	D	11	9% 18% 82%
4	H	11	9% 45% 55%
5	I	65	14% 58% 22%
5	J	65	2% 22% 55% 20%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 27007 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 RNA chain called RNA (34-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	34	Total	C	N	O	P	0	0	0
			725	325	127	239	34			
1	E	31	Total	C	N	O	P	0	0	0
			663	297	118	217	31			

- Molecule 2 is a protein called CRISPR-associated endonuclease Cas9/Csn1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1326	Total	C	N	O	S	0	0	0
			10769	6854	1869	2024	22			
2	F	1327	Total	C	N	O	S	0	0	0
			10698	6816	1845	2014	23			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	10	ALA	ASP	engineered mutation	UNP Q99ZW2
B	840	ALA	HIS	engineered mutation	UNP Q99ZW2
F	10	ALA	ASP	engineered mutation	UNP Q99ZW2
F	840	ALA	HIS	engineered mutation	UNP Q99ZW2

- Molecule 3 is a DNA chain called DNA (25-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	25	Total	C	N	O	P	0	0	0
			501	244	83	150	24			
3	G	25	Total	C	N	O	P	0	0	0
			501	244	83	150	24			

- Molecule 4 is a DNA chain called DNA (5'-D(*TP*TP*TP*AP*GP*GP*TP*AP*TP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	11	Total	C	N	O	P	0	0	0
			225	110	37	68	10			
4	H	11	Total	C	N	O	P	0	0	0
			225	110	37	68	10			

- Molecule 5 is a RNA chain called RNA (65-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	63	Total	C	N	O	P	0	0	0
			1348	603	245	437	63			
5	J	63	Total	C	N	O	P	0	0	0
			1348	603	245	437	63			

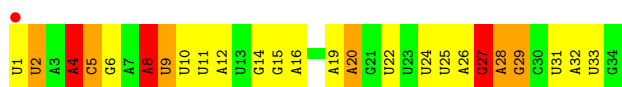
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	O	0	0
			1	1		
6	F	3	Total	O	0	0
			3	3		

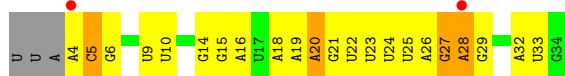
3 Residue-property plots

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

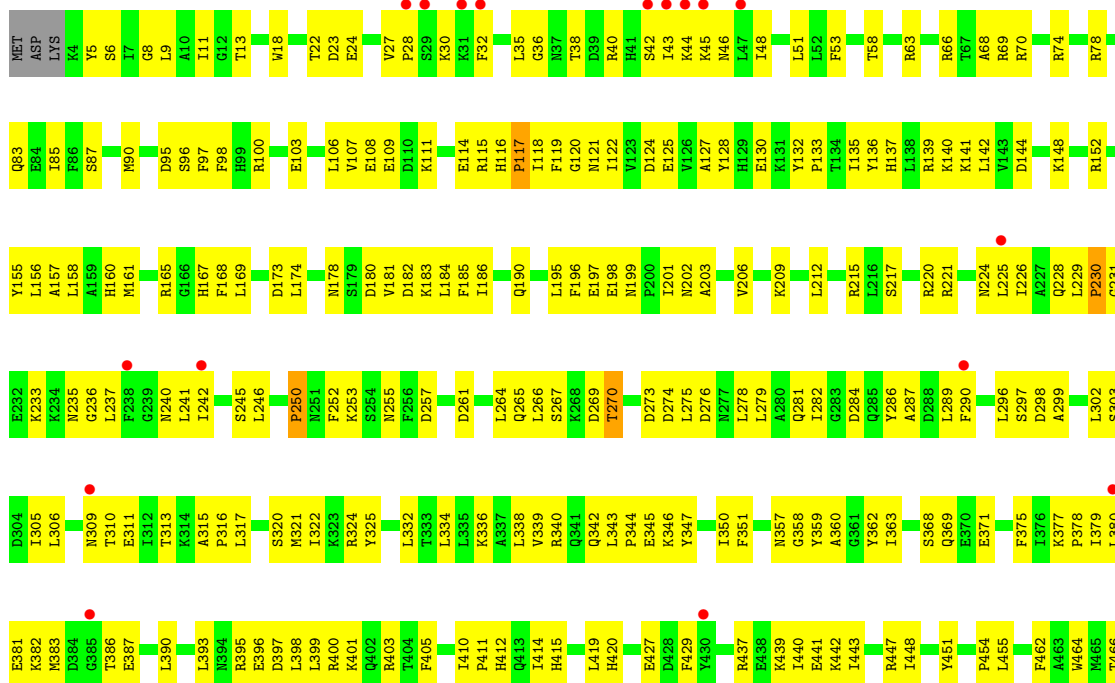
- Molecule 1: RNA (34-MER)

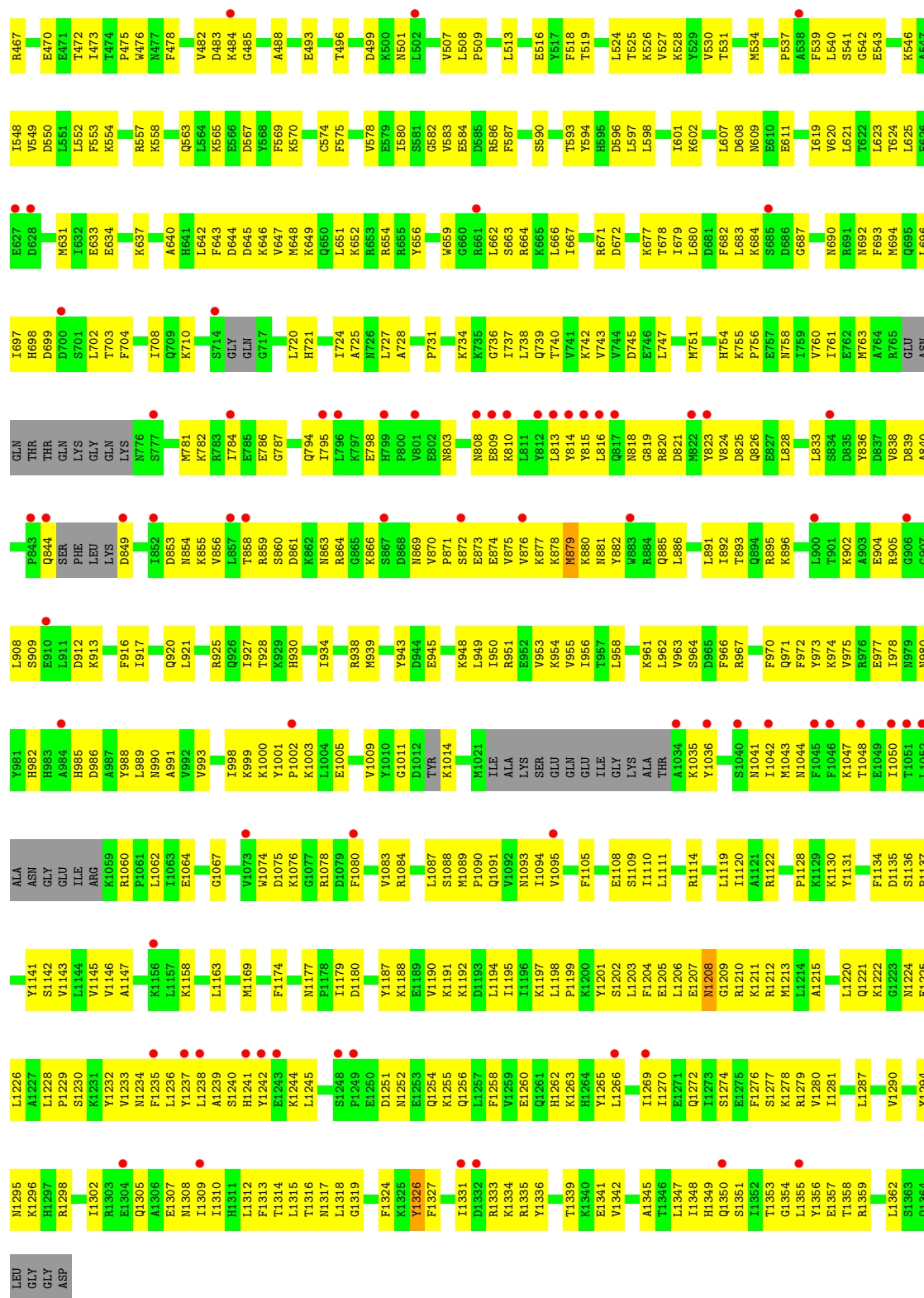


- Molecule 1: RNA (34-MER)

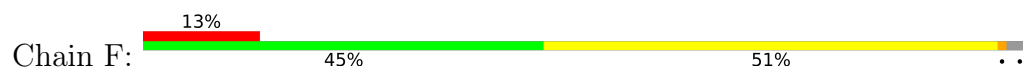


- Molecule 2: CRISPR-associated endonuclease Cas9/Csn1

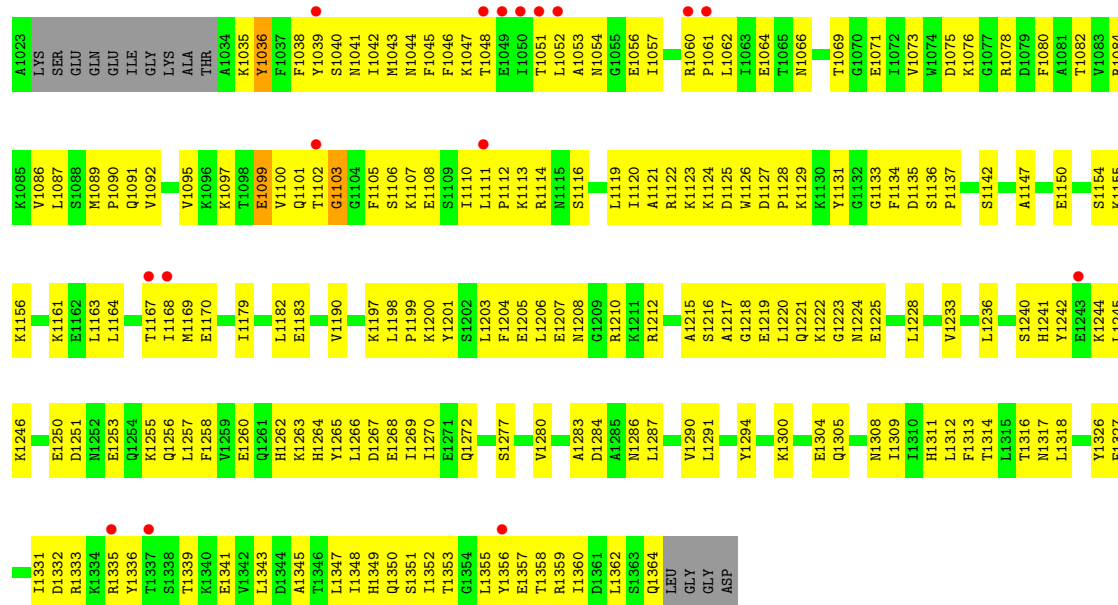




● Molecule 2: CRISPR-associated endonuclease Cas9/Csn1



N946	K377	R802	W724	R654	F587	L514	K442	Y373	L301	N235	R165	L101	MET
L949	K378	R803	S730	R655	M838	Y516	T443	K374	L302	G236	G166	E102	ASP
R951	M879	T804	P731	G658	A589	E516	T445	F375	D304	F237	F168	E103	LYS
E952	Y882	Q807	A732	G659	F518	F518	F446	K376	I305	G239	L169	L106	K4
V953	U883	L811	I733	G660	T519	T519	R447	K377	L306	N240	I170	V107	Y5
	U884	L812	K734	R661	T593	V520	T448	P378	R307	L241	E171	E108	G8
	Q885	R813	K735	L662	Y594	Y521	F449	I379	V308	I242	G172		
	Q886	L814	G736	S663	H595	N522	Y450	L390	N309	A243	D173	K111	K31
	L886	R815	I737	R664	D596	E523	V451	L391	L307	L244	L174	K112	F32
		Y815	L738	K665	L597	L524	V452	K392	S318	S245		H113	
		R816	K739	L666	L598	T525	G453	K393	S320	G246	D177	H114	L35
		Q817	T740	L667	K599	K526	P454	L394	S321	G247	N178	H115	L36
		R818	V741		I600	V527	L455	T386	A315	L248	S179	H116	R37
			K742	R671	I601	K528		L389	P316	P250	D180	P117	T38
			E745	D672	K602			L390	L317	T249	V181	I118	D39
			E746	S675	D803	T531		L391	S318	P250	L184	F119	R40
			W751	G676	F606	M534		K392	A319	K253	K183	G120	H41
				K677	L607	R535		N394	S320	F256	F185	I122	S42
				T678	N612	K536		N395	M321	D257	I186	I123	I43
				L679		P537		E396	K323	L258	Q187	I124	K44
				L680				D397	R324	A259	L188	E125	K45
				D681		Q544		L398	Y325	E260	V189	V126	N46
				F682		K545		L399	D326	D261	F196	A127	L47
				L683		K546		R400	E327	A262		Y128	I48
				L684		A547		K401	H328	LYS		H129	T58
				S685		L548		Q402	L332	LEU			
				D686		V549		R403	T333	GLN		Y132	R63
				G687		D550		T404	L334	S267	A203	P133	
				F688		L551		F405	L335	K668	S204	T134	R66
				R689		L552		D406	L336	GLY	VAL	I135	T67
				R690		F553		N407	K336	D269	ALA	I136	A68
				R691		K554		G408	A337	T270	ARG	H137	R69
				N692		T555		S409	L338	D272	LEU	L138	R70
				F693		D628		P411	V339	D273	LYS	R139	R71
				M694		R629		H412	Q342	D274	LYS	K140	Y72
				Q695		E630		Q413		L275	L211	K141	T73
				L696		M631		L414	K346	D276	S213	L142	T74
				L697		E632		H415	Y347	N277	ALA	V143	R75
				H698		Q563		L416	K348	L278	ARG	D144	K76
				D699		L564		G417	E349	L279	LEU	S145	N77
				D700		K565		E418	I350		SER	K148	R78
				T701		E566		L419	F351		LYS	A149	I79
				L702		D567		T422	F352		SER	D150	C80
				T703		Y568		L423	N357	Q285	R220	L151	L82
				A711		K570		R424	G358	A287	R221	L153	L82
				Q712		F569		R425	X359	D288	N224	L154	F86
				V713		D640		Q426	A360	L289	L225	Y155	E89
				S714		F573		E427	G361	F290	I226	Y156	M90
				GLY		D645		D428	Y362	L291	O228	A157	A91
				R715		K646		F429	I363	A292	Q228	L158	K92
				D717		V647		F432	D364		L229	A159	V93
				R718		M648		L433	N295		P230	H160	D94
				S719		E579			L296		G231	M161	
				L720		I580			S297		L232	I162	
				H721		S581			S368		K233	K163	
				L722		G582			Q369			F164	
				E722		V583			E370				
				H723		E584							



• Molecule 3: DNA (25-MER)



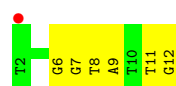
• Molecule 3: DNA (25-MER)



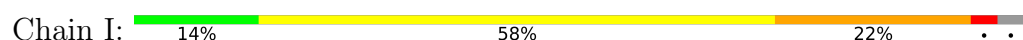
• Molecule 4: DNA (5'-D(*TP*TP*TP*AP*GP*GP*TP*AP*TP*TP*G)-3')

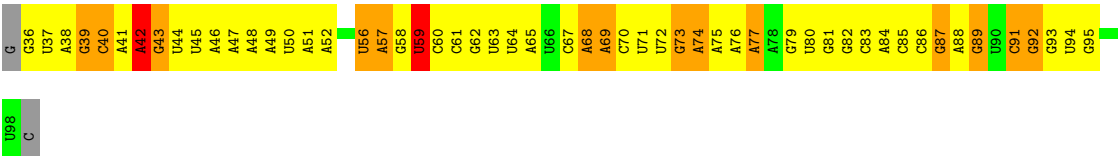


• Molecule 4: DNA (5'-D(*TP*TP*TP*AP*GP*GP*TP*AP*TP*TP*G)-3')

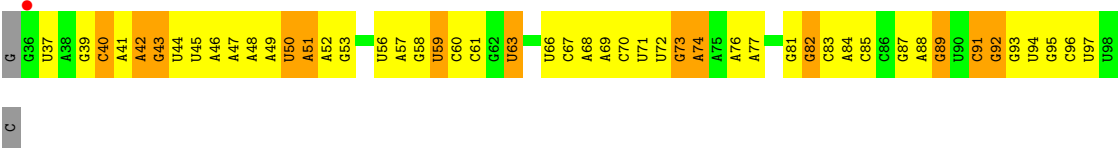


• Molecule 5: RNA (65-MER)





● Molecule 5: RNA (65-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	144.30Å 130.19Å 146.41Å 90.00° 104.02° 90.00°	Depositor
Resolution (Å)	48.57 – 3.49 48.57 – 3.49	Depositor EDS
% Data completeness (in resolution range)	79.0 (48.57-3.49) 79.0 (48.57-3.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.225 , 0.294 0.224 , 0.289	Depositor DCC
R_{free} test set	2620 reflections (3.77%)	wwPDB-VP
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 76.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.087 for l,-k,h	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	27007	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.65	0/811	1.03	4/1261 (0.3%)
1	E	0.61	0/742	0.93	0/1154
2	B	0.65	0/10954	0.97	6/14725 (0.0%)
2	F	0.67	2/10882 (0.0%)	0.96	7/14639 (0.0%)
3	C	0.81	0/559	1.03	0/859
3	G	0.77	0/559	0.99	0/859
4	D	0.86	0/251	0.87	0/387
4	H	0.78	0/251	0.93	0/387
5	I	0.66	0/1509	0.93	2/2350 (0.1%)
5	J	0.58	0/1509	0.91	0/2350
All	All	0.66	2/28027 (0.0%)	0.96	19/38971 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1103	GLY	C-O	-17.89	1.14	1.24
2	F	425	ARG	CG-CD	-6.61	1.32	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1326	TYR	N-CA-C	-6.60	102.02	110.53
1	A	27	G	C4'-C3'-O3'	6.20	122.29	113.00
2	F	226	ILE	CA-CB-CG1	-6.15	99.95	110.40
5	I	42	A	C2'-C3'-O3'	6.11	122.86	113.70
2	F	902	LYS	CD-CE-NZ	-5.97	92.78	111.90
2	B	879	MET	CA-CB-CG	-5.89	102.32	114.10
2	F	896	LYS	CD-CE-NZ	-5.85	93.18	111.90
2	F	139	ARG	CB-CG-CD	5.71	124.42	111.30
2	F	1036	TYR	CB-CA-C	-5.64	110.06	116.54
1	A	8	A	C4'-C3'-O3'	5.58	121.38	113.00
2	B	343	LEU	CA-CB-CG	5.50	135.57	116.30
2	B	250	PRO	CA-N-CD	-5.38	104.46	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	8	A	P-O3'-C3'	5.30	128.15	120.20
2	B	1208	ASN	O-C-N	-5.24	115.62	122.59
1	A	4	A	N9-C1'-C2'	5.22	119.82	112.00
2	F	425	ARG	CB-CG-CD	-5.20	99.34	111.30
2	B	684	LYS	N-CA-C	-5.13	102.93	110.52
5	I	59	U	O5'-P-OP2	-5.13	92.62	108.00
2	F	1099	GLU	N-CA-C	5.12	116.74	108.34

There are no chirality outliers.

There are no planarity outliers.

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	725	0	362	29	0
1	E	663	0	331	30	0
2	B	10769	0	10863	722	2
2	F	10698	0	10745	835	0
3	C	501	0	287	12	0
3	G	501	0	287	19	0
4	D	225	0	129	7	0
4	H	225	0	129	11	0
5	I	1348	0	678	70	0
5	J	1348	0	678	69	0
6	B	1	0	0	0	0
6	F	3	0	0	0	0
All	All	27007	0	24489	1682	2

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 33.

All (1682) 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)
2:B:380:LEU:O	2:B:386:THR:CG2	1.70	1.39

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1222:LYS:NZ	2:B:1315:LEU:O	1.59	1.33
2:F:878:LYS:HB3	2:F:879:MET:SD	1.74	1.28
2:F:878:LYS:CD	2:F:879:MET:HE1	1.65	1.24
2:F:878:LYS:HD2	2:F:879:MET:CE	1.76	1.16
2:B:410:ILE:HG23	2:B:414:ILE:HD11	1.26	1.15
2:B:1258:PHE:CE1	2:B:1262:HIS:CD2	2.38	1.11
2:B:1258:PHE:HE1	2:B:1262:HIS:CD2	1.68	1.11
2:F:1060:ARG:HE	2:F:1061:PRO:HD2	1.04	1.09
2:F:137:HIS:CD2	2:F:322:ILE:HG12	1.86	1.09
2:F:137:HIS:HD2	2:F:322:ILE:HG12	1.06	1.08
2:B:380:LEU:O	2:B:386:THR:HG21	0.89	1.06
2:B:410:ILE:HG23	2:B:414:ILE:CD1	1.85	1.04
2:F:521:TYR:HD1	2:F:684:LYS:HG2	1.20	1.04
2:F:878:LYS:HB3	2:F:879:MET:CE	1.87	1.04
2:B:1179:ILE:HD11	2:B:1192:LYS:HE2	1.41	1.02
2:F:1108:GLU:HB2	3:G:9:DT:H5"	1.44	1.00
2:B:410:ILE:CG2	2:B:414:ILE:HD11	1.91	0.99
1:E:23:U:H5"	2:F:1112:PRO:HG3	1.44	0.99
2:F:922:VAL:HG11	2:F:1007:GLU:HB3	1.44	0.99
2:B:727:LEU:HD12	2:B:927:ILE:HD12	1.42	0.99
2:F:1205:GLU:OE1	2:F:1359:ARG:NH2	1.97	0.98
2:F:168:PHE:HB2	2:F:447:ARG:HH11	1.26	0.97
2:F:521:TYR:CD1	2:F:684:LYS:CD	2.48	0.96
2:B:1000:LYS:HG3	2:B:1001:TYR:CE1	2.01	0.95
2:F:521:TYR:CE1	2:F:684:LYS:CD	2.48	0.95
2:F:522:ASN:OD1	2:F:692:ASN:ND2	1.99	0.94
2:B:1109:SER:OG	3:C:9:DT:OP2	1.84	0.94
2:F:165:ARG:HD2	2:F:168:PHE:HE1	1.33	0.93
2:B:46:ASN:ND2	2:B:1091:GLN:OE1	2.01	0.93
2:B:727:LEU:HD12	2:B:927:ILE:CD1	1.97	0.93
2:F:1060:ARG:NE	2:F:1061:PRO:HD2	1.82	0.93
2:B:279:LEU:HD11	2:B:284:ASP:HA	1.51	0.93
2:F:923:GLU:HG2	2:F:928:THR:HG21	1.52	0.92
2:B:70:ARG:NH2	5:I:61:C:OP1	2.03	0.92
2:F:527:VAL:HA	2:F:582:GLY:HA3	1.51	0.92
2:F:138:LEU:HD21	2:F:153:LEU:HD21	1.49	0.92
2:F:140:LYS:NZ	2:F:313:THR:HB	1.84	0.92
2:B:212:LEU:HD21	2:B:225:LEU:HD12	1.50	0.92
2:F:140:LYS:HZ2	2:F:313:THR:HB	1.34	0.92
2:F:760:VAL:HG22	2:F:956:ILE:HD12	1.52	0.91
2:F:180:ASP:HB3	2:F:183:LYS:HB2	1.48	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:521:TYR:CD1	2:F:684:LYS:HG2	2.06	0.91
2:F:90:MET:HA	2:F:151:LEU:HD21	1.51	0.90
2:F:860:SER:OG	2:F:863:ASN:OD1	1.90	0.90
2:F:521:TYR:CE1	2:F:684:LYS:HD2	2.04	0.90
2:F:139:ARG:HH12	2:F:418:GLU:CD	1.78	0.90
2:F:174:LEU:HD21	2:F:413:GLN:CG	2.02	0.89
2:B:1351:SER:OG	5:I:68:A:N6	2.05	0.89
2:F:174:LEU:HD21	2:F:413:GLN:CD	1.96	0.89
2:F:1045:PHE:HB2	2:F:1064:GLU:HG2	1.54	0.89
2:F:249:THR:OG1	2:F:267:SER:N	2.06	0.89
2:F:521:TYR:CD1	2:F:684:LYS:HD3	2.08	0.89
2:F:855:LYS:NZ	2:F:1246:LYS:O	2.06	0.89
2:F:521:TYR:CD1	2:F:684:LYS:CG	2.57	0.88
2:F:44:LYS:NZ	5:J:92:G:O6	2.05	0.88
2:F:521:TYR:HD1	2:F:684:LYS:CG	1.86	0.88
2:B:336:LYS:NZ	5:I:43:G:O6	2.06	0.87
5:J:46:A:H2'	5:J:47:A:C8	2.10	0.87
2:B:1251:ASP:HA	2:B:1254:GLN:HE21	1.39	0.87
2:F:187:GLN:NE2	2:F:292:ALA:HB1	1.90	0.87
2:B:1222:LYS:NZ	2:B:1315:LEU:C	2.33	0.87
3:C:6:DC:O2	4:D:7:DG:N2	2.08	0.86
2:F:451:TYR:O	2:F:464:TRP:NE1	2.08	0.86
2:B:1277:SER:HA	2:B:1281:ILE:HG12	1.56	0.85
2:B:1003:LYS:HG3	2:B:1036:TYR:HE2	1.41	0.85
2:B:220:ARG:O	2:B:224:ASN:ND2	2.10	0.84
2:B:1241:HIS:CE1	2:B:1244:LYS:HA	2.11	0.84
2:F:207:ASP:O	2:F:211:ILE:HD13	1.77	0.84
2:F:249:THR:HG1	2:F:267:SER:N	1.75	0.84
2:F:933:GLN:HG2	2:F:1010:TYR:OH	1.77	0.84
5:I:83:C:H2'	5:I:84:A:H8	1.41	0.84
2:F:1357:GLU:O	5:J:81:G:N2	2.10	0.84
2:B:299:ALA:O	2:B:303:SER:OG	1.94	0.83
2:F:478:PHE:HE2	2:F:482:VAL:HB	1.41	0.83
2:B:1228:LEU:HD12	2:B:1229:PRO:HD2	1.61	0.83
2:B:1245:LEU:HB2	2:B:1252:ASN:ND2	1.93	0.83
2:F:627:GLU:HA	2:F:655:ARG:HH12	1.44	0.83
2:F:1256:GLN:NE2	2:F:1260:GLU:OE2	2.12	0.83
2:B:557:ARG:NH2	2:B:596:ASP:OD1	2.12	0.83
2:F:136:TYR:CE1	2:F:139:ARG:NH2	2.45	0.83
2:B:508:LEU:HD21	2:B:664:ARG:HB2	1.61	0.82
2:F:672:ASP:OD1	2:F:703:THR:HG22	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:671:ARG:HG3	2:B:678:THR:HG22	1.61	0.82
2:F:211:ILE:HG22	2:F:212:LEU:HD23	1.61	0.82
2:F:878:LYS:CB	2:F:879:MET:CE	2.57	0.81
2:B:241:LEU:HD13	2:B:289:LEU:HD21	1.60	0.81
2:F:226:ILE:CD1	2:F:232:GLU:HB3	2.09	0.81
2:F:633:GLU:HG2	2:F:652:LYS:HD3	1.60	0.81
2:B:212:LEU:O	2:B:221:ARG:NH1	2.13	0.81
2:F:143:VAL:HG23	2:F:422:ILE:HD11	1.62	0.81
2:F:878:LYS:CG	2:F:879:MET:CE	2.58	0.81
2:F:923:GLU:OE2	2:F:925:ARG:NH1	2.12	0.81
2:B:978:ILE:HD12	2:B:1233:VAL:HG22	1.62	0.81
2:F:94:ASP:HB3	2:F:97:PHE:HB2	1.63	0.81
2:F:878:LYS:CB	2:F:879:MET:SD	2.66	0.81
1:A:27:G:H5'	1:A:28:A:H5''	1.60	0.81
2:F:1041:ASN:O	2:F:1042:ILE:HG22	1.81	0.81
1:A:14:G:OP2	2:B:63:ARG:NH1	2.13	0.80
2:B:45:LYS:NZ	2:B:1357:GLU:OE2	2.14	0.80
2:F:165:ARG:HD2	2:F:168:PHE:CE1	2.16	0.80
2:F:1210:ARG:NH2	2:F:1341:GLU:OE1	2.15	0.80
2:F:380:LEU:HD11	2:F:390:LEU:HG	1.62	0.80
2:B:967:ARG:HE	2:B:974:LYS:HB2	1.47	0.80
2:B:395:ARG:NH2	2:B:397:ASP:OD2	2.14	0.80
2:B:524:LEU:HD12	2:B:587:PHE:HE2	1.44	0.79
2:B:525:THR:HG23	2:B:690:ASN:HB3	1.63	0.79
2:B:881:ASN:OD1	2:B:885:GLN:NE2	2.15	0.79
2:B:1211:LYS:H	2:B:1224:ASN:HD21	1.30	0.79
2:F:921:LEU:HD22	2:F:1042:ILE:HD12	1.63	0.79
2:B:939:MET:HE2	2:B:953:VAL:HG21	1.65	0.79
2:F:921:LEU:HD22	2:F:1042:ILE:CD1	2.13	0.79
2:B:1074:TRP:HZ2	2:B:1080:PHE:HE2	1.31	0.79
2:F:1119:LEU:HD23	2:F:1128:PRO:HB2	1.65	0.78
2:B:634:GLU:HA	2:B:637:LYS:NZ	1.98	0.78
2:F:184:LEU:HD13	2:F:295:ASN:HB3	1.65	0.78
1:A:20:A:OP2	2:B:403:ARG:NH1	2.15	0.78
2:B:229:LEU:HB2	2:B:230:PRO:HD2	1.66	0.77
2:F:1290:VAL:HG22	2:F:1331:ILE:HD13	1.66	0.77
2:F:466:THR:O	2:F:482:VAL:HG13	1.84	0.77
2:B:563:GLN:O	2:B:567:ASP:HB2	1.82	0.77
5:I:52:A:OP2	5:I:62:G:N2	2.18	0.77
2:B:1108:GLU:N	3:C:9:DT:OP1	2.13	0.77
2:B:824:VAL:HG11	2:B:859:ARG:HH12	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1074:TRP:HZ2	2:B:1080:PHE:CE2	2.03	0.77
2:F:48:ILE:HG12	2:F:984:ALA:HB1	1.66	0.77
2:F:933:GLN:HG2	2:F:1010:TYR:CZ	2.20	0.77
1:E:10:U:O4	3:G:19:DA:N6	2.18	0.77
2:B:1326:TYR:HD2	2:B:1327:PHE:H	1.32	0.77
2:F:870:VAL:HG11	2:F:899:ASN:O	1.85	0.77
2:F:1001:TYR:HE2	2:F:1045:PHE:CE1	2.03	0.77
2:F:1286:ASN:ND2	2:F:1332:ASP:O	2.17	0.77
2:F:165:ARG:C	2:F:415:HIS:HD2	1.93	0.76
2:F:174:LEU:HG	2:F:413:GLN:HB2	1.66	0.76
2:F:644:ASP:OD2	2:F:646:LYS:N	2.17	0.76
2:B:83:GLN:HG2	2:B:98:PHE:CE1	2.21	0.76
2:F:853:ASP:OD1	2:F:893:THR:HG21	1.85	0.76
2:B:860:SER:OG	2:B:863:ASN:OD1	2.03	0.76
2:B:69:ARG:HD3	5:I:62:G:N7	2.01	0.76
2:F:253:LYS:HB2	2:F:262:ALA:H	1.51	0.76
2:F:921:LEU:HG	2:F:1008:PHE:HE2	1.51	0.76
2:F:89:GLU:OE2	2:F:92:LYS:NZ	2.19	0.75
2:F:413:GLN:O	2:F:417:GLY:N	2.14	0.75
2:B:1147:ALA:HB2	2:B:1190:VAL:HA	1.67	0.75
2:F:826:GLN:NE2	2:F:859:ARG:HD3	2.01	0.75
2:B:368:SER:OG	2:B:371:GLU:OE1	2.04	0.75
2:F:826:GLN:HE22	2:F:859:ARG:HD3	1.50	0.75
2:F:1091:GLN:HG3	5:J:91:C:H5"	1.69	0.75
2:B:525:THR:CG2	2:B:690:ASN:HB3	2.16	0.75
2:F:1241:HIS:CE1	2:F:1244:LYS:HA	2.22	0.75
2:F:521:TYR:HE1	2:F:684:LYS:HD2	1.51	0.75
2:B:383:MET:O	2:B:386:THR:HG23	1.87	0.75
1:E:27:G:N2	5:J:44:U:OP2	2.19	0.75
2:F:1236:LEU:O	2:F:1240:SER:OG	2.04	0.75
2:F:643:PHE:HD1	2:F:647:VAL:HG11	1.52	0.74
2:B:342:GLN:HG3	2:B:383:MET:HE3	1.68	0.74
2:F:921:LEU:HD13	2:F:1042:ILE:HD13	1.69	0.74
2:F:187:GLN:HE21	2:F:292:ALA:HB1	1.51	0.74
2:F:978:ILE:HD12	2:F:1233:VAL:HG22	1.68	0.74
2:F:958:LEU:HD22	2:F:962:LEU:HD12	1.68	0.74
2:B:1011:GLY:O	2:B:1014:LYS:N	2.20	0.74
2:B:1356:TYR:HB3	5:I:81:G:N1	2.02	0.74
2:F:411:PRO:HB2	2:F:413:GLN:OE1	1.87	0.74
2:B:531:THR:HG21	2:B:575:PHE:HE2	1.53	0.74
2:B:1119:LEU:HD23	2:B:1128:PRO:HB2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:473:ILE:HG12	2:F:481:VAL:HG11	1.69	0.74
2:F:489:GLN:HG3	2:F:625:LEU:HD21	1.69	0.74
2:B:725:ALA:O	2:B:734:LYS:NZ	2.21	0.73
2:F:174:LEU:CD2	2:F:413:GLN:CG	2.66	0.73
2:F:521:TYR:CE1	2:F:684:LYS:HD3	2.22	0.73
2:B:594:TYR:OH	2:B:608:ASP:OD1	2.06	0.73
2:B:38:THR:HG22	2:B:40:ARG:H	1.52	0.73
2:B:114:GLU:HG3	2:B:116:HIS:H	1.52	0.73
2:F:258:LEU:HD22	2:F:260:GLU:H	1.54	0.73
2:B:549:VAL:HA	2:B:553:PHE:HD2	1.54	0.72
2:F:878:LYS:CG	2:F:879:MET:HE3	2.19	0.72
2:F:1262:HIS:HB3	2:F:1265:TYR:CD2	2.24	0.72
2:B:1047:LYS:HB2	2:B:1050:ILE:HG22	1.71	0.72
2:F:318:SER:OG	2:F:418:GLU:OE2	2.05	0.72
2:F:649:LYS:O	2:F:653:ARG:NE	2.21	0.72
2:F:886:LEU:HA	2:F:891:LEU:HD21	1.70	0.72
2:F:841:ILE:CD1	2:F:896:LYS:HG3	2.19	0.72
2:F:969:ASP:HB2	2:F:970:PHE:CE2	2.25	0.72
2:B:181:VAL:O	2:B:185:PHE:N	2.22	0.72
2:B:687:GLY:O	2:B:690:ASN:ND2	2.23	0.72
2:F:499:ASP:HB2	2:F:663:SER:HB3	1.72	0.72
2:F:646:LYS:O	2:F:650:GLN:NE2	2.23	0.72
2:B:139:ARG:HD3	2:B:161:MET:HE2	1.71	0.72
2:F:481:VAL:HG12	2:F:482:VAL:HG23	1.72	0.72
2:F:178:ASN:ND2	2:F:295:ASN:OD1	2.23	0.71
2:B:229:LEU:HD12	2:B:231:GLY:H	1.55	0.71
2:B:975:VAL:HG11	2:B:1310:ILE:HD11	1.72	0.71
2:F:174:LEU:HD21	2:F:413:GLN:HG2	1.69	0.71
2:B:745:ASP:OD2	2:B:938:ARG:NH2	2.22	0.71
2:B:1177:ASN:ND2	2:B:1180:ASP:OD2	2.23	0.71
2:F:531:THR:HG21	2:F:575:PHE:CE1	2.26	0.71
2:F:1217:ALA:O	2:F:1339:THR:HG21	1.91	0.71
2:F:686:ASP:HB3	2:F:689:ALA:O	1.90	0.71
2:F:1212:ARG:NH2	2:F:1280:VAL:O	2.24	0.71
2:B:1307:GLU:O	2:B:1310:ILE:HG22	1.89	0.71
2:F:980:ASN:HB2	2:F:1225:GLU:OE2	1.90	0.71
2:F:413:GLN:HA	2:F:416:LEU:HB3	1.73	0.71
2:F:505:GLU:HG3	2:F:665:LYS:HB2	1.72	0.71
2:F:1167:THR:HG23	2:F:1170:GLU:H	1.54	0.71
2:B:1315:LEU:HB2	2:B:1324:PHE:CZ	2.26	0.71
2:B:184:LEU:HD12	2:B:299:ALA:HB2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:640:ALA:HA	2:B:648:MET:HE2	1.73	0.71
2:F:820:ARG:HG3	2:F:826:GLN:O	1.91	0.71
2:B:509:PRO:HB3	2:B:624:THR:HG21	1.73	0.70
2:B:1276:PHE:HE2	2:B:1316:THR:HB	1.55	0.70
2:F:838:VAL:HG11	2:F:855:LYS:HE3	1.72	0.70
2:F:903:ALA:HA	2:F:907:GLY:HA2	1.73	0.70
2:F:1060:ARG:HH21	2:F:1061:PRO:HG2	1.56	0.70
2:F:826:GLN:OE1	2:F:859:ARG:NH1	2.22	0.70
2:B:137:HIS:HA	2:B:322:ILE:HD11	1.72	0.70
2:B:448:ILE:HD13	2:B:455:LEU:HD13	1.72	0.70
2:F:185:PHE:O	2:F:189:VAL:HG23	1.90	0.70
2:F:1206:LEU:HD11	2:F:1210:ARG:HH22	1.54	0.70
2:B:925:ARG:HB3	2:B:928:THR:HG23	1.72	0.70
2:F:174:LEU:CD2	2:F:413:GLN:HG2	2.22	0.70
2:F:74:ARG:O	2:F:78:ARG:HG3	1.91	0.70
2:F:889:ALA:HB3	2:F:891:LEU:HD23	1.73	0.70
2:F:967:ARG:NH1	2:F:974:LYS:HE3	2.06	0.70
2:B:114:GLU:HG2	2:B:120:GLY:O	1.91	0.70
2:B:1003:LYS:HG3	2:B:1036:TYR:CE2	2.25	0.70
2:F:338:LEU:HB3	2:F:383:MET:CE	2.22	0.70
2:F:692:ASN:O	2:F:696:LEU:HG	1.91	0.70
2:B:849:ASP:OD2	2:B:895:ARG:NH1	2.25	0.70
2:F:878:LYS:CG	2:F:879:MET:HE1	2.22	0.70
2:F:627:GLU:HA	2:F:655:ARG:NH1	2.05	0.70
2:F:632:ILE:O	2:F:636:LEU:N	2.20	0.70
2:F:1221:GLN:NE2	4:H:6:DG:OP2	2.24	0.70
2:B:1356:TYR:HB3	5:I:81:G:C6	2.26	0.70
5:J:40:C:H2'	5:J:41:A:C8	2.26	0.70
2:B:524:LEU:HD12	2:B:587:PHE:CE2	2.26	0.69
2:F:1001:TYR:HE2	2:F:1045:PHE:CD1	2.10	0.69
2:B:9:LEU:HD12	2:B:761:ILE:HG22	1.72	0.69
2:B:1147:ALA:HB1	2:B:1188:LYS:O	1.90	0.69
2:F:1045:PHE:HA	2:F:1060:ARG:HH11	1.58	0.69
2:F:878:LYS:HD2	2:F:879:MET:HE1	0.81	0.69
2:B:1208:ASN:ND2	2:B:1208:ASN:O	2.25	0.69
2:F:161:MET:HE2	2:F:419:LEU:HD12	1.75	0.69
2:F:1286:ASN:O	2:F:1290:VAL:HG23	1.92	0.69
2:B:107:VAL:HG22	2:B:1131:TYR:OH	1.93	0.69
2:B:386:THR:O	2:B:390:LEU:N	2.25	0.69
2:B:672:ASP:HA	2:B:703:THR:HG21	1.72	0.69
2:B:1211:LYS:N	2:B:1224:ASN:HD21	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1135:ASP:OD1	2:F:1136:SER:N	2.26	0.69
2:F:446:PHE:HZ	2:F:478:PHE:HD1	1.41	0.69
2:F:1062:LEU:O	2:F:1076:LYS:HG3	1.93	0.69
2:F:1021:MET:HG3	2:F:1036:TYR:HD2	1.57	0.68
2:F:271:TYR:O	2:F:275:LEU:N	2.22	0.68
2:F:823:TYR:CD2	2:F:858:THR:HG21	2.29	0.68
2:F:1167:THR:HG22	2:F:1170:GLU:HG3	1.74	0.68
2:B:526:LYS:HE2	2:B:692:ASN:HB2	1.75	0.68
2:F:832:ARG:HD2	2:F:835:ASP:OD2	1.92	0.68
5:I:83:C:H2'	5:I:84:A:C8	2.26	0.68
2:B:1211:LYS:H	2:B:1224:ASN:ND2	1.92	0.68
2:B:1305:GLN:O	2:B:1309:ILE:HG13	1.93	0.68
2:F:672:ASP:HB3	2:F:675:SER:HB2	1.76	0.68
2:F:114:GLU:OE1	2:F:116:HIS:N	2.24	0.68
2:F:603:ASP:OD1	2:F:606:PHE:N	2.25	0.68
2:F:1219:GLU:OE1	2:F:1335:ARG:NH2	2.26	0.68
2:B:240:ASN:HB3	2:B:252:PHE:CE2	2.28	0.68
2:F:1045:PHE:O	2:F:1060:ARG:NH1	2.25	0.68
2:B:305:ILE:HD13	2:B:411:PRO:HD2	1.74	0.68
2:B:1333:ARG:NH1	2:B:1335:ARG:HD2	2.07	0.68
2:B:1349:HIS:HB3	5:I:68:A:N3	2.09	0.68
2:F:1182:LEU:HD13	2:F:1190:VAL:HG21	1.75	0.68
5:J:48:A:H2'	5:J:49:A:C8	2.28	0.68
2:B:369:GLN:NE2	2:B:405:PHE:HZ	1.90	0.67
2:B:116:HIS:CE1	2:B:122:ILE:HG23	2.30	0.67
2:B:1220:LEU:HD11	2:B:1339:THR:HA	1.76	0.67
2:F:168:PHE:HB2	2:F:447:ARG:NH1	2.06	0.67
2:F:234:LYS:H	2:F:234:LYS:HD3	1.57	0.67
2:F:646:LYS:HG3	2:F:650:GLN:HE21	1.59	0.67
2:B:8:GLY:HA3	2:B:991:ALA:HB2	1.76	0.67
2:F:621:LEU:O	2:F:625:LEU:N	2.26	0.67
2:F:878:LYS:HG2	2:F:879:MET:HE3	1.76	0.67
2:B:240:ASN:HB3	2:B:252:PHE:HE2	1.58	0.67
2:F:153:LEU:HD23	2:F:153:LEU:O	1.93	0.67
2:B:558:LYS:HE3	2:B:590:SER:HB3	1.76	0.67
2:F:136:TYR:HE1	2:F:139:ARG:NH2	1.92	0.67
2:F:878:LYS:HB3	2:F:879:MET:HE3	1.75	0.67
5:I:36:G:H2'	5:I:37:U:H6	1.60	0.67
2:B:565:LYS:HD3	2:B:578:VAL:HG13	1.77	0.67
5:J:95:G:H2'	5:J:96:C:C6	2.29	0.67
1:A:15:G:H2'	1:A:16:A:H8	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:143:VAL:HG21	2:F:315:ALA:HB2	1.76	0.67
2:F:472:THR:O	2:F:477:ASN:ND2	2.27	0.67
2:F:943:TYR:HE2	2:F:949:LEU:HD13	1.60	0.67
2:F:46:ASN:ND2	2:F:1089:MET:SD	2.69	0.66
2:B:971:GLN:O	2:B:971:GLN:HG2	1.94	0.66
2:B:1120:ILE:HD11	2:B:1137:PRO:HG3	1.76	0.66
2:B:1226:LEU:HB2	2:B:1276:PHE:CE2	2.31	0.66
2:F:1116:SER:HB3	2:F:1119:LEU:HB2	1.75	0.66
2:B:1262:HIS:O	2:B:1265:TYR:HB2	1.94	0.66
2:F:90:MET:SD	2:F:151:LEU:HD23	2.35	0.66
2:B:233:LYS:HG2	2:B:235:ASN:HB2	1.76	0.66
2:B:526:LYS:NZ	2:B:690:ASN:O	2.27	0.66
2:B:755:LYS:NZ	2:B:939:MET:O	2.22	0.66
2:F:143:VAL:CG2	2:F:422:ILE:HD11	2.24	0.66
2:F:323:LYS:HE3	2:F:327:GLU:OE2	1.94	0.66
2:B:1047:LYS:CB	2:B:1050:ILE:HG22	2.26	0.66
2:F:922:VAL:HG11	2:F:1007:GLU:CB	2.24	0.66
2:B:237:LEU:HA	2:B:255:ASN:HD21	1.60	0.66
2:B:1276:PHE:CE2	2:B:1316:THR:HB	2.30	0.66
1:A:22:U:O2'	2:B:1110:ILE:HB	1.96	0.66
2:F:118:ILE:H	2:F:118:ILE:HD12	1.60	0.66
5:I:39:G:H5'	5:I:40:C:OP2	1.96	0.66
2:F:174:LEU:HD22	2:F:174:LEU:N	2.10	0.66
2:B:117:PRO:HD2	2:B:125:GLU:OE2	1.96	0.66
2:F:163:LYS:HG2	2:F:164:PHE:CE1	2.30	0.66
2:F:566:GLU:O	2:F:570:LYS:HE2	1.95	0.66
2:B:182:ASP:OD1	2:B:209:LYS:HB2	1.96	0.66
2:B:317:LEU:HD11	2:B:410:ILE:HD11	1.77	0.66
2:B:420:HIS:ND1	2:B:441:GLU:OE2	2.28	0.66
2:F:551:LEU:HD23	2:F:568:TYR:HD1	1.60	0.66
2:B:531:THR:HG21	2:B:575:PHE:CE2	2.31	0.65
2:B:971:GLN:HA	2:B:973:TYR:CE2	2.30	0.65
2:B:313:THR:HG23	2:B:315:ALA:H	1.60	0.65
2:B:844:GLN:C	2:B:1041:ASN:HB3	2.22	0.65
2:F:392:LYS:HD3	2:F:397:ASP:O	1.96	0.65
2:F:986:ASP:O	2:F:990:ASN:ND2	2.29	0.65
1:E:15:G:OP1	2:F:66:ARG:NH2	2.28	0.65
2:F:618:ASP:HA	2:F:621:LEU:HD22	1.79	0.65
2:B:874:GLU:HA	2:B:877:LYS:HE3	1.76	0.65
2:F:640:ALA:HA	2:F:648:MET:HE3	1.79	0.65
2:F:1084:ARG:HB3	2:F:1084:ARG:CZ	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:672:ASP:HA	2:B:703:THR:CG2	2.26	0.65
2:F:272:ASP:HA	2:F:275:LEU:HB3	1.77	0.65
1:A:27:G:H5'	1:A:28:A:C5'	2.27	0.65
2:B:66:ARG:HD2	2:B:462:PHE:HE2	1.62	0.65
2:B:970:PHE:CD1	2:B:1080:PHE:HZ	2.14	0.65
3:G:6:DC:H2''	3:G:7:DC:O5'	1.97	0.65
2:B:493:GLU:O	2:B:496:THR:OG1	2.14	0.65
2:B:107:VAL:HG13	2:B:1131:TYR:CE1	2.32	0.65
2:F:671:ARG:HB3	2:F:676:GLY:HA2	1.79	0.65
2:F:966:PHE:O	2:F:970:PHE:HD2	1.80	0.65
2:B:378:PRO:O	2:B:382:LYS:HG2	1.96	0.64
2:B:633:GLU:OE1	2:B:652:LYS:HE3	1.96	0.64
1:E:14:G:OP2	2:F:63:ARG:HD3	1.98	0.64
2:F:143:VAL:O	2:F:425:ARG:NH1	2.30	0.64
2:F:274:ASP:O	2:F:278:LEU:HD12	1.95	0.64
2:F:943:TYR:CE2	2:F:949:LEU:HD13	2.32	0.64
2:B:619:ILE:O	2:B:623:LEU:HB2	1.98	0.64
2:B:1308:ASN:ND2	2:B:1327:PHE:CB	2.59	0.64
2:F:142:LEU:HB3	2:F:422:ILE:HD12	1.79	0.64
2:F:180:ASP:HB3	2:F:183:LYS:HD3	1.80	0.64
2:F:208:ALA:O	2:F:212:LEU:HG	1.96	0.64
2:F:622:THR:HG21	2:F:635:ARG:HG3	1.79	0.64
2:B:317:LEU:HD11	2:B:410:ILE:CD1	2.27	0.64
2:F:623:LEU:HD11	2:F:654:ARG:O	1.96	0.64
2:B:970:PHE:CD1	2:B:1080:PHE:CZ	2.86	0.64
2:F:791:LEU:HD22	2:F:891:LEU:HD22	1.79	0.64
2:F:828:LEU:HD22	2:F:836:TYR:CE2	2.32	0.64
2:F:328:HIS:NE2	2:F:359:TYR:OH	2.29	0.64
2:F:762:GLU:OE1	2:F:990:ASN:ND2	2.30	0.64
2:B:1003:LYS:CG	2:B:1036:TYR:HE2	2.10	0.64
3:C:18:DA:H2'	3:C:19:DA:C8	2.32	0.64
2:F:478:PHE:CE2	2:F:482:VAL:HB	2.28	0.64
2:B:892:ILE:HB	2:B:896:LYS:HD3	1.80	0.64
2:F:103:GLU:OE2	2:F:113:HIS:N	2.31	0.64
2:F:545:LYS:NZ	2:F:683:LEU:O	2.31	0.64
1:E:25:U:H5'	2:F:107:VAL:HG12	1.80	0.64
2:F:143:VAL:CG2	2:F:422:ILE:CD1	2.75	0.63
2:F:891:LEU:HD12	2:F:892:ILE:HG23	1.80	0.63
2:B:893:THR:HG23	2:B:896:LYS:H	1.64	0.63
2:F:900:LEU:H	2:F:900:LEU:HD12	1.63	0.63
2:F:921:LEU:CG	2:F:1008:PHE:HE2	2.10	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:36:G:H2'	5:I:37:U:C6	2.34	0.63
2:F:1347:LEU:N	2:F:1360:ILE:O	2.31	0.63
2:F:432:PHE:CE1	2:F:433:LEU:HG	2.34	0.63
2:F:691:ARG:HG2	2:F:695:GLN:HE21	1.63	0.63
2:F:821:ASP:HB2	2:F:828:LEU:HD21	1.80	0.63
2:B:282:ILE:HG22	2:B:286:TYR:CD1	2.33	0.63
2:F:158:LEU:HA	2:F:161:MET:SD	2.39	0.63
2:F:817:GLN:NE2	2:F:857:LEU:O	2.29	0.63
2:B:278:LEU:O	2:B:282:ILE:HG13	1.98	0.63
2:B:548:ILE:HG23	2:B:552:LEU:CD1	2.29	0.63
2:B:139:ARG:CZ	2:B:161:MET:HG2	2.29	0.62
2:F:649:LYS:HB3	2:F:653:ARG:HH21	1.64	0.62
2:F:933:GLN:HE22	2:F:937:SER:HB3	1.64	0.62
2:F:1123:LYS:HG3	5:J:53:G:OP1	1.99	0.62
2:F:1326:TYR:HE2	2:F:1327:PHE:CD2	2.16	0.62
2:B:275:LEU:O	2:B:279:LEU:HB2	1.99	0.62
2:B:782:LYS:O	2:B:786:GLU:HG3	1.99	0.62
2:F:5:TYR:CZ	2:F:751:MET:HG3	2.34	0.62
2:F:359:TYR:CE2	2:F:363:ILE:HG13	2.34	0.62
2:F:1311:HIS:O	2:F:1314:THR:HG22	1.98	0.62
2:B:824:VAL:HG22	2:B:863:ASN:HD22	1.65	0.62
2:B:985:HIS:ND1	2:B:1087:LEU:HD13	2.14	0.62
2:B:1290:VAL:HG22	2:B:1331:ILE:HD13	1.81	0.62
2:F:1206:LEU:HD11	2:F:1210:ARG:NH2	2.14	0.62
2:B:1207:GLU:HG3	2:B:1208:ASN:H	1.62	0.62
2:B:5:TYR:OH	2:B:754:HIS:O	2.18	0.62
2:B:121:ASN:OD1	2:B:124:ASP:HB2	1.99	0.62
2:B:631:MET:HE2	2:B:631:MET:HA	1.81	0.62
2:B:864:ARG:O	2:B:872:SER:N	2.32	0.62
2:F:143:VAL:HG22	2:F:422:ILE:CD1	2.30	0.62
2:F:171:GLU:HG2	2:F:269:ASP:CB	2.30	0.62
2:F:553:PHE:CE2	2:F:559:VAL:HG21	2.35	0.62
2:B:720:LEU:HD13	2:B:938:ARG:NH1	2.14	0.62
2:F:1253:GLU:O	2:F:1257:LEU:HD12	2.00	0.62
2:F:289:LEU:O	2:F:292:ALA:HB3	2.00	0.62
5:I:94:U:H2'	5:I:95:G:C8	2.35	0.62
2:B:45:LYS:NZ	2:B:1354:GLY:O	2.32	0.62
2:B:245:SER:HA	2:B:297:SER:HB2	1.82	0.62
2:B:970:PHE:HD1	2:B:1080:PHE:CZ	2.17	0.62
2:B:44:LYS:HE2	5:I:92:G:O6	1.99	0.61
2:F:1167:THR:CG2	2:F:1170:GLU:HG3	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:410:ILE:HG21	2:F:415:HIS:CE1	2.35	0.61
5:I:42:A:H8	5:I:42:A:H5''	1.65	0.61
2:B:955:VAL:O	2:B:1009:VAL:HG13	1.99	0.61
2:F:485:GLY:HA3	2:F:631:MET:HG3	1.82	0.61
2:F:777:SER:HA	2:F:807:GLN:HE21	1.66	0.61
2:F:842:VAL:HG12	2:F:854:ASN:HD21	1.65	0.61
2:B:1245:LEU:HB2	2:B:1252:ASN:HD21	1.64	0.61
5:I:94:U:H2'	5:I:95:G:H8	1.66	0.61
2:B:640:ALA:HA	2:B:648:MET:CE	2.29	0.61
2:B:1236:LEU:O	2:B:1240:SER:OG	2.16	0.61
2:F:383:MET:HE3	2:F:386:THR:HG21	1.83	0.61
2:F:471:GLU:OE1	2:F:477:ASN:ND2	2.33	0.61
2:F:978:ILE:HD13	2:F:1228:LEU:HD23	1.81	0.61
2:F:1051:THR:HG22	2:F:1053:ALA:H	1.65	0.61
2:B:879:MET:HE2	2:B:882:TYR:CD2	2.36	0.61
2:B:1002:PRO:HD2	2:B:1036:TYR:OH	2.00	0.61
2:F:933:GLN:NE2	2:F:937:SER:HB3	2.16	0.61
2:B:634:GLU:HA	2:B:637:LYS:HZ3	1.64	0.61
2:B:1228:LEU:HD12	2:B:1229:PRO:CD	2.29	0.61
2:B:1349:HIS:CE1	5:I:69:A:H4'	2.36	0.61
2:F:776:ASN:O	2:F:780:ARG:HG2	1.99	0.61
2:B:351:PHE:C	2:B:360:ALA:HB2	2.26	0.61
2:F:788:ILE:O	2:F:792:GLY:N	2.29	0.60
2:F:961:LYS:HG2	2:F:965:ASP:OD2	2.00	0.60
2:B:40:ARG:NE	2:B:43:ILE:HD11	2.15	0.60
2:B:158:LEU:HD22	2:B:419:LEU:HG	1.81	0.60
2:B:1105:PHE:CG	2:B:1169:MET:HG3	2.36	0.60
2:F:174:LEU:CG	2:F:413:GLN:HB2	2.31	0.60
2:B:644:ASP:HB3	2:B:647:VAL:HG23	1.83	0.60
2:B:1205:GLU:HG3	2:B:1209:GLY:HA2	1.82	0.60
2:F:730:SER:HB2	2:F:733:ILE:HG22	1.84	0.60
2:F:1000:LYS:HG3	2:F:1001:TYR:CD2	2.36	0.60
2:B:542:GLY:O	2:B:546:LYS:HG3	2.01	0.60
2:B:809:GLU:OE1	2:B:855:LYS:HE2	2.00	0.60
2:F:32:PHE:CE1	2:F:1355:LEU:HB3	2.37	0.60
2:F:328:HIS:CG	5:J:44:U:C2	2.90	0.60
2:F:528:LYS:O	2:F:581:SER:N	2.25	0.60
2:F:82:LEU:HD11	2:F:162:ILE:HD13	1.83	0.60
2:F:1218:GLY:C	2:F:1339:THR:HG23	2.27	0.60
2:B:96:SER:O	2:B:100:ARG:HG3	2.01	0.60
2:B:310:THR:OG1	2:B:316:PRO:HB3	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:19:DA:H2'	3:C:20:DA:C8	2.36	0.60
3:G:3:DA:N6	4:H:9:DA:H61	2.00	0.60
2:B:6:SER:HB3	2:B:758:ASN:HB2	1.83	0.60
2:B:148:LYS:HB2	2:B:429:PHE:CD1	2.36	0.60
2:B:645:ASP:O	2:B:649:LYS:HG2	2.02	0.60
2:B:692:ASN:O	2:B:696:LEU:HD23	2.02	0.60
2:B:973:TYR:HB3	2:B:1237:TYR:CD1	2.37	0.60
2:B:1251:ASP:O	2:B:1255:LYS:HG3	2.02	0.60
2:F:226:ILE:HG13	2:F:232:GLU:HB3	1.84	0.60
2:F:279:LEU:HD21	2:F:287:ALA:HB2	1.84	0.60
2:F:598:LEU:HG	2:F:607:LEU:HD12	1.83	0.60
2:F:733:ILE:HD11	2:F:763:MET:HE2	1.84	0.60
2:F:794:GLN:O	2:F:798:GLU:HG3	2.02	0.60
2:B:455:LEU:HD23	2:B:473:ILE:HD12	1.84	0.60
2:B:1091:GLN:HG3	5:I:91:C:H5''	1.83	0.60
2:F:38:THR:HG22	2:F:40:ARG:H	1.66	0.60
2:F:921:LEU:CD2	2:F:1042:ILE:CD1	2.79	0.60
2:F:1169:MET:HE3	5:J:52:A:N3	2.16	0.60
2:B:140:LYS:HD3	2:B:322:ILE:HD12	1.84	0.60
2:B:549:VAL:HA	2:B:553:PHE:CD2	2.36	0.60
2:F:780:ARG:HD2	2:F:812:TYR:CE2	2.37	0.60
2:B:35:LEU:HB2	2:B:1358:THR:HG22	1.84	0.59
2:F:619:ILE:HD11	2:F:651:LEU:HD11	1.84	0.59
2:F:1095:VAL:HG13	2:F:1350:GLN:OE1	2.01	0.59
2:B:180:ASP:HB3	2:B:183:LYS:HB2	1.83	0.59
3:C:22:DT:H2''	3:C:23:DC:O5'	2.02	0.59
2:F:44:LYS:HD3	5:J:92:G:N7	2.17	0.59
2:B:823:TYR:HA	2:B:875:VAL:CG1	2.33	0.59
2:F:791:LEU:HD11	2:F:885:GLN:HB3	1.84	0.59
2:B:1215:ALA:HB2	2:B:1221:GLN:HB2	1.84	0.59
1:A:8:A:H2'	1:A:9:U:C6	2.37	0.59
2:B:550:ASP:HA	2:B:554:LYS:HD3	1.84	0.59
2:F:720:LEU:HD13	2:F:938:ARG:HD2	1.84	0.59
2:F:921:LEU:HG	2:F:1008:PHE:CE2	2.37	0.59
2:F:942:LYS:HE3	2:F:952:GLU:OE2	2.03	0.59
2:F:1001:TYR:CE2	2:F:1045:PHE:CE1	2.87	0.59
2:F:1272:GLN:HE22	5:J:89:G:H1	1.51	0.59
3:G:3:DA:H61	4:H:9:DA:H61	1.51	0.59
5:I:37:U:H2'	5:I:38:A:H8	1.68	0.59
2:B:338:LEU:O	2:B:383:MET:HE1	2.01	0.59
2:B:1236:LEU:HA	2:B:1239:ALA:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1060:ARG:HE	2:F:1061:PRO:CD	1.96	0.59
2:F:1266:LEU:HD12	2:F:1309:ILE:HD12	1.85	0.59
2:B:917:ILE:HD11	2:B:1042:ILE:HG22	1.84	0.59
2:F:818:ASN:O	2:F:818:ASN:ND2	2.36	0.59
2:B:332:LEU:HD13	2:B:359:TYR:CE1	2.38	0.59
2:B:720:LEU:HD13	2:B:938:ARG:HH11	1.67	0.59
2:F:134:THR:HG22	5:J:45:U:H4'	1.84	0.59
2:F:784:ILE:HG21	2:F:815:TYR:HD1	1.68	0.59
2:F:1270:ILE:HG13	2:F:1294:TYR:CD2	2.38	0.59
2:F:1314:THR:HA	2:F:1317:ASN:CG	2.27	0.59
2:B:516:GLU:O	2:B:519:THR:HG22	2.02	0.59
2:B:1235:PHE:CE1	2:B:1239:ALA:HB2	2.37	0.59
2:F:531:THR:HG1	2:F:575:PHE:HD1	1.49	0.59
2:B:345:GLU:OE1	2:B:345:GLU:N	2.36	0.59
2:F:1270:ILE:HG13	2:F:1294:TYR:CE2	2.38	0.59
2:B:527:VAL:HA	2:B:582:GLY:HA3	1.84	0.58
2:B:594:TYR:O	2:B:598:LEU:N	2.31	0.58
2:F:359:TYR:HE2	2:F:363:ILE:HG13	1.67	0.58
2:F:841:ILE:HD13	2:F:896:LYS:HG3	1.85	0.58
2:F:923:GLU:HG3	2:F:925:ARG:H	1.67	0.58
2:F:1250:GLU:HG3	2:F:1251:ASP:N	2.17	0.58
5:J:42:A:O2'	5:J:43:G:OP1	2.19	0.58
2:B:977:GLU:N	2:B:977:GLU:OE1	2.35	0.58
1:E:27:G:H1'	2:F:129:HIS:CD2	2.37	0.58
2:F:515:TYR:O	2:F:519:THR:HG22	2.03	0.58
2:F:1218:GLY:HA2	2:F:1339:THR:CG2	2.33	0.58
2:B:1263:LYS:HG3	2:B:1302:ILE:HD13	1.85	0.58
2:B:1315:LEU:HB2	2:B:1324:PHE:CE1	2.38	0.58
2:F:1047:LYS:O	2:F:1076:LYS:NZ	2.37	0.58
3:G:19:DA:H2'	3:G:20:DA:C8	2.38	0.58
2:F:475:PRO:HG3	5:J:59:U:O4	2.03	0.58
2:F:878:LYS:CB	2:F:879:MET:HE3	2.31	0.58
2:B:1000:LYS:O	2:B:1000:LYS:HD3	2.04	0.58
2:F:836:TYR:HB2	2:F:857:LEU:HD11	1.85	0.58
2:B:48:ILE:O	2:B:1093:ASN:ND2	2.36	0.58
1:A:15:G:H2'	1:A:16:A:C8	2.38	0.58
2:F:226:ILE:CG1	2:F:232:GLU:HB3	2.33	0.58
2:B:1207:GLU:CG	2:B:1208:ASN:H	2.15	0.58
2:F:971:GLN:HG2	2:F:973:TYR:CE2	2.39	0.58
2:F:1038:PHE:CD2	2:F:1039:TYR:HE1	2.21	0.58
2:F:922:VAL:CG1	2:F:1007:GLU:HB3	2.25	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:70:ARG:HH21	5:I:61:C:P	2.24	0.57
2:B:121:ASN:H	2:B:121:ASN:ND2	2.01	0.57
2:B:978:ILE:HG22	2:B:1313:PHE:CE2	2.39	0.57
2:F:1312:LEU:HD21	2:F:1326:TYR:HD1	1.68	0.57
5:I:88:A:N6	5:I:91:C:H42	2.02	0.57
2:B:83:GLN:HG2	2:B:98:PHE:CZ	2.39	0.57
2:B:1210:ARG:NH2	2:B:1341:GLU:OE1	2.36	0.57
2:F:339:VAL:HG12	2:F:347:TYR:HB2	1.86	0.57
2:F:535:ARG:HH11	2:F:535:ARG:HG3	1.69	0.57
2:B:1041:ASN:ND2	2:B:1044:ASN:HD21	2.03	0.57
2:F:967:ARG:NH1	2:F:986:ASP:OD1	2.37	0.57
5:J:40:C:H2'	5:J:41:A:H8	1.66	0.57
2:B:168:PHE:CD2	2:B:447:ARG:HD3	2.39	0.57
1:E:23:U:O2	2:F:1122:ARG:NH2	2.37	0.57
2:F:144:ASP:OD1	2:F:144:ASP:N	2.36	0.57
2:B:279:LEU:CD1	2:B:284:ASP:HA	2.31	0.57
2:B:1111:LEU:HD12	2:B:1135:ASP:CB	2.35	0.57
2:F:174:LEU:CD2	2:F:174:LEU:N	2.67	0.57
2:B:853:ASP:OD2	2:B:893:THR:HG21	2.04	0.57
2:B:866:LYS:HB3	2:B:869:ASN:HB2	1.87	0.57
2:B:1266:LEU:O	2:B:1270:ILE:HG12	2.03	0.57
2:F:174:LEU:CD2	2:F:413:GLN:CB	2.83	0.57
2:F:618:ASP:OD2	2:F:639:TYR:OH	2.22	0.57
2:F:969:ASP:HB2	2:F:970:PHE:CD2	2.40	0.57
2:B:278:LEU:HG	2:B:282:ILE:HD11	1.87	0.57
2:B:727:LEU:HD21	2:B:934:ILE:HD11	1.87	0.57
2:B:781:MET:HG3	2:B:803:ASN:ND2	2.19	0.57
2:F:63:ARG:HA	2:F:66:ARG:HD3	1.86	0.57
2:F:221:ARG:HA	2:F:224:ASN:HB2	1.87	0.57
2:F:550:ASP:HA	2:F:554:LYS:HG3	1.85	0.57
2:F:630:GLU:HG3	2:F:631:MET:N	2.19	0.57
1:A:10:U:H2'	1:A:11:U:C6	2.39	0.57
3:C:2:DA:H2'	3:C:3:DA:C8	2.40	0.57
2:F:112:LYS:O	2:F:113:HIS:ND1	2.34	0.57
2:B:340:ARG:HH21	5:I:41:A:P	2.28	0.57
2:B:620:VAL:HG13	2:B:656:TYR:HD2	1.70	0.57
2:B:1208:ASN:OD1	2:B:1279:ARG:HG3	2.04	0.57
2:F:662:LEU:HB3	2:F:666:LEU:HD23	1.87	0.57
2:F:1108:GLU:N	3:G:9:DT:OP1	2.33	0.57
2:B:109:GLU:OE1	2:B:1130:LYS:HD3	2.04	0.56
2:B:1000:LYS:HG3	2:B:1001:TYR:CZ	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:523:GLU:OE1	2:F:589:ALA:N	2.37	0.56
2:F:870:VAL:HB	2:F:903:ALA:HB2	1.85	0.56
5:J:44:U:O2'	5:J:45:U:H5'	2.04	0.56
2:B:241:LEU:CD1	2:B:289:LEU:HD21	2.32	0.56
2:B:948:LYS:H	2:B:948:LYS:HD2	1.70	0.56
2:F:241:LEU:HD23	2:F:241:LEU:H	1.70	0.56
2:F:936:ASP:CB	2:F:1010:TYR:CD2	2.88	0.56
2:F:981:TYR:CZ	2:F:1092:VAL:HB	2.40	0.56
2:B:378:PRO:HG2	2:B:379:ILE:HD12	1.86	0.56
2:B:410:ILE:CG2	2:B:414:ILE:CD1	2.64	0.56
2:F:117:PRO:HD2	2:F:118:ILE:HD12	1.88	0.56
2:F:563:GLN:O	2:F:567:ASP:HB2	2.04	0.56
2:F:841:ILE:HD12	2:F:854:ASN:HA	1.88	0.56
2:F:1011:GLY:O	2:F:1012:ASP:HB2	2.05	0.56
2:F:1215:ALA:HB2	2:F:1221:GLN:HG3	1.86	0.56
2:B:74:ARG:O	2:B:78:ARG:HG3	2.05	0.56
2:B:824:VAL:HG22	2:B:863:ASN:ND2	2.21	0.56
2:B:1048:THR:HG22	2:B:1076:LYS:CB	2.35	0.56
2:F:76:LYS:O	2:F:80:CYS:HB2	2.06	0.56
2:F:362:TYR:OH	2:F:401:LYS:HG3	2.04	0.56
2:F:373:TYR:HE1	2:F:398:LEU:HB3	1.71	0.56
2:F:620:VAL:O	2:F:624:THR:N	2.28	0.56
2:F:622:THR:HG21	2:F:635:ARG:CG	2.35	0.56
2:F:893:THR:HG23	2:F:896:LYS:HB3	1.88	0.56
2:F:1267:ASP:OD1	2:F:1294:TYR:OH	2.22	0.56
2:B:970:PHE:HD1	2:B:1080:PHE:CE1	2.24	0.56
2:B:198:GLU:HG2	2:B:199:ASN:N	2.19	0.56
2:B:679:ILE:O	2:B:683:LEU:HD13	2.05	0.56
2:B:814:TYR:HD1	2:B:815:TYR:CD1	2.23	0.56
2:B:1075:ASP:OD1	2:B:1078:ARG:N	2.27	0.56
2:F:40:ARG:HD3	2:F:43:ILE:HD11	1.88	0.56
2:F:595:HIS:HD1	2:F:595:HIS:H	1.53	0.56
2:B:451:TYR:CD1	2:B:488:ALA:HB2	2.40	0.56
2:B:662:LEU:HD23	2:B:666:LEU:HD22	1.86	0.56
2:B:821:ASP:OD2	2:B:828:LEU:HG	2.06	0.56
2:B:609:ASN:ND2	2:B:611:GLU:OE1	2.39	0.56
2:B:1041:ASN:ND2	2:B:1044:ASN:ND2	2.54	0.56
2:B:1295:ASN:HA	2:B:1298:ARG:NH1	2.20	0.56
2:F:623:LEU:HD11	2:F:655:ARG:HA	1.88	0.56
2:F:781:MET:HG3	2:F:803:ASN:ND2	2.21	0.56
2:B:784:ILE:HD13	2:B:815:TYR:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1326:TYR:CE2	2:F:1327:PHE:CD2	2.94	0.56
3:G:3:DA:H61	4:H:9:DA:N6	2.04	0.56
2:B:727:LEU:O	2:B:734:LYS:NZ	2.34	0.56
2:F:221:ARG:O	2:F:225:LEU:N	2.33	0.56
2:F:895:ARG:O	2:F:899:ASN:ND2	2.39	0.56
2:F:1106:SER:HA	2:F:1137:PRO:HA	1.88	0.56
2:B:816:LEU:HD12	2:B:891:LEU:O	2.04	0.55
2:B:821:ASP:O	2:B:879:MET:HE1	2.06	0.55
2:B:1345:ALA:O	2:B:1362:LEU:HG	2.07	0.55
2:F:32:PHE:O	2:F:42:SER:HA	2.06	0.55
2:F:180:ASP:CB	2:F:183:LYS:HB2	2.29	0.55
5:J:92:G:H2'	5:J:93:G:C8	2.42	0.55
2:B:118:ILE:HG22	2:B:119:PHE:CE1	2.41	0.55
2:B:379:ILE:HD12	2:B:379:ILE:H	1.71	0.55
2:F:936:ASP:HB3	2:F:1010:TYR:CD2	2.41	0.55
2:F:1207:GLU:OE2	2:F:1210:ARG:NH1	2.40	0.55
2:F:1313:PHE:O	2:F:1316:THR:N	2.39	0.55
2:B:317:LEU:CD1	2:B:410:ILE:HD13	2.37	0.55
2:F:48:ILE:CG1	2:F:984:ALA:HB1	2.37	0.55
2:F:724:ILE:HD13	2:F:738:LEU:HG	1.88	0.55
2:B:531:THR:HG23	2:B:534:MET:HG3	1.88	0.55
2:B:1197:LYS:O	2:B:1199:PRO:HD3	2.06	0.55
2:F:391:VAL:HA	2:F:394:ASN:OD1	2.07	0.55
5:I:37:U:H2'	5:I:38:A:C8	2.42	0.55
2:B:383:MET:O	2:B:386:THR:CG2	2.53	0.55
2:B:905:ARG:HG2	2:B:905:ARG:HH11	1.71	0.55
2:B:920:GLN:HG3	2:B:921:LEU:HD23	1.89	0.55
2:F:551:LEU:O	2:F:555:THR:OG1	2.17	0.55
2:F:699:ASP:OD1	2:F:701:SER:OG	2.23	0.55
2:B:183:LYS:NZ	2:B:311:GLU:OE2	2.39	0.55
2:B:823:TYR:CD1	2:B:875:VAL:HG11	2.41	0.55
2:F:97:PHE:O	2:F:101:LEU:HD13	2.07	0.55
2:F:621:LEU:O	2:F:625:LEU:HB2	2.07	0.55
2:F:742:LYS:HE2	2:F:1352:ILE:HD13	1.89	0.55
2:F:1000:LYS:HG3	2:F:1001:TYR:CE2	2.42	0.55
2:F:1102:THR:OG1	2:F:1103:GLY:N	2.39	0.55
2:B:1062:LEU:HD23	2:B:1062:LEU:H	1.71	0.55
2:B:1318:LEU:HD23	2:B:1319:GLY:N	2.21	0.55
2:F:455:LEU:O	5:J:60:C:H5'	2.07	0.55
2:F:813:LEU:O	2:F:817:GLN:HG3	2.06	0.55
2:F:949:LEU:HD23	2:F:951:ARG:HH22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:114:GLU:HG3	2:B:115:ARG:N	2.22	0.55
2:F:869:ASN:HD21	2:F:907:GLY:HA3	1.71	0.55
2:B:1074:TRP:CZ2	2:B:1080:PHE:HE2	2.20	0.55
2:F:606:PHE:CE1	2:F:612:ASN:HB3	2.42	0.55
2:F:886:LEU:HB3	2:F:892:ILE:HG12	1.88	0.55
2:F:936:ASP:CG	2:F:1010:TYR:HD2	2.15	0.55
2:B:925:ARG:HG3	3:C:21:DT:OP1	2.07	0.55
2:B:1207:GLU:HG3	2:B:1208:ASN:N	2.22	0.54
2:F:351:PHE:HB3	5:J:43:G:O6	2.06	0.54
2:F:870:VAL:CG1	2:F:871:PRO:HD2	2.37	0.54
2:B:252:PHE:CE1	2:B:290:PHE:HE2	2.25	0.54
2:B:601:ILE:HD11	2:B:607:LEU:HD21	1.88	0.54
2:B:823:TYR:HA	2:B:875:VAL:HG11	1.89	0.54
2:B:943:TYR:CZ	2:B:949:LEU:HD13	2.42	0.54
1:E:22:U:O2	2:F:1110:ILE:HD12	2.07	0.54
2:B:118:ILE:HG22	2:B:119:PHE:CD1	2.43	0.54
2:B:165:ARG:O	2:B:412:HIS:HA	2.08	0.54
2:F:36:GLY:HA3	2:F:1359:ARG:O	2.08	0.54
2:F:90:MET:HA	2:F:151:LEU:CD2	2.32	0.54
2:F:467:ARG:HD3	2:F:470:GLU:HA	1.88	0.54
2:B:980:ASN:HB2	2:B:1225:GLU:CD	2.31	0.54
2:B:338:LEU:C	2:B:383:MET:HE1	2.31	0.54
2:B:699:ASP:HB3	2:B:702:LEU:HB2	1.90	0.54
2:B:949:LEU:HD12	2:B:950:ILE:H	1.72	0.54
2:B:1251:ASP:O	2:B:1254:GLN:HG2	2.07	0.54
2:F:535:ARG:H	2:F:535:ARG:HD2	1.73	0.54
2:F:677:LYS:NZ	2:F:685:SER:O	2.40	0.54
2:F:1147:ALA:HB2	2:F:1190:VAL:HA	1.90	0.54
2:B:332:LEU:HD21	2:B:336:LYS:HE3	1.88	0.54
2:B:682:PHE:HB3	2:B:696:LEU:HD11	1.90	0.54
2:B:963:VAL:HG21	2:B:990:ASN:OD1	2.07	0.54
1:E:20:A:OP1	2:F:404:THR:N	2.40	0.54
2:F:925:ARG:HB3	2:F:928:THR:HG22	1.88	0.54
2:B:32:PHE:N	2:B:43:ILE:O	2.29	0.54
2:F:70:ARG:HH21	5:J:61:C:P	2.31	0.54
2:F:410:ILE:HG21	2:F:415:HIS:NE2	2.22	0.54
2:F:1075:ASP:OD2	2:F:1078:ARG:NH2	2.40	0.54
2:B:253:LYS:HD3	2:B:261:ASP:HA	1.90	0.54
2:B:621:LEU:O	2:B:625:LEU:HB2	2.08	0.54
2:F:233:LYS:HG2	2:F:235:ASN:HB2	1.89	0.54
2:F:363:ILE:HD12	5:J:44:U:H5'	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1263:LYS:HG3	2:B:1302:ILE:CD1	2.38	0.54
2:F:467:ARG:HE	2:F:473:ILE:HD11	1.72	0.54
2:F:536:LYS:HD2	2:F:537:PRO:HD2	1.89	0.54
2:F:573:GLU:OE1	2:F:573:GLU:HA	2.07	0.54
2:F:643:PHE:CD1	2:F:647:VAL:HG11	2.38	0.54
2:B:825:ASP:OD1	2:B:879:MET:HE3	2.08	0.54
2:B:1110:ILE:CD1	2:B:1122:ARG:HD2	2.38	0.54
2:B:1143:VAL:HG13	2:B:1195:ILE:HG23	1.90	0.54
2:F:338:LEU:HB3	2:F:383:MET:HE1	1.87	0.54
2:F:963:VAL:HG21	2:F:990:ASN:OD1	2.08	0.54
3:G:23:DC:H2'	3:G:24:DG:O4'	2.06	0.54
2:B:972:PHE:HE1	2:B:1084:ARG:HB2	1.73	0.53
5:J:91:C:O2'	5:J:92:G:P	2.67	0.53
2:F:238:PHE:O	2:F:242:ILE:HG12	2.08	0.53
2:F:688:PHE:CD2	2:F:689:ALA:N	2.76	0.53
2:F:817:GLN:HB3	2:F:820:ARG:O	2.09	0.53
2:F:1343:LEU:O	2:F:1362:LEU:HB2	2.08	0.53
2:B:386:THR:OG1	2:B:387:GLU:OE1	2.21	0.53
2:B:642:LEU:HB2	2:B:643:PHE:CE2	2.43	0.53
2:F:468:LYS:HE3	2:F:483:ASP:HB3	1.90	0.53
2:F:338:LEU:HB3	2:F:383:MET:HE2	1.90	0.53
2:F:596:ASP:CG	2:F:654:ARG:HH21	2.16	0.53
2:F:632:ILE:HG22	2:F:636:LEU:HD13	1.91	0.53
2:F:795:ILE:HG13	2:F:795:ILE:O	2.07	0.53
2:F:896:LYS:O	2:F:900:LEU:HD12	2.09	0.53
5:J:45:U:C2	5:J:46:A:C8	2.96	0.53
2:B:787:GLY:HA3	2:B:891:LEU:HD21	1.89	0.53
2:B:876:VAL:O	2:B:880:LYS:N	2.41	0.53
2:F:253:LYS:HG3	2:F:261:ASP:HA	1.89	0.53
2:B:225:LEU:HD13	2:B:242:ILE:HG21	1.91	0.53
2:B:824:VAL:HG11	2:B:859:ARG:NH1	2.20	0.53
2:B:1314:THR:CG2	2:B:1324:PHE:HB3	2.38	0.53
2:F:644:ASP:HB3	2:F:647:VAL:HG23	1.90	0.53
2:F:867:SER:HB2	2:F:1053:ALA:C	2.32	0.53
2:F:949:LEU:HD12	2:F:950:ILE:H	1.73	0.53
2:F:1161:LYS:NZ	2:F:1364:GLN:HG2	2.23	0.53
2:B:751:MET:O	2:B:754:HIS:HB2	2.08	0.53
2:B:951:ARG:CZ	2:B:1011:GLY:HA2	2.38	0.53
2:B:1211:LYS:HB2	2:B:1224:ASN:ND2	2.24	0.53
2:F:424:ARG:O	2:F:427:GLU:HG2	2.09	0.53
2:B:30:LYS:HD3	5:I:83:C:P	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:839:ASP:O	2:B:856:VAL:N	2.42	0.53
2:B:985:HIS:O	2:B:989:LEU:HG	2.08	0.53
2:F:551:LEU:HG	2:F:552:LEU:HD23	1.91	0.53
2:F:616:LEU:HA	2:F:619:ILE:HG22	1.89	0.53
2:F:829:ASP:OD1	2:F:831:ASN:N	2.42	0.53
5:J:95:G:C6	5:J:96:C:N4	2.77	0.53
2:B:818:ASN:ND2	2:B:818:ASN:O	2.42	0.53
2:F:108:GLU:CD	2:F:115:ARG:HD3	2.34	0.53
2:F:442:LYS:HA	2:F:445:THR:HG22	1.91	0.53
2:F:1204:PHE:CE1	2:F:1347:LEU:HG	2.44	0.53
2:F:1241:HIS:HE1	2:F:1244:LYS:HA	1.68	0.53
2:B:22:THR:HG22	2:B:23:ASP:H	1.74	0.53
2:B:302:LEU:HA	2:B:305:ILE:HG12	1.90	0.53
2:B:340:ARG:NH2	5:I:41:A:P	2.82	0.53
2:F:309:ASN:OD1	2:F:312:ILE:HG23	2.09	0.53
2:F:1351:SER:OG	2:F:1356:TYR:HB2	2.09	0.53
2:F:136:TYR:CE2	2:F:160:HIS:NE2	2.77	0.52
2:F:616:LEU:O	2:F:620:VAL:HG23	2.09	0.52
2:F:1066:ASN:OD1	2:F:1069:THR:OG1	2.22	0.52
2:F:1263:LYS:O	2:F:1266:LEU:HD22	2.09	0.52
2:F:1264:HIS:O	2:F:1268:GLU:HG3	2.09	0.52
5:I:57:A:N6	5:J:74:A:H1'	2.24	0.52
2:B:144:ASP:OD1	2:B:313:THR:OG1	2.27	0.52
2:B:289:LEU:C	2:B:289:LEU:HD23	2.34	0.52
1:A:20:A:P	2:B:403:ARG:NH1	2.83	0.52
2:B:106:LEU:O	2:B:111:LYS:HE3	2.09	0.52
2:B:527:VAL:HG12	2:B:540:LEU:CD1	2.39	0.52
2:F:189:VAL:HG13	2:F:201:ILE:HG22	1.92	0.52
2:F:363:ILE:HD12	5:J:44:U:C5'	2.40	0.52
2:F:939:MET:HG3	2:F:953:VAL:HG11	1.91	0.52
2:F:1108:GLU:HB2	3:G:9:DT:C5'	2.29	0.52
2:B:677:LYS:HD3	2:B:682:PHE:CZ	2.44	0.52
2:F:735:LYS:HE3	5:J:66:U:OP2	2.09	0.52
2:B:135:ILE:HG21	2:B:160:HIS:NE2	2.25	0.52
2:F:446:PHE:CZ	2:F:478:PHE:HD1	2.24	0.52
2:F:921:LEU:CD2	2:F:1008:PHE:HE2	2.22	0.52
5:I:64:U:C2	5:I:65:A:C8	2.97	0.52
2:B:462:PHE:N	2:B:462:PHE:CD1	2.76	0.52
2:B:864:ARG:NH2	2:B:871:PRO:HD3	2.24	0.52
2:B:939:MET:HG3	2:B:953:VAL:HG11	1.92	0.52
2:B:1312:LEU:O	2:B:1315:LEU:HB3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1357:GLU:O	5:I:81:G:N2	2.43	0.52
1:E:27:G:H5'	1:E:28:A:O5'	2.08	0.52
2:F:360:ALA:O	2:F:364:ASP:N	2.43	0.52
2:F:666:LEU:HD11	2:F:693:PHE:HE1	1.75	0.52
2:F:882:TYR:CD2	2:F:883:TRP:CD1	2.98	0.52
2:F:1090:PRO:HD2	5:J:88:A:C2	2.43	0.52
2:F:1312:LEU:HD21	2:F:1326:TYR:CD1	2.44	0.52
2:B:279:LEU:HD13	2:B:279:LEU:O	2.10	0.52
2:B:1041:ASN:HD22	2:B:1044:ASN:CG	2.16	0.52
2:B:1235:PHE:O	2:B:1239:ALA:N	2.28	0.52
4:D:11:DT:H2''	4:D:12:DG:C8	2.45	0.52
2:F:174:LEU:CD2	2:F:413:GLN:HB2	2.40	0.52
2:F:346:LYS:O	2:F:350:ILE:HG13	2.09	0.52
2:F:516:GLU:OE1	2:F:592:GLY:N	2.43	0.52
2:F:982:HIS:HA	2:F:985:HIS:HB2	1.91	0.52
2:F:35:LEU:HB2	2:F:1358:THR:HB	1.91	0.52
2:F:1304:GLU:O	2:F:1308:ASN:ND2	2.42	0.52
2:B:237:LEU:CA	2:B:255:ASN:HD21	2.23	0.52
2:B:507:VAL:HG12	2:B:508:LEU:O	2.09	0.52
2:B:1315:LEU:HD13	2:B:1324:PHE:HZ	1.75	0.52
2:F:226:ILE:HD12	2:F:232:GLU:HB3	1.90	0.52
2:F:496:THR:HG21	2:F:659:TRP:CZ2	2.45	0.52
2:F:633:GLU:O	2:F:637:LYS:N	2.42	0.52
2:F:1212:ARG:HD2	2:F:1336:TYR:HD2	1.74	0.52
2:B:30:LYS:HD3	5:I:83:C:OP2	2.10	0.51
2:B:945:GLU:N	2:B:945:GLU:OE1	2.42	0.51
2:B:975:VAL:CG1	2:B:1310:ILE:HD11	2.40	0.51
2:B:1000:LYS:HG3	2:B:1001:TYR:CD1	2.44	0.51
1:E:16:A:H5''	2:F:74:ARG:HH12	1.75	0.51
2:F:138:LEU:HD21	2:F:153:LEU:CD2	2.31	0.51
2:F:846:PHE:O	2:F:1040:SER:OG	2.16	0.51
2:F:967:ARG:CZ	2:F:974:LYS:HB2	2.40	0.51
2:B:252:PHE:CE1	2:B:264:LEU:HD13	2.44	0.51
2:B:317:LEU:O	2:B:320:SER:HB3	2.11	0.51
2:B:332:LEU:HD21	2:B:336:LYS:CE	2.40	0.51
2:F:544:GLN:O	2:F:548:ILE:HG13	2.10	0.51
2:B:548:ILE:HG23	2:B:552:LEU:HD12	1.91	0.51
2:B:763:MET:SD	2:B:928:THR:HG22	2.50	0.51
2:B:828:LEU:HD21	2:B:859:ARG:HG2	1.92	0.51
2:B:1146:VAL:HG13	2:B:1191:LYS:HG3	1.92	0.51
2:F:321:MET:HE2	2:F:321:MET:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:514:LEU:HD21	2:F:664:ARG:HH21	1.76	0.51
2:F:1114:ARG:NH1	4:H:9:DA:OP1	2.44	0.51
2:B:736:GLY:O	2:B:740:THR:N	2.39	0.51
2:B:823:TYR:HD2	2:B:858:THR:HG21	1.76	0.51
2:B:913:LYS:O	2:B:916:PHE:HB2	2.11	0.51
2:B:1270:ILE:HG13	2:B:1294:TYR:CE2	2.46	0.51
2:F:165:ARG:O	2:F:412:HIS:HA	2.11	0.51
2:F:893:THR:HG23	2:F:896:LYS:H	1.75	0.51
2:F:1269:ILE:O	2:F:1272:GLN:HB2	2.11	0.51
1:E:4:A:C2	1:E:5:C:C4	2.99	0.51
2:F:122:ILE:O	2:F:126:VAL:HG23	2.10	0.51
2:F:730:SER:O	2:F:733:ILE:HG22	2.10	0.51
2:F:1097:LYS:HE2	2:F:1099:GLU:OE2	2.10	0.51
5:J:94:U:H2'	5:J:95:G:C8	2.45	0.51
2:B:66:ARG:CD	2:B:462:PHE:HE2	2.23	0.51
2:B:874:GLU:O	2:B:878:LYS:HE3	2.10	0.51
2:B:1213:MET:HE1	2:B:1318:LEU:HD21	1.92	0.51
2:B:1263:LYS:O	2:B:1263:LYS:HG2	2.11	0.51
2:F:413:GLN:CD	2:F:413:GLN:H	2.18	0.51
2:F:733:ILE:HD11	2:F:763:MET:CE	2.41	0.51
5:I:92:G:H2'	5:I:93:G:H8	1.76	0.51
5:J:91:C:O2'	5:J:92:G:O5'	2.25	0.51
2:B:620:VAL:HG13	2:B:656:TYR:CD2	2.45	0.51
2:B:1199:PRO:O	2:B:1202:SER:HB2	2.11	0.51
5:I:45:U:H2'	5:I:46:A:O4'	2.11	0.51
2:B:11:ILE:O	2:B:763:MET:HA	2.09	0.51
2:B:554:LYS:HG3	2:B:594:TYR:CE2	2.46	0.51
2:B:943:TYR:CE2	2:B:949:LEU:HA	2.46	0.51
2:B:1226:LEU:HB2	2:B:1276:PHE:CZ	2.46	0.51
2:F:1125:ASP:OD2	2:F:1125:ASP:N	2.44	0.51
2:F:1127:ASP:OD1	2:F:1129:LYS:N	2.43	0.51
2:F:1218:GLY:HA2	2:F:1339:THR:HG23	1.93	0.51
2:B:181:VAL:CG2	2:B:209:LYS:HA	2.41	0.51
2:B:967:ARG:NE	2:B:974:LYS:HB2	2.23	0.51
2:F:140:LYS:HB3	2:F:322:ILE:CD1	2.41	0.51
2:F:233:LYS:HG2	2:F:236:GLY:N	2.26	0.51
2:F:1000:LYS:HB2	2:F:1073:VAL:HG21	1.93	0.51
2:B:201:ILE:HG22	2:B:202:ASN:H	1.76	0.50
2:B:879:MET:HG2	2:B:882:TYR:HB2	1.92	0.50
2:B:1270:ILE:HG13	2:B:1294:TYR:CD2	2.46	0.50
2:B:1326:TYR:HD2	2:B:1327:PHE:N	2.07	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:19:A:H4'	2:F:407:ASN:C	2.35	0.50
2:F:688:PHE:HD2	2:F:689:ALA:N	2.08	0.50
2:B:334:LEU:O	2:B:338:LEU:HG	2.11	0.50
2:B:973:TYR:CD1	2:B:1237:TYR:CD1	2.99	0.50
2:B:1349:HIS:ND1	5:I:69:A:H4'	2.26	0.50
1:E:25:U:O5'	1:E:25:U:H6	1.93	0.50
2:F:40:ARG:NE	2:F:43:ILE:HD11	2.26	0.50
2:F:412:HIS:CD2	2:F:413:GLN:NE2	2.80	0.50
2:F:597:LEU:O	2:F:601:ILE:HG12	2.11	0.50
2:F:936:ASP:CB	2:F:1010:TYR:HD2	2.24	0.50
2:B:136:TYR:HE2	2:B:403:ARG:HD3	1.75	0.50
2:B:1111:LEU:HD12	2:B:1135:ASP:HB2	1.93	0.50
1:E:19:A:O3'	2:F:407:ASN:HB2	2.11	0.50
2:F:138:LEU:HD11	2:F:153:LEU:HD21	1.92	0.50
2:F:165:ARG:O	2:F:415:HIS:HD2	1.93	0.50
2:F:921:LEU:CD1	2:F:1042:ILE:HD13	2.39	0.50
2:F:939:MET:CE	2:F:953:VAL:HG21	2.41	0.50
2:B:358:GLY:O	2:B:362:TYR:N	2.40	0.50
2:B:737:ILE:O	2:B:740:THR:HG22	2.11	0.50
2:B:866:LYS:HB3	2:B:869:ASN:CB	2.41	0.50
2:F:561:VAL:O	2:F:565:LYS:HG3	2.12	0.50
2:B:499:ASP:OD2	2:B:663:SER:HB3	2.12	0.50
5:I:71:U:O2'	5:I:72:U:H5'	2.12	0.50
2:F:622:THR:HG23	2:F:626:PHE:CD1	2.47	0.50
1:A:24:U:O2	1:A:25:U:C2	2.65	0.50
2:B:902:LYS:HE3	2:B:908:LEU:HA	1.93	0.50
2:B:1258:PHE:CE1	2:B:1262:HIS:HD2	2.17	0.50
2:F:69:ARG:NH2	5:J:63:U:OP2	2.45	0.50
2:F:140:LYS:HB3	2:F:322:ILE:HD11	1.94	0.50
2:F:390:LEU:O	2:F:394:ASN:ND2	2.45	0.50
2:F:882:TYR:HD2	2:F:883:TRP:CD1	2.29	0.50
2:F:1283:ALA:HB1	2:F:1286:ASN:HB2	1.93	0.50
2:B:317:LEU:CD1	2:B:410:ILE:CD1	2.90	0.50
2:B:342:GLN:CG	2:B:383:MET:HE3	2.40	0.50
2:F:878:LYS:CD	2:F:879:MET:CE	2.49	0.50
2:F:1082:THR:O	2:F:1086:VAL:HG23	2.12	0.50
2:B:1145:VAL:HG11	2:B:1187:TYR:CD2	2.46	0.50
2:B:1314:THR:HG21	2:B:1324:PHE:HB3	1.93	0.50
2:F:570:LYS:HA	2:F:575:PHE:O	2.11	0.50
2:F:583:VAL:HG22	2:F:584:GLU:N	2.27	0.50
2:F:999:LYS:HB3	2:F:1073:VAL:HG12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:95:G:H2'	5:J:96:C:H6	1.75	0.50
2:B:36:GLY:HA3	2:B:1359:ARG:O	2.11	0.49
2:B:927:ILE:HG23	2:B:928:THR:N	2.26	0.49
2:B:954:LYS:HG3	2:B:1009:VAL:HG11	1.94	0.49
2:B:989:LEU:HD21	2:B:1087:LEU:HD21	1.94	0.49
2:B:1296:LYS:HD3	2:B:1296:LYS:N	2.26	0.49
5:I:85:C:H2'	5:I:86:C:C6	2.47	0.49
2:B:518:PHE:C	2:B:518:PHE:CD2	2.90	0.49
2:F:1216:SER:OG	2:F:1217:ALA:N	2.45	0.49
2:B:5:TYR:CE2	2:B:756:PRO:HB3	2.47	0.49
2:B:108:GLU:HG3	2:B:115:ARG:HG2	1.93	0.49
2:B:340:ARG:HA	2:B:344:PRO:HB3	1.94	0.49
2:B:410:ILE:HG23	2:B:414:ILE:HD13	1.86	0.49
2:B:467:ARG:HD3	2:B:470:GLU:HA	1.95	0.49
2:B:913:LYS:HA	2:B:916:PHE:HD2	1.77	0.49
2:B:1041:ASN:ND2	2:B:1044:ASN:OD1	2.41	0.49
2:B:1110:ILE:CD1	2:B:1122:ARG:NH1	2.75	0.49
2:B:548:ILE:HG23	2:B:552:LEU:HD13	1.94	0.49
2:B:882:TYR:O	2:B:886:LEU:HG	2.12	0.49
2:B:951:ARG:NH2	2:B:1011:GLY:HA2	2.27	0.49
2:F:1105:PHE:CD1	2:F:1169:MET:HG3	2.47	0.49
3:G:2:DA:H2''	3:G:3:DA:OP1	2.10	0.49
2:B:1308:ASN:HD22	2:B:1327:PHE:CA	2.24	0.49
2:F:402:GLN:OE1	5:J:44:U:O2'	2.26	0.49
5:I:56:U:O2'	5:I:57:A:H5''	2.13	0.49
2:B:95:ASP:OD1	2:B:95:ASP:N	2.45	0.49
2:B:167:HIS:CE1	2:B:411:PRO:HA	2.47	0.49
2:B:369:GLN:OE1	2:B:400:ARG:NH1	2.46	0.49
2:B:704:PHE:O	2:B:708:ILE:HG12	2.13	0.49
2:B:988:TYR:HE2	2:B:1083:VAL:HG13	1.77	0.49
2:B:1094:ILE:HG21	2:B:1225:GLU:OE2	2.12	0.49
2:F:554:LYS:HB3	2:F:594:TYR:CE2	2.47	0.49
2:F:621:LEU:HD23	2:F:622:THR:H	1.76	0.49
2:F:737:ILE:O	2:F:741:VAL:HG23	2.13	0.49
2:B:321:MET:HE1	2:B:324:ARG:NH2	2.28	0.49
2:B:448:ILE:HD13	2:B:455:LEU:CD1	2.41	0.49
4:D:5:DA:H1'	4:D:6:DG:C8	2.47	0.49
2:F:167:HIS:CD2	2:F:169:LEU:HB2	2.47	0.49
2:F:1147:ALA:HB2	2:F:1190:VAL:HG22	1.95	0.49
5:J:49:A:H2'	5:J:50:U:O4'	2.13	0.49
2:B:270:THR:O	2:B:270:THR:OG1	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:U:O2'	2:F:111:LYS:NZ	2.45	0.49
2:F:143:VAL:HG22	2:F:422:ILE:HD13	1.95	0.49
2:F:691:ARG:HG2	2:F:695:GLN:NE2	2.27	0.49
2:F:746:GLU:OE2	2:F:1353:THR:OG1	2.24	0.49
2:B:956:ILE:HG12	2:B:1009:VAL:HG22	1.94	0.49
2:B:1005:GLU:O	2:B:1009:VAL:HB	2.12	0.49
2:B:1147:ALA:HB2	2:B:1190:VAL:CA	2.39	0.49
2:B:1308:ASN:ND2	2:B:1327:PHE:CA	2.75	0.49
2:B:1326:TYR:CD2	2:B:1327:PHE:N	2.73	0.49
2:F:165:ARG:C	2:F:415:HIS:CD2	2.84	0.49
2:F:491:PHE:O	2:F:494:ARG:HG2	2.13	0.49
2:F:902:LYS:NZ	2:F:912:ASP:OD1	2.46	0.49
2:F:1333:ARG:CZ	2:F:1335:ARG:HD2	2.43	0.49
2:B:369:GLN:HE22	2:B:400:ARG:NH1	2.10	0.49
2:B:909:SER:H	2:B:912:ASP:CB	2.26	0.49
2:B:1236:LEU:HD11	2:B:1269:ILE:HD13	1.95	0.49
2:F:90:MET:SD	2:F:151:LEU:CD2	3.01	0.49
2:F:140:LYS:NZ	2:F:144:ASP:OD2	2.46	0.49
2:F:153:LEU:HD23	2:F:153:LEU:C	2.38	0.49
2:F:258:LEU:CD2	2:F:260:GLU:H	2.25	0.49
2:F:821:ASP:OD1	2:F:858:THR:OG1	2.30	0.49
2:B:1041:ASN:O	2:B:1044:ASN:ND2	2.46	0.48
2:F:114:GLU:HG2	2:F:120:GLY:HA2	1.95	0.48
2:F:135:ILE:HG21	5:J:46:A:H5'	1.94	0.48
2:F:794:GLN:CD	2:F:794:GLN:H	2.21	0.48
2:F:915:GLY:O	2:F:919:ARG:HB2	2.13	0.48
2:B:814:TYR:HD1	2:B:815:TYR:HD1	1.60	0.48
2:F:32:PHE:HD1	2:F:45:LYS:HD3	1.77	0.48
2:F:816:LEU:HD22	2:F:891:LEU:O	2.14	0.48
2:F:1126:TRP:HB3	2:F:1131:TYR:CD2	2.48	0.48
2:B:309:ASN:OD1	2:B:311:GLU:HB2	2.13	0.48
2:B:925:ARG:HG2	2:B:927:ILE:HG22	1.96	0.48
2:B:1110:ILE:HD11	2:B:1122:ARG:NH1	2.28	0.48
2:B:1256:GLN:NE2	2:B:1256:GLN:O	2.46	0.48
2:B:1277:SER:HA	2:B:1281:ILE:CG1	2.35	0.48
2:F:143:VAL:HG23	2:F:422:ILE:CD1	2.37	0.48
2:F:601:ILE:HD11	2:F:607:LEU:HD11	1.95	0.48
2:B:1211:LYS:HB2	2:B:1224:ASN:HD21	1.77	0.48
2:F:870:VAL:HG12	2:F:871:PRO:HD2	1.95	0.48
5:J:82:G:N7	5:J:97:U:O2	2.46	0.48
5:J:96:C:H2'	5:J:97:U:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:237:LEU:HA	2:B:255:ASN:ND2	2.27	0.48
2:B:381:GLU:O	2:B:382:LYS:HD3	2.14	0.48
2:B:427:GLU:OE1	2:B:437:ARG:NH1	2.46	0.48
2:B:925:ARG:HB3	2:B:928:THR:CG2	2.43	0.48
4:D:6:DG:H2''	4:D:7:DG:H5''	1.95	0.48
2:F:58:THR:HG22	2:F:731:PRO:CG	2.43	0.48
2:F:836:TYR:CB	2:F:857:LEU:HD11	2.44	0.48
2:F:1056:GLU:O	2:F:1057:ILE:HD12	2.14	0.48
5:J:76:A:C5	5:J:77:A:H1'	2.49	0.48
2:B:565:LYS:HA	2:B:569:PHE:HB2	1.95	0.48
2:F:738:LEU:HA	2:F:738:LEU:HD23	1.54	0.48
2:F:1224:ASN:HB2	2:F:1280:VAL:HG11	1.94	0.48
2:B:934:ILE:O	2:B:938:ARG:HG3	2.14	0.48
2:F:140:LYS:NZ	2:F:313:THR:CB	2.67	0.48
2:F:163:LYS:HG2	2:F:164:PHE:CD1	2.49	0.48
2:F:671:ARG:HG2	2:F:676:GLY:O	2.14	0.48
2:F:853:ASP:HB3	2:F:895:ARG:HH11	1.78	0.48
2:B:18:TRP:HZ2	2:B:1353:THR:O	1.97	0.48
2:B:141:LYS:HD3	2:B:141:LYS:C	2.39	0.48
2:B:527:VAL:HG12	2:B:540:LEU:HD11	1.95	0.48
2:B:625:LEU:CD1	2:B:659:TRP:HZ2	2.27	0.48
2:B:1105:PHE:CD2	2:B:1169:MET:HG3	2.48	0.48
2:F:594:TYR:O	2:F:598:LEU:HB2	2.14	0.48
2:F:848:LYS:HE2	2:F:965:ASP:HB3	1.96	0.48
2:B:276:ASP:HA	2:B:279:LEU:HB3	1.95	0.48
2:B:1000:LYS:HZ3	2:B:1067:GLY:H	1.62	0.48
2:B:1111:LEU:HD23	2:B:1111:LEU:HA	1.50	0.48
2:B:1240:SER:HB2	2:B:1242:TYR:CD1	2.48	0.48
2:F:163:LYS:HG2	2:F:164:PHE:HE1	1.75	0.48
2:F:902:LYS:NZ	2:F:912:ASP:CG	2.72	0.48
2:F:1287:LEU:HD12	2:F:1287:LEU:O	2.13	0.48
2:B:325:TYR:CD1	5:I:44:U:C2	3.02	0.48
2:B:362:TYR:OH	2:B:401:LYS:HG3	2.14	0.48
2:F:140:LYS:HZ1	2:F:313:THR:HB	1.72	0.48
2:F:464:TRP:CD1	2:F:464:TRP:C	2.92	0.48
2:F:583:VAL:HG22	2:F:584:GLU:H	1.79	0.48
2:F:1251:ASP:O	2:F:1255:LYS:HG2	2.13	0.48
5:I:47:A:C6	5:I:48:A:C6	3.02	0.48
2:B:42:SER:O	2:B:43:ILE:HG13	2.13	0.47
2:B:167:HIS:HB2	2:B:169:LEU:HG	1.96	0.47
2:B:273:ASP:OD1	2:B:273:ASP:N	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:485:GLY:HA3	2:B:631:MET:SD	2.54	0.47
2:B:570:LYS:O	2:B:574:CYS:HA	2.13	0.47
2:F:921:LEU:HD21	2:F:1008:PHE:CE2	2.48	0.47
2:B:40:ARG:HH21	2:B:43:ILE:HG12	1.79	0.47
2:B:63:ARG:O	2:B:66:ARG:HB3	2.14	0.47
2:B:119:PHE:CD1	2:B:152:ARG:NH1	2.82	0.47
2:F:139:ARG:NH1	2:F:418:GLU:CD	2.60	0.47
2:F:1111:LEU:N	2:F:1133:GLY:O	2.40	0.47
1:A:31:U:C2	1:A:32:A:C8	3.02	0.47
2:B:270:THR:O	2:B:274:ASP:HB2	2.14	0.47
2:B:958:LEU:HD22	2:B:962:LEU:HD12	1.97	0.47
2:B:973:TYR:CE1	2:B:1238:LEU:HD21	2.49	0.47
2:F:246:LEU:CD2	2:F:248:LEU:HD12	2.44	0.47
2:F:325:TYR:O	2:F:328:HIS:HB3	2.13	0.47
2:B:325:TYR:HD1	5:I:44:U:C2	2.32	0.47
4:D:3:DT:H1'	4:D:4:DT:H5'	1.97	0.47
2:F:253:LYS:HA	2:F:256:PHE:CD2	2.49	0.47
2:F:279:LEU:CD2	2:F:287:ALA:HB2	2.43	0.47
2:F:531:THR:HG22	2:F:534:MET:HG2	1.97	0.47
5:I:92:G:H2'	5:I:93:G:C8	2.49	0.47
1:A:16:A:H4'	2:B:448:ILE:O	2.14	0.47
2:B:1158:LYS:HB2	2:B:1158:LYS:HE3	1.47	0.47
2:B:1204:PHE:CG	2:B:1342:VAL:HG13	2.49	0.47
2:B:1207:GLU:CD	2:B:1210:ARG:HH11	2.22	0.47
2:F:143:VAL:HG21	2:F:315:ALA:CB	2.43	0.47
2:F:527:VAL:HA	2:F:582:GLY:CA	2.35	0.47
2:F:730:SER:HB2	2:F:733:ILE:H	1.80	0.47
2:F:1101:GLN:O	2:F:1168:ILE:HD11	2.15	0.47
2:F:1312:LEU:O	2:F:1314:THR:N	2.47	0.47
1:A:11:U:C2	1:A:12:A:C8	3.02	0.47
2:B:212:LEU:O	2:B:221:ARG:HD2	2.14	0.47
2:B:338:LEU:O	2:B:383:MET:CE	2.62	0.47
2:F:32:PHE:CZ	2:F:1355:LEU:HB3	2.50	0.47
2:F:97:PHE:CE2	2:F:152:ARG:HA	2.50	0.47
2:F:499:ASP:CB	2:F:663:SER:HB3	2.43	0.47
2:F:939:MET:HE3	2:F:953:VAL:HG21	1.95	0.47
2:F:1150:GLU:HB3	2:F:1155:LYS:HA	1.97	0.47
4:H:11:DT:H2''	4:H:12:DG:H8	1.78	0.47
2:B:197:GLU:N	2:B:197:GLU:OE1	2.47	0.47
2:B:242:ILE:O	2:B:246:LEU:HG	2.14	0.47
2:B:252:PHE:CE1	2:B:290:PHE:CE2	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:451:TYR:HE1	2:B:484:LYS:HG2	1.80	0.47
2:B:466:THR:OG1	2:B:483:ASP:HB3	2.14	0.47
2:B:870:VAL:HG21	2:B:908:LEU:H	1.80	0.47
2:B:1213:MET:CE	2:B:1318:LEU:HD21	2.44	0.47
2:B:1295:ASN:HA	2:B:1298:ARG:HH11	1.80	0.47
1:E:27:G:H5'	1:E:28:A:C5'	2.45	0.47
2:F:150:ASP:O	2:F:154:ILE:HD12	2.15	0.47
2:F:351:PHE:CD1	5:J:43:G:O6	2.68	0.47
2:F:404:THR:HG22	2:F:405:PHE:H	1.79	0.47
2:F:622:THR:HG21	2:F:635:ARG:CB	2.44	0.47
2:F:737:ILE:HA	2:F:740:THR:HG22	1.97	0.47
2:F:921:LEU:CD2	2:F:1042:ILE:HD11	2.44	0.47
2:F:1216:SER:HB3	2:F:1219:GLU:H	1.78	0.47
2:F:1345:ALA:O	2:F:1362:LEU:HD12	2.14	0.47
5:J:43:G:H3'	5:J:44:U:H6	1.80	0.47
1:A:31:U:N3	1:A:32:A:N7	2.62	0.47
2:B:530:VAL:CG2	2:B:537:PRO:HB3	2.45	0.47
2:B:625:LEU:HD12	2:B:625:LEU:HA	1.60	0.47
2:B:840:ALA:HA	2:B:854:ASN:O	2.14	0.47
2:B:1226:LEU:HD13	2:B:1276:PHE:CG	2.49	0.47
2:F:908:LEU:HA	2:F:908:LEU:HD23	1.61	0.47
2:B:869:ASN:OD1	2:B:870:VAL:N	2.48	0.47
2:B:1208:ASN:O	2:B:1208:ASN:CG	2.57	0.47
1:E:15:G:P	2:F:66:ARG:HH12	2.38	0.47
2:F:135:ILE:CG2	5:J:46:A:H5'	2.45	0.47
2:F:509:PRO:HB3	2:F:624:THR:HG21	1.97	0.47
2:F:526:LYS:HD3	2:F:526:LYS:HA	1.38	0.47
2:F:1222:LYS:NZ	2:F:1314:THR:O	2.48	0.47
1:A:26:A:C6	5:I:46:A:C2	3.04	0.47
2:B:22:THR:HG22	2:B:23:ASP:N	2.30	0.47
2:B:133:PRO:HD2	2:B:137:HIS:CG	2.50	0.47
2:B:334:LEU:HD12	2:B:338:LEU:HG	1.96	0.47
2:B:380:LEU:O	2:B:386:THR:CB	2.54	0.47
2:B:1000:LYS:NZ	2:B:1067:GLY:H	2.13	0.47
2:B:1241:HIS:HE1	2:B:1244:LYS:HA	1.76	0.47
2:B:1256:GLN:HE22	2:B:1260:GLU:HG2	1.79	0.47
1:E:4:A:N1	3:G:25:DT:O4	2.48	0.47
2:F:58:THR:HG22	2:F:731:PRO:HG3	1.96	0.47
2:F:422:ILE:O	2:F:425:ARG:HG2	2.16	0.47
2:F:780:ARG:HD2	2:F:812:TYR:HE2	1.77	0.47
2:F:1001:TYR:CE2	2:F:1045:PHE:CD1	2.99	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1001:TYR:HB3	2:F:1004:LEU:HD12	1.97	0.47
2:F:1207:GLU:HG3	2:F:1208:ASN:N	2.29	0.47
2:F:1294:TYR:HE1	2:F:1305:GLN:HE21	1.61	0.47
1:A:19:A:H61	3:C:10:DT:H3	1.63	0.46
2:B:114:GLU:CG	2:B:120:GLY:O	2.63	0.46
2:B:472:THR:HG23	5:I:59:U:OP2	2.15	0.46
2:B:864:ARG:HB2	2:B:871:PRO:HA	1.97	0.46
2:F:262:ALA:C	2:F:278:LEU:HD21	2.40	0.46
2:B:51:LEU:HA	2:B:1095:VAL:HG23	1.97	0.46
2:B:909:SER:O	2:B:913:LYS:N	2.29	0.46
2:B:1241:HIS:ND1	2:B:1244:LYS:HA	2.30	0.46
2:F:253:LYS:HE3	2:F:261:ASP:HB3	1.97	0.46
2:F:531:THR:HB	2:F:578:VAL:HG23	1.98	0.46
2:B:32:PHE:CE1	2:B:1355:LEU:HD22	2.51	0.46
2:B:398:LEU:HG	2:B:399:LEU:HG	1.97	0.46
2:B:558:LYS:HE2	2:B:587:PHE:O	2.15	0.46
2:B:694:MET:HG3	2:B:698:HIS:CD2	2.50	0.46
2:B:739:GLN:NE2	5:I:67:C:OP1	2.49	0.46
2:F:40:ARG:CD	2:F:43:ILE:HD11	2.45	0.46
2:F:628:ASP:O	2:F:632:ILE:HG13	2.16	0.46
2:F:719:SER:HB3	2:F:722:GLU:OE2	2.14	0.46
2:F:1089:MET:HA	2:F:1090:PRO:HD3	1.76	0.46
2:F:1198:LEU:HA	2:F:1198:LEU:HD23	1.63	0.46
2:F:1258:PHE:O	2:F:1258:PHE:HD1	1.98	0.46
2:B:139:ARG:NH2	2:B:161:MET:HG2	2.30	0.46
2:B:217:SER:O	2:B:221:ARG:HG3	2.15	0.46
2:B:478:PHE:CZ	2:B:482:VAL:HG11	2.49	0.46
2:B:1204:PHE:HE1	2:B:1347:LEU:HB2	1.81	0.46
2:B:1226:LEU:HB2	2:B:1276:PHE:CD2	2.49	0.46
2:F:8:GLY:O	2:F:987:ALA:HB1	2.15	0.46
2:F:623:LEU:HD12	2:F:623:LEU:O	2.14	0.46
2:F:791:LEU:HD12	2:F:791:LEU:HA	1.71	0.46
2:F:894:GLN:HE22	2:F:898:ASP:CG	2.24	0.46
2:F:1042:ILE:HG23	2:F:1043:MET:HE2	1.97	0.46
2:F:1100:VAL:N	5:J:67:C:H42	2.13	0.46
2:B:395:ARG:O	2:B:396:GLU:HB2	2.16	0.46
2:B:866:LYS:HE2	2:B:866:LYS:HB2	1.56	0.46
2:B:1135:ASP:OD1	2:B:1136:SER:N	2.48	0.46
2:B:1260:GLU:HA	2:B:1260:GLU:OE2	2.16	0.46
1:E:18:A:OP2	2:F:71:ARG:HD2	2.16	0.46
2:F:237:LEU:HD12	2:F:238:PHE:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:324:ARG:O	2:F:327:GLU:HB2	2.15	0.46
2:F:406:ASP:N	2:F:406:ASP:OD1	2.41	0.46
2:F:632:ILE:O	2:F:636:LEU:HD13	2.15	0.46
2:F:653:ARG:H	2:F:653:ARG:HG2	1.48	0.46
2:F:967:ARG:NH2	2:F:974:LYS:HB2	2.31	0.46
2:B:127:ALA:O	2:B:130:GLU:HB2	2.16	0.46
2:B:269:ASP:OD1	2:B:270:THR:N	2.49	0.46
2:B:623:LEU:HG	2:B:654:ARG:O	2.15	0.46
2:B:646:LYS:HA	2:B:649:LYS:HG3	1.96	0.46
2:B:1204:PHE:CE2	2:B:1342:VAL:HG11	2.50	0.46
2:B:1206:LEU:HG	2:B:1207:GLU:HG2	1.97	0.46
3:C:19:DA:H2''	3:C:20:DA:O4'	2.15	0.46
1:E:23:U:C5'	2:F:1112:PRO:HG3	2.32	0.46
2:F:1019:ARG:O	2:F:1021:MET:N	2.48	0.46
2:F:1046:PHE:C	2:F:1076:LYS:HZ2	2.24	0.46
2:F:1203:LEU:HD23	2:F:1348:ILE:HB	1.98	0.46
2:B:27:VAL:HG21	2:B:48:ILE:HB	1.96	0.46
2:B:74:ARG:HH21	5:I:60:C:P	2.38	0.46
2:B:336:LYS:HG2	2:B:347:TYR:HE2	1.81	0.46
2:B:410:ILE:HG21	2:B:414:ILE:HD11	1.89	0.46
2:B:838:VAL:HG11	2:B:855:LYS:HE3	1.96	0.46
2:B:978:ILE:CD1	2:B:1233:VAL:HG22	2.38	0.46
2:F:174:LEU:HD23	2:F:413:GLN:CB	2.46	0.46
2:F:465:MET:SD	2:F:482:VAL:HG11	2.56	0.46
2:F:1042:ILE:O	2:F:1045:PHE:CE1	2.68	0.46
2:F:1272:GLN:NE2	5:J:89:G:H1	2.14	0.46
2:B:111:LYS:HD3	2:B:115:ARG:HA	1.98	0.46
2:B:808:ASN:HD22	2:B:1244:LYS:HE3	1.81	0.46
2:B:1141:TYR:CD1	2:B:1141:TYR:C	2.94	0.46
3:C:12:DA:OP1	3:C:12:DA:H4'	2.16	0.46
2:F:272:ASP:HA	2:F:275:LEU:CB	2.44	0.46
2:F:380:LEU:CD1	2:F:390:LEU:HG	2.38	0.46
2:F:918:LYS:HD3	2:F:918:LYS:HA	1.74	0.46
2:F:967:ARG:HH12	2:F:974:LYS:HE3	1.80	0.46
2:F:1019:ARG:C	2:F:1021:MET:H	2.24	0.46
2:B:83:GLN:O	2:B:87:SER:N	2.49	0.46
2:B:282:ILE:HG22	2:B:286:TYR:CE1	2.50	0.46
2:B:340:ARG:NH2	5:I:41:A:OP2	2.48	0.46
2:B:880:LYS:HE2	2:B:904:GLU:OE2	2.16	0.46
2:B:954:LYS:HB2	2:B:954:LYS:HE3	1.53	0.46
2:B:1202:SER:O	2:B:1213:MET:HA	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:212:LEU:HD13	2:F:300:ILE:HD11	1.98	0.46
2:F:352:PHE:CE1	5:J:42:A:N6	2.84	0.46
2:F:601:ILE:CD1	2:F:607:LEU:HD21	2.46	0.46
2:F:813:LEU:HB3	2:F:857:LEU:HB3	1.96	0.46
2:F:892:ILE:HB	2:F:896:LYS:NZ	2.30	0.46
2:F:1120:ILE:CD1	2:F:1134:PHE:HB2	2.45	0.46
2:F:1212:ARG:CZ	2:F:1336:TYR:HE2	2.29	0.46
2:B:68:ALA:O	2:B:69:ARG:C	2.57	0.46
2:B:142:LEU:HD12	2:B:157:ALA:HB2	1.98	0.46
2:B:279:LEU:HD21	2:B:287:ALA:HB2	1.96	0.46
2:B:281:GLN:OE1	2:B:281:GLN:N	2.31	0.46
2:B:455:LEU:HD12	2:B:455:LEU:N	2.31	0.46
2:B:1062:LEU:O	2:B:1075:ASP:HA	2.15	0.46
2:B:1211:LYS:CB	2:B:1224:ASN:HD21	2.28	0.46
2:B:1245:LEU:CB	2:B:1252:ASN:ND2	2.71	0.46
2:F:74:ARG:NE	5:J:60:C:OP2	2.39	0.46
2:F:93:VAL:CG2	2:F:151:LEU:HD22	2.46	0.46
2:F:134:THR:O	2:F:137:HIS:HB2	2.16	0.46
2:F:672:ASP:OD2	2:F:675:SER:OG	2.25	0.46
2:F:1084:ARG:CZ	2:F:1084:ARG:CB	2.94	0.46
2:F:1167:THR:OG1	2:F:1168:ILE:N	2.49	0.46
2:B:203:ALA:O	2:B:206:VAL:HG22	2.17	0.45
2:F:97:PHE:CE1	2:F:101:LEU:HD11	2.51	0.45
2:F:246:LEU:HD22	2:F:248:LEU:HD12	1.98	0.45
2:F:253:LYS:HB2	2:F:262:ALA:N	2.27	0.45
2:F:554:LYS:HD3	2:F:594:TYR:CZ	2.52	0.45
2:F:632:ILE:HG22	2:F:636:LEU:CD1	2.46	0.45
2:F:682:PHE:O	2:F:686:ASP:OD2	2.34	0.45
2:F:886:LEU:HD22	2:F:891:LEU:HD11	1.97	0.45
4:H:12:DG:H2'	4:H:12:DG:OP2	2.15	0.45
2:B:114:GLU:HG3	2:B:116:HIS:N	2.27	0.45
2:B:1313:PHE:O	2:B:1317:ASN:N	2.48	0.45
2:B:1333:ARG:NH2	2:B:1335:ARG:HH11	2.14	0.45
2:F:527:VAL:HG22	2:F:582:GLY:HA3	1.98	0.45
2:F:846:PHE:O	2:F:1040:SER:C	2.59	0.45
2:F:1044:ASN:O	2:F:1047:LYS:N	2.43	0.45
2:F:1111:LEU:HD23	2:F:1111:LEU:HA	1.63	0.45
2:F:1236:LEU:HD11	2:F:1269:ILE:HD13	1.98	0.45
5:J:91:C:H6	5:J:91:C:H2'	1.34	0.45
2:B:743:VAL:O	2:B:747:LEU:HD23	2.16	0.45
2:B:820:ARG:HA	2:B:826:GLN:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:839:ASP:N	2:B:856:VAL:O	2.28	0.45
2:F:148:LYS:HA	2:F:429:PHE:CD2	2.51	0.45
2:F:737:ILE:O	2:F:740:THR:HG22	2.16	0.45
2:F:933:GLN:CG	2:F:1010:TYR:OH	2.57	0.45
2:F:1300:LYS:NZ	2:F:1304:GLU:OE1	2.49	0.45
2:B:265:GLN:HG2	2:B:267:SER:H	1.81	0.45
2:B:359:TYR:CE2	2:B:363:ILE:HG13	2.52	0.45
2:B:1145:VAL:HG11	2:B:1187:TYR:CE2	2.51	0.45
2:F:600:ILE:HG23	2:F:650:GLN:HB2	1.99	0.45
2:B:24:GLU:OE1	2:B:24:GLU:HA	2.16	0.45
2:B:137:HIS:HE1	2:B:325:TYR:CD2	2.33	0.45
2:B:1041:ASN:ND2	2:B:1044:ASN:CG	2.75	0.45
2:F:377:LYS:N	2:F:378:PRO:HD2	2.32	0.45
2:F:495:MET:O	3:G:17:DT:H2'	2.17	0.45
2:F:760:VAL:HG13	2:F:956:ILE:HB	1.98	0.45
5:J:46:A:C2	5:J:47:A:C5	3.05	0.45
2:B:642:LEU:HB2	2:B:643:PHE:CD2	2.51	0.45
2:B:930:HIS:O	2:B:934:ILE:HG13	2.16	0.45
2:B:1043:MET:HB2	2:B:1043:MET:HE3	1.62	0.45
2:B:1163:LEU:HD23	2:B:1163:LEU:HA	1.69	0.45
2:F:43:ILE:HD12	2:F:43:ILE:HG23	1.64	0.45
2:F:211:ILE:HG13	2:F:224:ASN:HB3	1.97	0.45
3:G:24:DG:C3'	3:G:25:DT:H4'	2.47	0.45
2:B:128:TYR:CD1	2:B:132:TYR:HD2	2.35	0.45
2:B:178:ASN:HD22	2:B:298:ASP:HB2	1.82	0.45
2:B:390:LEU:HD23	2:B:393:LEU:HB3	1.98	0.45
2:B:593:THR:O	2:B:594:TYR:C	2.59	0.45
2:F:118:ILE:HD13	2:F:125:GLU:OE2	2.17	0.45
2:F:332:LEU:HD13	2:F:359:TYR:CE1	2.52	0.45
2:F:844:GLN:OE1	2:F:848:LYS:HD2	2.16	0.45
2:B:513:LEU:HD23	2:B:513:LEU:HA	1.77	0.45
2:B:794:GLN:HG2	2:B:798:GLU:HG3	1.99	0.45
2:B:1280:VAL:HG12	2:B:1281:ILE:HD13	1.98	0.45
2:F:401:LYS:HB3	5:J:45:U:OP1	2.17	0.45
2:F:684:LYS:HB2	2:F:684:LYS:HE3	1.32	0.45
2:F:971:GLN:HG2	2:F:973:TYR:HE2	1.82	0.45
2:F:1105:PHE:CG	2:F:1169:MET:HG3	2.51	0.45
2:F:1126:TRP:N	2:F:1126:TRP:CD1	2.85	0.45
5:I:48:A:H2'	5:I:49:A:C8	2.51	0.45
2:B:32:PHE:CZ	2:B:1355:LEU:HD13	2.52	0.45
2:B:233:LYS:O	2:B:236:GLY:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:357:ASN:O	2:B:375:PHE:CD2	2.70	0.45
2:B:509:PRO:HG3	2:B:621:LEU:HD12	1.99	0.45
2:B:760:VAL:HG11	2:B:958:LEU:HD12	1.98	0.45
2:F:119:PHE:HE1	2:F:150:ASP:OD2	2.00	0.45
2:F:128:TYR:CD1	2:F:132:TYR:HD2	2.34	0.45
2:F:821:ASP:OD1	2:F:822:MET:N	2.50	0.45
2:F:842:VAL:CG1	2:F:854:ASN:HD21	2.29	0.45
2:F:911:LEU:H	2:F:911:LEU:HD12	1.82	0.45
2:F:949:LEU:HD23	2:F:951:ARG:NH2	2.31	0.45
2:F:1135:ASP:OD1	4:H:8:DT:H5"	2.17	0.45
2:F:1347:LEU:HD22	2:F:1349:HIS:CD2	2.51	0.45
3:G:19:DA:C2'	3:G:20:DA:C8	2.99	0.45
1:A:15:G:OP1	2:B:70:ARG:NH1	2.44	0.45
1:A:29:G:N3	5:I:41:A:C2	2.84	0.45
2:B:1274:SER:O	2:B:1278:LYS:HG3	2.17	0.45
2:F:306:LEU:HD21	2:F:414:ILE:HD12	1.98	0.45
2:F:1256:GLN:HE21	2:F:1260:GLU:CD	2.25	0.45
2:B:215:ARG:NE	2:B:215:ARG:O	2.50	0.44
2:B:597:LEU:O	2:B:601:ILE:HG12	2.17	0.44
2:B:651:LEU:HA	2:B:651:LEU:HD23	1.73	0.44
2:B:724:ILE:O	2:B:727:LEU:HB2	2.17	0.44
2:B:737:ILE:O	2:B:738:LEU:C	2.59	0.44
2:B:970:PHE:CE2	2:B:1047:LYS:HD3	2.51	0.44
2:F:390:LEU:HD23	2:F:390:LEU:HA	1.83	0.44
2:F:592:GLY:O	2:F:596:ASP:OD1	2.35	0.44
2:F:640:ALA:HA	2:F:648:MET:CE	2.44	0.44
2:B:229:LEU:O	2:B:231:GLY:N	2.51	0.44
2:B:1315:LEU:HD13	2:B:1324:PHE:CZ	2.51	0.44
2:F:693:PHE:HA	2:F:696:LEU:HD12	1.98	0.44
2:F:742:LYS:HE2	2:F:742:LYS:HB3	1.63	0.44
2:B:710:LYS:HZ1	2:F:480:GLU:HB3	1.82	0.44
2:B:721:HIS:O	2:B:725:ALA:N	2.32	0.44
2:F:138:LEU:CD2	2:F:153:LEU:HD21	2.34	0.44
2:F:917:ILE:HA	2:F:917:ILE:HD13	1.70	0.44
2:B:377:LYS:N	2:B:378:PRO:HD2	2.33	0.44
2:B:1207:GLU:HG2	2:B:1210:ARG:NH1	2.32	0.44
2:F:616:LEU:O	2:F:619:ILE:HG22	2.18	0.44
2:F:893:THR:HG23	2:F:896:LYS:CB	2.46	0.44
2:F:1219:GLU:OE2	2:F:1335:ARG:HB3	2.18	0.44
1:A:27:G:N2	5:I:44:U:OP2	2.51	0.44
2:B:161:MET:SD	2:B:419:LEU:HB2	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:528:LYS:HD2	2:B:539:PHE:CE1	2.53	0.44
2:B:973:TYR:HD1	2:B:1237:TYR:CE1	2.35	0.44
2:F:677:LYS:HE2	2:F:681:ASP:HB3	2.00	0.44
2:F:791:LEU:HD23	2:F:818:ASN:OD1	2.18	0.44
2:F:883:TRP:HB3	2:F:897:PHE:HD1	1.82	0.44
2:F:1228:LEU:HD12	2:F:1228:LEU:HA	1.82	0.44
5:I:58:G:C2	5:I:60:C:O2	2.71	0.44
2:B:155:TYR:HD2	2:B:156:LEU:HD23	1.83	0.44
2:B:1110:ILE:HD13	2:B:1134:PHE:CE1	2.53	0.44
2:F:177:ASP:OD1	2:F:177:ASP:N	2.50	0.44
2:F:1215:ALA:O	4:H:6:DG:H5''	2.18	0.44
2:F:1218:GLY:CA	2:F:1339:THR:HG23	2.48	0.44
5:I:76:A:H2'	5:I:77:A:O4'	2.17	0.44
2:B:1201:TYR:N	2:B:1201:TYR:CD1	2.86	0.44
2:F:546:LYS:HE3	2:F:546:LYS:HB3	1.81	0.44
2:F:760:VAL:CG2	2:F:956:ILE:HD12	2.35	0.44
2:F:794:GLN:HE21	2:F:798:GLU:CD	2.25	0.44
2:F:1123:LYS:HG3	2:F:1124:LYS:H	1.82	0.44
2:B:528:LYS:HG2	2:B:539:PHE:CD1	2.53	0.44
2:B:530:VAL:HG22	2:B:537:PRO:HB3	1.98	0.44
2:B:989:LEU:O	2:B:993:VAL:HG23	2.18	0.44
4:D:2:DT:H6	4:D:2:DT:H2'	1.56	0.44
2:F:835:ASP:OD1	2:F:835:ASP:N	2.51	0.44
2:F:1163:LEU:HD12	2:F:1339:THR:HB	1.99	0.44
2:F:1210:ARG:HG3	2:F:1280:VAL:HA	2.00	0.44
2:F:1218:GLY:HA2	2:F:1339:THR:HG21	2.00	0.44
5:I:37:U:C2	5:I:38:A:C8	3.05	0.44
2:B:13:THR:O	2:B:53:PHE:HE1	2.00	0.44
2:B:185:PHE:HE1	2:B:242:ILE:HD11	1.82	0.44
2:B:784:ILE:HD13	2:B:815:TYR:CB	2.47	0.44
2:B:810:LYS:O	2:B:833:LEU:HD13	2.18	0.44
2:F:1161:LYS:HZ2	2:F:1364:GLN:HG2	1.83	0.44
5:I:40:C:H2'	5:I:41:A:C8	2.52	0.44
1:A:26:A:O3'	2:B:116:HIS:CD2	2.71	0.43
2:B:265:GLN:HG2	2:B:266:LEU:N	2.32	0.43
2:B:472:THR:HG23	5:I:59:U:P	2.58	0.43
2:B:601:ILE:HA	2:B:647:VAL:HG13	2.00	0.43
2:B:607:LEU:HD23	2:B:607:LEU:HA	1.72	0.43
2:B:1336:TYR:N	2:B:1336:TYR:CD1	2.84	0.43
2:F:114:GLU:CD	2:F:116:HIS:H	2.22	0.43
2:F:514:LEU:H	2:F:514:LEU:HD12	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:46:A:C2	5:J:47:A:C6	3.06	0.43
2:B:346:LYS:O	2:B:350:ILE:HG13	2.18	0.43
2:B:478:PHE:CE2	2:B:482:VAL:HG11	2.53	0.43
2:B:1089:MET:HA	2:B:1090:PRO:HD3	1.70	0.43
2:F:285:GLN:OE1	2:F:285:GLN:N	2.51	0.43
5:J:84:A:C2	5:J:85:C:C2	3.06	0.43
2:B:195:LEU:HB3	2:B:196:PHE:HD1	1.82	0.43
2:B:524:LEU:CD1	2:B:587:PHE:CE2	2.99	0.43
2:B:980:ASN:HB2	2:B:1225:GLU:OE2	2.18	0.43
1:E:16:A:OP1	2:F:454:PRO:HG3	2.18	0.43
2:F:82:LEU:HD23	2:F:82:LEU:HA	1.79	0.43
2:F:119:PHE:CD2	2:F:124:ASP:HB3	2.53	0.43
2:F:332:LEU:HD11	2:F:336:LYS:HE3	2.01	0.43
2:F:425:ARG:HG3	2:F:426:GLN:N	2.33	0.43
2:F:779:GLU:O	2:F:783:ARG:HD3	2.18	0.43
2:F:918:LYS:HE3	2:F:1018:VAL:HG11	1.99	0.43
2:F:1039:TYR:CD1	2:F:1039:TYR:N	2.87	0.43
2:F:1120:ILE:HD11	2:F:1135:ASP:N	2.32	0.43
2:F:1124:LYS:N	5:J:53:G:OP1	2.41	0.43
2:F:1147:ALA:CB	2:F:1190:VAL:HG22	2.48	0.43
2:F:1245:LEU:HD23	2:F:1245:LEU:HA	1.81	0.43
5:I:75:A:C2	5:I:76:A:C4	3.06	0.43
2:B:142:LEU:HD23	2:B:142:LEU:HA	1.74	0.43
2:B:201:ILE:HG22	2:B:202:ASN:N	2.33	0.43
2:B:565:LYS:HE2	2:B:580:ILE:HG12	2.00	0.43
2:B:781:MET:HG3	2:B:803:ASN:CG	2.43	0.43
2:B:813:LEU:HD11	2:B:855:LYS:HB3	1.99	0.43
2:B:1229:PRO:HB2	2:B:1232:TYR:CD2	2.52	0.43
2:F:121:ASN:HB2	2:F:123:VAL:HG12	2.00	0.43
2:F:351:PHE:HD1	5:J:43:G:O6	2.00	0.43
2:F:1255:LYS:N	2:F:1255:LYS:HE2	2.34	0.43
2:B:69:ARG:HD3	5:I:62:G:C5	2.53	0.43
2:B:119:PHE:CD2	2:B:124:ASP:HB3	2.54	0.43
2:B:682:PHE:CB	2:B:696:LEU:HD11	2.48	0.43
2:B:1035:LYS:HD3	2:B:1035:LYS:HA	1.60	0.43
2:F:4:LYS:HE2	2:F:4:LYS:HB2	1.71	0.43
2:F:31:LYS:HD2	5:J:83:C:H41	1.83	0.43
2:F:137:HIS:CD2	2:F:322:ILE:CG1	2.79	0.43
2:F:243:ALA:HB3	2:F:250:PRO:HG3	2.01	0.43
2:F:473:ILE:HG13	5:J:59:U:OP1	2.18	0.43
2:F:508:LEU:HD11	2:F:664:ARG:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:848:LYS:CE	2:F:965:ASP:HB3	2.48	0.43
2:F:942:LYS:HE3	2:F:952:GLU:CD	2.43	0.43
2:F:1060:ARG:HH22	2:F:1064:GLU:HB2	1.83	0.43
2:B:369:GLN:NE2	2:B:405:PHE:CZ	2.79	0.43
2:F:137:HIS:HA	2:F:322:ILE:HG12	2.01	0.43
2:F:601:ILE:HD11	2:F:607:LEU:HD21	2.01	0.43
2:F:1113:LYS:HB2	2:F:1129:LYS:O	2.19	0.43
2:F:1197:LYS:O	2:F:1199:PRO:HD3	2.19	0.43
1:A:2:U:H3	1:A:4:A:H3'	1.83	0.43
2:B:967:ARG:HH11	2:B:989:LEU:HD12	1.83	0.43
2:B:1294:TYR:HE1	2:B:1305:GLN:HE21	1.65	0.43
2:F:140:LYS:HZ2	2:F:313:THR:CB	2.18	0.43
2:F:174:LEU:HA	2:F:174:LEU:HD13	1.79	0.43
2:F:795:ILE:HA	2:F:798:GLU:OE1	2.19	0.43
5:I:47:A:H2'	5:I:48:A:C8	2.54	0.43
5:I:87:G:N2	5:I:92:G:C5	2.86	0.43
2:B:90:MET:HE3	2:B:97:PHE:CD2	2.54	0.43
2:B:226:ILE:HA	2:B:229:LEU:HG	2.01	0.43
2:B:1114:ARG:NH1	4:D:9:DA:OP1	2.51	0.43
2:F:233:LYS:HG2	2:F:236:GLY:H	1.84	0.43
2:F:531:THR:HG21	2:F:575:PHE:HE1	1.75	0.43
2:F:553:PHE:CD2	2:F:559:VAL:HG21	2.53	0.43
2:F:662:LEU:HD22	2:F:666:LEU:HD21	2.01	0.43
2:F:970:PHE:CD1	2:F:1080:PHE:CZ	3.07	0.43
2:F:1052:LEU:C	2:F:1054:ASN:H	2.26	0.43
5:J:70:C:H2'	5:J:71:U:H6	1.84	0.43
2:B:139:ARG:CD	2:B:161:MET:HE2	2.44	0.43
2:B:253:LYS:O	2:B:257:ASP:N	2.51	0.43
2:B:917:ILE:HG12	2:B:1042:ILE:HB	2.00	0.43
2:B:986:ASP:O	2:B:990:ASN:N	2.45	0.43
2:B:1003:LYS:CG	2:B:1036:TYR:CE2	2.95	0.43
2:B:1110:ILE:HD12	2:B:1122:ARG:HD2	2.01	0.43
2:B:1191:LYS:HD2	2:B:1194:LEU:HD12	2.00	0.43
2:F:621:LEU:HD23	2:F:622:THR:N	2.33	0.43
2:F:844:GLN:HG2	2:F:848:LYS:HA	2.00	0.43
2:F:847:LEU:N	2:F:847:LEU:HD23	2.33	0.43
3:G:4:DT:H2''	3:G:5:DA:H5'	2.01	0.43
1:A:4:A:H2'	1:A:5:C:C6	2.54	0.43
2:B:501:ASN:HB2	2:B:666:LEU:CD1	2.49	0.43
2:B:870:VAL:HG13	2:B:871:PRO:HD2	2.01	0.43
2:B:1041:ASN:HD22	2:B:1044:ASN:ND2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:21:G:H2'	1:E:22:U:O4'	2.18	0.43
2:F:226:ILE:HA	2:F:226:ILE:HD13	1.55	0.43
2:F:465:MET:SD	2:F:482:VAL:HG21	2.59	0.43
2:F:619:ILE:HD13	2:F:619:ILE:HG21	1.79	0.43
2:F:675:SER:HB3	2:F:682:PHE:CZ	2.54	0.43
2:F:1182:LEU:HD12	2:F:1183:GLU:N	2.34	0.43
2:B:103:GLU:OE2	2:B:111:LYS:HG2	2.19	0.42
2:B:332:LEU:HD11	2:B:336:LYS:HE2	2.01	0.42
2:B:369:GLN:HE22	2:B:400:ARG:HH12	1.65	0.42
2:B:1333:ARG:CZ	2:B:1335:ARG:HD2	2.48	0.42
2:F:134:THR:HG22	5:J:45:U:C4'	2.48	0.42
2:F:401:LYS:HD3	5:J:45:U:OP2	2.19	0.42
2:F:404:THR:HG22	2:F:405:PHE:N	2.33	0.42
2:F:1041:ASN:C	2:F:1043:MET:H	2.26	0.42
2:F:1056:GLU:C	2:F:1057:ILE:HD12	2.44	0.42
2:F:1062:LEU:HD12	2:F:1076:LYS:HB2	2.00	0.42
2:B:27:VAL:HA	2:B:28:PRO:HD3	1.89	0.42
2:F:136:TYR:CZ	2:F:160:HIS:NE2	2.83	0.42
2:F:332:LEU:HD11	2:F:336:LYS:CE	2.49	0.42
2:F:535:ARG:HG3	2:F:535:ARG:NH1	2.34	0.42
2:F:1207:GLU:HG3	2:F:1208:ASN:H	1.85	0.42
2:F:1312:LEU:O	2:F:1313:PHE:C	2.62	0.42
5:I:42:A:C8	5:I:42:A:H3'	2.54	0.42
1:A:16:A:OP1	2:B:454:PRO:HG3	2.19	0.42
2:B:168:PHE:HA	2:B:412:HIS:HD2	1.84	0.42
2:B:475:PRO:HG3	5:I:59:U:O4	2.19	0.42
2:B:516:GLU:HA	2:B:519:THR:HG22	2.01	0.42
2:B:633:GLU:CD	2:B:652:LYS:HE3	2.44	0.42
2:B:810:LYS:C	2:B:833:LEU:HD13	2.44	0.42
2:B:814:TYR:CE2	2:B:819:GLY:HA2	2.54	0.42
2:B:1169:MET:HE3	5:I:52:A:N3	2.35	0.42
2:F:373:TYR:CE1	2:F:398:LEU:HB3	2.53	0.42
2:F:684:LYS:O	2:F:685:SER:C	2.61	0.42
2:B:35:LEU:HD12	2:B:1358:THR:HG22	2.02	0.42
2:B:339:VAL:HA	2:B:383:MET:HE1	2.01	0.42
2:B:439:LYS:O	2:B:476:TRP:NE1	2.52	0.42
2:B:464:TRP:CD1	2:B:464:TRP:C	2.97	0.42
2:B:518:PHE:CG	2:B:667:ILE:HD13	2.54	0.42
2:B:734:LYS:O	2:B:737:ILE:HB	2.20	0.42
2:F:226:ILE:O	2:F:230:PRO:HA	2.19	0.42
2:F:359:TYR:CE2	2:F:363:ILE:CG1	3.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:370:GLU:OE2	2:F:374:LYS:NZ	2.50	0.42
2:F:406:ASP:C	2:F:408:GLY:H	2.27	0.42
2:F:551:LEU:HG	2:F:552:LEU:CD2	2.49	0.42
2:F:1207:GLU:CG	2:F:1208:ASN:H	2.32	0.42
2:B:728:ALA:O	2:B:927:ILE:HD13	2.20	0.42
2:B:1095:VAL:HG12	2:B:1350:GLN:CD	2.44	0.42
2:B:1110:ILE:HD12	2:B:1122:ARG:CZ	2.49	0.42
2:B:1279:ARG:HG2	2:B:1280:VAL:HG23	2.02	0.42
2:B:1351:SER:O	2:B:1354:GLY:N	2.53	0.42
2:F:89:GLU:HG3	2:F:432:PHE:CD2	2.55	0.42
2:F:256:PHE:CD1	2:F:282:ILE:HD11	2.55	0.42
2:F:274:ASP:O	2:F:277:ASN:OD1	2.37	0.42
2:F:451:TYR:HB2	2:F:488:ALA:HA	2.01	0.42
2:F:842:VAL:HG23	2:F:908:LEU:HD11	2.00	0.42
2:F:902:LYS:NZ	2:F:912:ASP:OD2	2.52	0.42
2:F:936:ASP:OD1	2:F:940:ASN:ND2	2.53	0.42
2:F:1038:PHE:CD2	2:F:1039:TYR:CE1	3.03	0.42
5:I:73:G:H5'	5:I:74:A:OP2	2.20	0.42
2:B:864:ARG:HH21	2:B:871:PRO:HD3	1.84	0.42
2:B:1119:LEU:HD12	2:B:1119:LEU:HA	1.84	0.42
2:F:118:ILE:HD13	2:F:125:GLU:CD	2.44	0.42
2:F:1069:THR:HB	2:F:1071:GLU:H	1.85	0.42
2:F:1265:TYR:O	2:F:1268:GLU:N	2.53	0.42
1:A:11:U:N3	1:A:12:A:N7	2.67	0.42
2:B:828:LEU:HD13	2:B:836:TYR:CD2	2.55	0.42
2:B:998:ILE:HG13	2:B:999:LYS:N	2.34	0.42
1:E:25:U:H2'	1:E:26:A:H8	1.84	0.42
2:F:1090:PRO:HD2	5:J:88:A:N3	2.35	0.42
3:G:24:DG:O3'	3:G:25:DT:H4'	2.20	0.42
2:B:760:VAL:HG11	2:B:990:ASN:O	2.20	0.42
2:B:1110:ILE:HD13	2:B:1134:PHE:HE1	1.85	0.42
2:F:90:MET:SD	2:F:97:PHE:HD2	2.42	0.42
2:F:167:HIS:HD2	2:F:169:LEU:HD12	1.85	0.42
2:F:226:ILE:HD11	2:F:232:GLU:HB3	1.98	0.42
2:F:308:VAL:HG21	2:F:319:ALA:HB1	2.02	0.42
2:F:518:PHE:CD1	2:F:667:ILE:HD13	2.54	0.42
2:F:1045:PHE:CA	2:F:1060:ARG:HH11	2.30	0.42
2:F:1142:SER:HA	2:F:1164:LEU:O	2.20	0.42
2:F:1179:ILE:O	2:F:1183:GLU:HG3	2.19	0.42
2:F:1277:SER:CB	2:F:1287:LEU:HD22	2.49	0.42
2:F:1343:LEU:H	2:F:1343:LEU:HG	1.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:42:A:H5''	5:I:42:A:C8	2.49	0.42
5:J:73:G:C5'	5:J:73:G:H8	2.33	0.42
2:B:478:PHE:CE1	2:B:482:VAL:HG21	2.55	0.42
2:B:558:LYS:HD2	2:B:586:ARG:HD2	2.01	0.42
2:B:795:ILE:O	2:B:795:ILE:HG13	2.20	0.42
2:B:973:TYR:HD2	2:B:1234:ASN:OD1	2.03	0.42
2:F:106:LEU:HD23	2:F:106:LEU:HA	1.65	0.42
2:F:444:LEU:HD23	2:F:444:LEU:C	2.45	0.42
2:F:1110:ILE:HD13	2:F:1110:ILE:HG21	1.87	0.42
2:F:1336:TYR:N	2:F:1336:TYR:CD1	2.85	0.42
3:G:1:DC:H2'	3:G:2:DA:C8	2.55	0.42
5:I:69:A:H2'	5:I:70:C:C6	2.55	0.42
5:J:58:G:C4	5:J:60:C:H1'	2.55	0.42
2:B:38:THR:HG22	2:B:40:ARG:N	2.28	0.42
2:B:602:LYS:HB2	2:B:602:LYS:HE3	1.83	0.42
2:B:738:LEU:HD23	2:B:742:LYS:HG3	2.02	0.42
2:B:1334:LYS:NZ	3:C:3:DA:OP2	2.53	0.42
1:E:4:A:C2	1:E:5:C:C5	3.08	0.42
2:F:70:ARG:NH2	5:J:61:C:OP1	2.50	0.42
2:F:189:VAL:CG1	2:F:201:ILE:HG22	2.50	0.42
2:F:561:VAL:HG22	2:F:583:VAL:HG21	2.01	0.42
2:F:595:HIS:ND1	2:F:595:HIS:N	2.67	0.42
2:F:821:ASP:HA	2:F:828:LEU:HD11	2.01	0.42
2:F:867:SER:HB2	2:F:1054:ASN:N	2.34	0.42
1:A:11:U:O5'	1:A:11:U:H6	2.03	0.41
2:B:85:ILE:HD12	2:B:440:ILE:HG12	2.02	0.41
2:B:114:GLU:HG2	2:B:120:GLY:HA2	2.01	0.41
1:E:15:G:P	2:F:66:ARG:HH22	2.41	0.41
2:F:444:LEU:HD23	2:F:444:LEU:O	2.19	0.41
2:F:448:ILE:HA	2:F:449:PRO:HD3	1.91	0.41
2:F:487:SER:O	2:F:491:PHE:N	2.48	0.41
1:A:29:G:C4	5:I:41:A:C2	3.07	0.41
2:B:40:ARG:HE	2:B:43:ILE:HD11	1.84	0.41
2:B:442:LYS:HE3	2:B:476:TRP:HA	2.02	0.41
2:B:873:GLU:O	2:B:877:LYS:HG2	2.20	0.41
2:B:988:TYR:CE2	2:B:1083:VAL:HG13	2.55	0.41
2:F:1111:LEU:HD12	2:F:1135:ASP:HB2	2.02	0.41
2:B:276:ASP:HA	2:B:279:LEU:CB	2.51	0.41
2:B:1002:PRO:O	2:B:1005:GLU:HB2	2.19	0.41
2:B:1222:LYS:HD2	2:B:1317:ASN:O	2.20	0.41
2:F:524:LEU:HD23	2:F:587:PHE:HE2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:566:GLU:O	2:F:570:LYS:HB3	2.20	0.41
2:F:1022:ILE:HG23	2:F:1038:PHE:HA	2.01	0.41
2:F:1284:ASP:OD1	2:F:1284:ASP:N	2.41	0.41
2:B:184:LEU:HD23	2:B:184:LEU:HA	1.42	0.41
2:B:275:LEU:O	2:B:275:LEU:HD12	2.20	0.41
2:B:321:MET:HE1	2:B:324:ARG:HH21	1.86	0.41
2:B:440:ILE:O	2:B:443:ILE:N	2.50	0.41
2:B:1088:SER:HA	2:B:1230:SER:OG	2.21	0.41
2:B:1147:ALA:HB2	2:B:1190:VAL:HG22	2.02	0.41
2:F:761:ILE:HD13	2:F:761:ILE:HG21	1.76	0.41
2:F:918:LYS:HZ2	2:F:1007:GLU:CD	2.28	0.41
2:F:1355:LEU:HA	2:F:1355:LEU:HD23	1.81	0.41
2:B:106:LEU:HA	2:B:106:LEU:HD12	1.81	0.41
2:B:114:GLU:OE2	2:B:120:GLY:O	2.38	0.41
2:B:173:ASP:C	2:B:174:LEU:HD12	2.45	0.41
2:B:823:TYR:HD1	2:B:875:VAL:HG11	1.83	0.41
2:B:982:HIS:HA	2:B:985:HIS:HB2	2.03	0.41
2:B:1203:LEU:HD23	2:B:1348:ILE:HB	2.02	0.41
2:F:342:GLN:HB2	2:F:383:MET:SD	2.60	0.41
2:F:935:LEU:O	2:F:939:MET:HG2	2.20	0.41
3:G:16:DA:H2'	3:G:17:DT:C6	2.56	0.41
5:J:91:C:HO2'	5:J:92:G:P	2.43	0.41
2:B:180:ASP:OD2	2:B:183:LYS:HE3	2.20	0.41
2:B:1060:ARG:HD3	2:B:1064:GLU:OE2	2.19	0.41
2:B:1143:VAL:HG21	2:B:1174:PHE:CZ	2.55	0.41
2:F:781:MET:HB2	2:F:803:ASN:HD22	1.85	0.41
2:F:1045:PHE:O	2:F:1076:LYS:NZ	2.38	0.41
2:F:1048:THR:HG22	2:F:1076:LYS:HD2	2.02	0.41
2:F:1121:ALA:HB2	2:F:1128:PRO:HD3	2.03	0.41
4:H:11:DT:H2''	4:H:12:DG:C8	2.56	0.41
2:B:305:ILE:HG13	2:B:306:LEU:N	2.34	0.41
2:B:1258:PHE:HE1	2:B:1262:HIS:NE2	2.09	0.41
2:B:1258:PHE:CZ	2:B:1262:HIS:CD2	3.03	0.41
2:B:1272:GLN:CD	5:I:89:G:H1	2.28	0.41
1:E:15:G:H4'	2:F:454:PRO:HD3	2.03	0.41
2:F:121:ASN:ND2	2:F:121:ASN:H	2.19	0.41
2:F:169:LEU:C	2:F:170:ILE:HD12	2.46	0.41
2:F:373:TYR:O	2:F:376:ILE:HG22	2.19	0.41
2:F:922:VAL:HG11	2:F:1007:GLU:C	2.46	0.41
5:J:72:U:H2'	5:J:73:G:H5''	2.01	0.41
2:B:970:PHE:CZ	2:B:1047:LYS:HD3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1224:ASN:N	2:B:1224:ASN:HD22	2.19	0.41
2:F:1087:LEU:HD23	2:F:1087:LEU:HA	1.83	0.41
2:F:1154:SER:OG	2:F:1156:LYS:HB3	2.20	0.41
2:B:127:ALA:HA	2:B:130:GLU:HB2	2.03	0.41
2:B:186:ILE:O	2:B:190:GLN:HG3	2.20	0.41
2:B:1136:SER:N	2:B:1137:PRO:HD3	2.36	0.41
2:B:1279:ARG:HH11	2:B:1279:ARG:HD2	1.77	0.41
1:E:27:G:H5'	1:E:28:A:H5''	2.02	0.41
2:F:43:ILE:HD13	2:F:43:ILE:HA	1.87	0.41
2:F:677:LYS:HG2	2:F:681:ASP:HB2	2.02	0.41
2:F:997:LEU:HD23	2:F:997:LEU:HA	1.89	0.41
2:F:1045:PHE:HB2	2:F:1064:GLU:CG	2.38	0.41
2:F:1054:ASN:C	2:F:1056:GLU:H	2.29	0.41
5:I:79:G:O2'	5:I:80:U:H5'	2.21	0.41
1:A:31:U:H1'	5:I:39:G:N2	2.36	0.41
2:B:296:LEU:O	2:B:297:SER:C	2.63	0.41
2:B:478:PHE:O	2:B:482:VAL:HB	2.21	0.41
2:B:1003:LYS:H	2:B:1003:LYS:HG2	1.51	0.41
2:B:1142:SER:O	2:B:1198:LEU:N	2.34	0.41
2:B:1146:VAL:CG1	2:B:1191:LYS:HB2	2.51	0.41
2:B:1169:MET:HE3	5:I:52:A:H1'	2.03	0.41
2:B:1203:LEU:HA	2:B:1203:LEU:HD12	1.79	0.41
2:F:182:ASP:CG	2:F:208:ALA:HB2	2.45	0.41
2:F:301:LEU:O	2:F:305:ILE:HG12	2.21	0.41
2:F:619:ILE:HD11	2:F:651:LEU:CD1	2.50	0.41
2:F:784:ILE:HD13	2:F:815:TYR:HB3	2.03	0.41
2:F:1242:TYR:H	2:F:1242:TYR:HD1	1.69	0.41
5:I:47:A:N6	5:I:48:A:C6	2.89	0.41
1:A:1:U:O5'	1:A:1:U:H6	2.04	0.40
2:B:114:GLU:CD	2:B:120:GLY:O	2.64	0.40
2:B:601:ILE:HG22	2:B:647:VAL:HG11	2.03	0.40
2:B:692:ASN:CG	2:B:693:PHE:H	2.29	0.40
2:F:565:LYS:HE2	2:F:565:LYS:HB3	1.84	0.40
2:F:936:ASP:CG	2:F:1010:TYR:CD2	2.98	0.40
2:B:35:LEU:HB2	2:B:1358:THR:CG2	2.51	0.40
2:B:118:ILE:HG12	2:B:156:LEU:HD11	2.03	0.40
2:B:861:ASP:O	2:B:864:ARG:HG2	2.20	0.40
2:B:1229:PRO:HB2	2:B:1232:TYR:HD2	1.87	0.40
2:F:224:ASN:C	2:F:226:ILE:N	2.76	0.40
2:F:553:PHE:HZ	2:F:587:PHE:CD2	2.38	0.40
2:F:781:MET:CB	2:F:803:ASN:HD22	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:956:ILE:H	2:F:956:ILE:HG13	1.69	0.40
2:F:1035:LYS:HD3	2:F:1035:LYS:HA	1.71	0.40
2:F:1052:LEU:HD12	2:F:1052:LEU:HA	1.96	0.40
2:F:1110:ILE:HD13	2:F:1122:ARG:CZ	2.52	0.40
2:F:1216:SER:OG	4:H:7:DG:OP1	2.32	0.40
2:B:342:GLN:CD	2:B:383:MET:HB3	2.47	0.40
2:B:583:VAL:HG22	2:B:584:GLU:N	2.37	0.40
2:B:692:ASN:CG	2:B:693:PHE:N	2.80	0.40
2:B:697:ILE:HG22	2:B:698:HIS:ND1	2.37	0.40
2:B:836:TYR:CD1	2:B:836:TYR:N	2.87	0.40
2:B:836:TYR:CD1	2:B:859:ARG:HA	2.57	0.40
2:B:961:LYS:HA	2:B:964:SER:HB3	2.03	0.40
2:B:966:PHE:CD2	2:B:966:PHE:C	2.99	0.40
2:B:1212:ARG:HD3	2:B:1212:ARG:HA	1.89	0.40
2:B:1287:LEU:HD12	2:B:1287:LEU:HA	1.82	0.40
1:E:27:G:H1	5:J:44:U:P	2.44	0.40
2:F:477:ASN:O	2:F:481:VAL:HG23	2.21	0.40
2:F:873:GLU:OE1	2:F:873:GLU:N	2.46	0.40
2:F:1207:GLU:CD	2:F:1210:ARG:HH11	2.29	0.40
2:F:1223:GLY:HA2	2:F:1318:LEU:HG	2.02	0.40
2:F:1351:SER:OG	2:F:1356:TYR:O	2.24	0.40
5:I:88:A:N1	5:I:91:C:N3	2.70	0.40
2:B:680:LEU:HD12	2:B:680:LEU:HA	1.84	0.40
2:B:973:TYR:CD1	2:B:1237:TYR:HD1	2.39	0.40
2:B:1205:GLU:CG	2:B:1209:GLY:HA2	2.49	0.40
2:B:1251:ASP:OD1	2:B:1254:GLN:NE2	2.54	0.40
2:F:1200:LYS:HG2	2:F:1201:TYR:CD1	2.56	0.40
2:F:1219:GLU:O	2:F:1220:LEU:HD23	2.22	0.40
2:F:1263:LYS:O	2:F:1266:LEU:CD2	2.70	0.40
2:F:1290:VAL:O	2:F:1291:LEU:C	2.63	0.40
2:F:1349:HIS:CE1	5:J:69:A:H5'	2.56	0.40
5:J:50:U:O3'	5:J:51:A:H4'	2.21	0.40
2:B:58:THR:HG22	2:B:731:PRO:HG3	2.04	0.40
2:B:165:ARG:O	2:B:415:HIS:HD2	2.04	0.40
2:B:317:LEU:HD13	2:B:410:ILE:HD13	2.03	0.40
2:F:44:LYS:O	5:J:91:C:H2'	2.22	0.40
2:F:336:LYS:HG2	2:F:351:PHE:CE1	2.57	0.40
2:F:842:VAL:HG12	2:F:854:ASN:ND2	2.35	0.40
2:F:945:GLU:HG2	2:F:946:ASN:N	2.36	0.40
2:F:1106:SER:O	2:F:1107:LYS:C	2.62	0.40
2:F:1120:ILE:H	2:F:1120:ILE:HG12	1.63	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:202:ASN:OD1	2:B:541:SER:OG[2_545]	2.07	0.13
2:B:228:GLN:NE2	2:B:543:GLU:OE2[2_545]	2.18	0.02

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 X-ray entries followed by that with respect to entries of similar resolution.

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	
2	B	1312/1368 (96%)	1279 (98%)	29 (2%)	4 (0%)	36	67
2	F	1313/1368 (96%)	1266 (96%)	45 (3%)	2 (0%)	43	74
All	All	2625/2736 (96%)	2545 (97%)	74 (3%)	6 (0%)	43	74

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	270	THR
2	F	1020	LYS
2	F	117	PRO
2	B	117	PRO
2	B	250	PRO
2	B	230	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	1173/1225 (96%)	1173 (100%)	0	100	100
2	F	1156/1225 (94%)	1156 (100%)	0	100	100
All	All	2329/2450 (95%)	2329 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	178	ASN
2	B	224	ASN
2	B	235	ASN
2	B	255	ASN
2	B	265	GLN
2	B	295	ASN
2	B	712	GLN
2	B	758	ASN
2	B	818	ASN
2	B	1041	ASN
2	B	1221	GLN
2	B	1224	ASN
2	B	1252	ASN
2	B	1254	GLN
2	B	1256	GLN
2	B	1262	HIS
2	B	1364	GLN
2	F	129	HIS
2	F	178	ASN
2	F	295	ASN
2	F	329	HIS
2	F	369	GLN
2	F	415	HIS
2	F	650	GLN
2	F	668	ASN
2	F	690	ASN
2	F	758	ASN
2	F	803	ASN
2	F	881	ASN
2	F	894	GLN
2	F	933	GLN
2	F	971	GLN
2	F	982	HIS

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Mol	Chain	Res	Type
2	F	985	HIS
2	F	1044	ASN
2	F	1305	GLN
2	F	1317	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	33/34 (97%)	9 (27%)	3 (9%)
1	E	30/34 (88%)	9 (30%)	1 (3%)
5	I	62/65 (95%)	20 (32%)	2 (3%)
5	J	62/65 (95%)	19 (30%)	1 (1%)
All	All	187/198 (94%)	57 (30%)	7 (3%)

All (57) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	U
1	A	4	A
1	A	5	C
1	A	6	G
1	A	9	U
1	A	20	A
1	A	28	A
1	A	29	G
1	A	33	U
1	E	5	C
1	E	6	G
1	E	9	U
1	E	20	A
1	E	24	U
1	E	28	A
1	E	29	G
1	E	32	A
1	E	33	U
5	I	39	G
5	I	40	C
5	I	42	A
5	I	43	G
5	I	50	U
5	I	51	A

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Mol	Chain	Res	Type
5	I	56	U
5	I	57	A
5	I	59	U
5	I	63	U
5	I	68	A
5	I	69	A
5	I	73	G
5	I	74	A
5	I	77	A
5	I	82	G
5	I	87	G
5	I	89	G
5	I	91	C
5	I	92	G
5	J	37	U
5	J	39	G
5	J	40	C
5	J	42	A
5	J	43	G
5	J	50	U
5	J	51	A
5	J	56	U
5	J	57	A
5	J	59	U
5	J	63	U
5	J	68	A
5	J	73	G
5	J	74	A
5	J	82	G
5	J	87	G
5	J	89	G
5	J	91	C
5	J	92	G

All (7) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	27	G
1	A	28	A
1	E	27	G
5	I	42	A

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Mol	Chain	Res	Type
5	I	68	A
5	J	42	A

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](#)

There are no ligands in this entry.

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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	34/34 (100%)	-0.36	1 (2%) 53 31	19, 34, 129, 166	0
1	E	31/34 (91%)	0.19	2 (6%) 25 15	40, 71, 175, 230	0
2	B	1326/1368 (96%)	0.34	89 (6%) 24 15	13, 62, 175, 215	0
2	F	1327/1368 (97%)	0.73	172 (12%) 7 6	11, 88, 145, 197	0
3	C	25/25 (100%)	-0.35	0 100 100	25, 38, 81, 88	0
3	G	25/25 (100%)	0.23	0 100 100	45, 59, 118, 139	0
4	D	11/11 (100%)	0.20	1 (9%) 15 10	30, 38, 122, 159	0
4	H	11/11 (100%)	0.20	1 (9%) 15 10	33, 60, 119, 189	0
5	I	63/65 (96%)	-0.41	0 100 100	17, 71, 122, 170	0
5	J	63/65 (96%)	-0.31	1 (1%) 70 45	26, 58, 137, 191	0
All	All	2916/3006 (97%)	0.47	267 (9%) 14 9	11, 70, 162, 230	0

All (267) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	305	ILE	7.8
2	B	801	VAL	7.1
2	F	73	THR	7.1
2	B	809	GLU	6.9
2	F	362	TYR	6.7
2	B	1243	GLU	6.7
2	F	402	GLN	6.3
2	B	1242	TYR	6.2
2	F	815	TYR	6.2
2	F	82	LEU	5.9
2	F	679	ILE	5.9
2	F	369	GLN	5.5
2	B	900	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
2	F	232	GLU	5.0
2	F	1049	GLU	5.0
2	F	224	ASN	5.0
2	F	400	ARG	4.9
2	B	883	TRP	4.8
2	B	47	LEU	4.8
2	F	301	LEU	4.7
2	F	230	PRO	4.7
2	B	44	LYS	4.6
2	B	813	LEU	4.5
2	F	802	GLU	4.4
2	F	811	LEU	4.3
2	F	693	PHE	4.3
2	F	451	TYR	4.2
2	B	1045	PHE	4.1
2	B	810	LYS	4.1
2	B	627	GLU	4.1
2	F	449	PRO	4.1
2	F	714	SER	4.0
2	F	688	PHE	4.0
2	F	128	TYR	3.9
2	F	244	LEU	3.9
2	B	1248	SER	3.8
2	F	419	LEU	3.8
2	F	682	PHE	3.8
2	B	812	TYR	3.8
2	F	213	SER	3.8
2	F	627	GLU	3.8
2	B	661	ARG	3.7
2	F	580	ILE	3.7
2	B	1052	LEU	3.7
2	B	1002	PRO	3.7
4	H	2	DT	3.7
2	F	818	ASN	3.7
2	F	777	SER	3.6
2	F	444	LEU	3.6
2	F	661	ARG	3.6
2	B	796	LEU	3.6
2	F	544	GLN	3.5
2	B	430	TYR	3.5
2	F	227	ALA	3.5
2	F	335	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	242	ILE	3.5
2	F	72	TYR	3.5
2	F	501	ASN	3.5
2	B	858	THR	3.5
2	F	225	LEU	3.5
2	B	784	ILE	3.4
2	B	1235	PHE	3.4
2	F	1050	ILE	3.4
2	F	74	ARG	3.4
2	F	247	GLY	3.4
2	B	822	MET	3.4
2	F	441	GLU	3.4
2	F	711	ALA	3.4
2	F	697	ILE	3.4
2	B	1238	LEU	3.3
2	F	856	VAL	3.3
2	F	68	ALA	3.3
2	F	297	SER	3.2
2	F	210	ALA	3.2
2	B	814	TYR	3.2
2	F	241	LEU	3.2
2	F	367	ALA	3.2
2	B	31	LYS	3.2
2	B	872	SER	3.2
2	F	79	ILE	3.2
2	F	796	LEU	3.1
2	F	452	VAL	3.1
2	B	867	SER	3.1
2	F	473	ILE	3.1
2	B	823	TYR	3.1
2	B	1355	LEU	3.0
2	B	1042	ILE	3.0
2	B	777	SER	3.0
2	F	478	PHE	3.0
2	B	1050	ILE	3.0
1	E	28	A	3.0
2	F	423	LEU	3.0
2	F	683	LEU	3.0
2	F	149	ALA	3.0
2	F	231	GLY	3.0
2	F	804	THR	3.0
2	F	207	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
2	F	1168	ILE	2.9
2	B	1048	THR	2.9
2	F	1039	TYR	2.9
2	F	338	LEU	2.9
2	B	32	PHE	2.9
2	F	238	PHE	2.9
2	F	211	ILE	2.9
2	F	690	ASN	2.9
2	F	1111	LEU	2.9
2	B	538	ALA	2.8
2	F	853	ASP	2.8
2	B	1237	TYR	2.8
2	F	246	LEU	2.8
2	F	389	LEU	2.8
2	F	445	THR	2.8
2	F	40	ARG	2.8
4	D	12	DG	2.8
2	F	1060	ARG	2.8
2	F	129	HIS	2.8
2	F	306	LEU	2.8
2	B	1051	THR	2.8
2	F	1243	GLU	2.8
2	F	245	SER	2.7
2	F	813	LEU	2.7
2	B	45	LYS	2.7
2	B	1073	VAL	2.7
2	F	308	VAL	2.7
2	F	481	VAL	2.7
2	B	1036	TYR	2.7
2	F	142	LEU	2.7
2	F	181	VAL	2.7
2	F	443	ILE	2.6
2	F	477	ASN	2.6
2	F	503	PRO	2.6
2	F	658	GLY	2.6
2	F	1051	THR	2.6
2	B	238	PHE	2.6
2	F	257	ASP	2.6
2	F	240	ASN	2.6
2	B	385	GLY	2.6
2	F	713	VAL	2.6
2	B	1249	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	844	GLN	2.6
2	B	502	LEU	2.6
2	F	237	LEU	2.6
2	B	1350	GLN	2.6
2	B	1269	ILE	2.5
2	B	28	PRO	2.5
2	B	685	SER	2.5
2	B	1309	ILE	2.5
2	F	531	THR	2.5
2	F	156	LEU	2.5
2	F	702	LEU	2.5
2	B	1241	HIS	2.5
2	F	1061	PRO	2.5
2	F	220	ARG	2.5
2	F	717	GLY	2.5
2	B	1332	ASP	2.5
2	F	162	ILE	2.5
2	F	1048	THR	2.5
2	B	984	ALA	2.5
2	B	43	ILE	2.5
2	B	910	GLU	2.5
2	B	799	HIS	2.5
2	F	322	ILE	2.4
2	F	795	ILE	2.4
2	B	700	ASP	2.4
2	B	1156	LYS	2.4
2	F	296	LEU	2.4
2	F	1356	TYR	2.4
2	B	817	GLN	2.4
2	F	312	ILE	2.4
2	B	628	ASP	2.4
2	F	1337	THR	2.4
2	B	1034	ALA	2.4
2	F	228	GLN	2.4
2	B	484	LYS	2.4
2	F	480	GLU	2.4
2	B	29	SER	2.4
2	B	834	SER	2.4
2	B	843	PRO	2.4
2	F	568	TYR	2.4
2	F	203	ALA	2.4
2	F	262	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
2	F	348	LYS	2.4
2	F	376	ILE	2.4
2	B	876	VAL	2.4
2	F	132	TYR	2.3
2	F	290	PHE	2.3
2	F	401	LYS	2.3
2	F	877	LYS	2.3
2	B	849	ASP	2.3
2	B	1046	PHE	2.3
2	F	662	LEU	2.3
2	B	1095	VAL	2.3
5	J	36	G	2.3
2	F	117	PRO	2.3
2	B	906	GLY	2.3
2	F	484	LYS	2.3
2	F	107	VAL	2.3
2	F	578	VAL	2.3
2	B	1331	ILE	2.3
2	B	225	LEU	2.3
2	F	67	THR	2.3
2	F	145	SER	2.3
2	F	303	SER	2.3
2	B	808	ASN	2.3
2	B	852	ILE	2.2
2	F	317	LEU	2.2
2	F	42	SER	2.2
2	F	742	LYS	2.2
2	F	803	ASN	2.2
2	F	440	ILE	2.2
2	B	380	LEU	2.2
2	B	857	LEU	2.2
2	F	196	PHE	2.2
2	F	386	THR	2.2
2	F	357	ASN	2.2
2	F	788	ILE	2.2
2	F	433	LEU	2.2
2	F	98	PHE	2.2
2	F	286	TYR	2.2
2	F	334	LEU	2.2
2	F	455	LEU	2.2
2	F	868	ASP	2.2
2	F	778	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
2	F	201	ILE	2.2
2	F	867	SER	2.2
2	F	229	LEU	2.2
2	F	321	MET	2.2
1	A	1	U	2.2
2	F	172	GLY	2.2
2	F	86	PHE	2.2
2	B	815	TYR	2.1
2	F	155	TYR	2.1
2	F	258	LEU	2.1
2	F	1052	LEU	2.1
2	F	315	ALA	2.1
2	F	701	SER	2.1
2	B	1304	GLU	2.1
2	F	361	GLY	2.1
2	F	863	ASN	2.1
2	B	290	PHE	2.1
2	B	795	ILE	2.1
2	F	536	LYS	2.1
2	F	1335	ARG	2.1
2	B	42	SER	2.1
2	B	1080	PHE	2.1
2	F	846	PHE	2.1
2	F	93	VAL	2.1
2	F	799	HIS	2.1
2	F	1102	THR	2.1
2	B	309	ASN	2.1
2	F	309	ASN	2.1
2	F	497	ASN	2.1
2	F	243	ALA	2.1
2	F	399	LEU	2.1
2	F	745	ASP	2.1
2	F	785	GLU	2.1
2	F	141	LYS	2.0
2	B	714	SER	2.0
2	B	1040	SER	2.0
1	E	4	A	2.0
2	F	446	PHE	2.0
2	F	712	GLN	2.0
2	B	816	LEU	2.0
2	F	1167	THR	2.0
2	F	189	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
2	F	396	GLU	2.0
2	B	1266	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.