



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 03:00 AM UTC

PDB ID : 1Y1W / pdb_00001y1w
Title : Complete RNA Polymerase II elongation complex
Authors : Cramer, P.; Kettenberger, H.; Armache, K.-J.
Deposited on : 2004-11-19
Resolution : 4.00 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

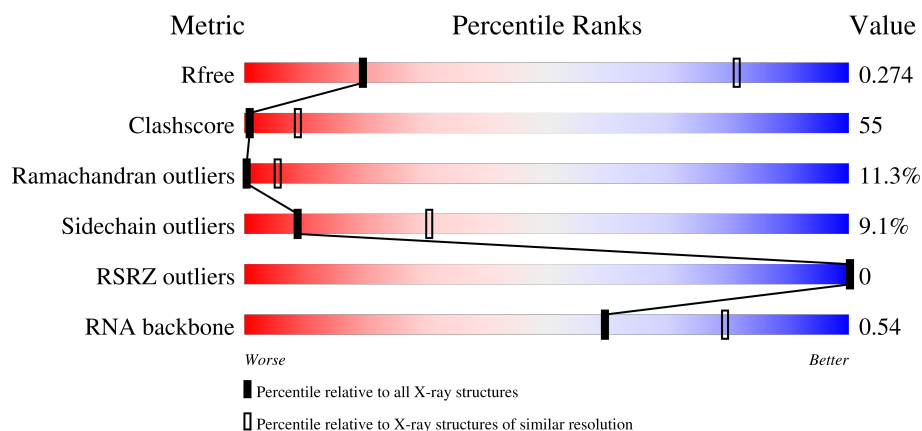
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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	1082 (4.20-3.80)
Clashscore	190562	1129 (4.20-3.80)
Ramachandran outliers	187476	1064 (4.20-3.80)
Sidechain outliers	187428	1055 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)
RNA backbone	3983	1017 (4.84-3.10)

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	T	19	32% 63% 5%
2	N	7	14% 71% 14%
3	P	10	80% 20%
4	A	1733	22% 45% 13% • 18%

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Mol	Chain	Length	Quality of chain
5	B	1224	
6	C	318	
7	D	221	
8	E	215	
9	F	155	
10	G	171	
11	H	146	
12	I	122	
13	J	70	
14	K	120	
15	L	70	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 31802 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 DNA chain called 5'-D(P*AP*GP*TP*AP*CP*TP*TP*AP*CP*GP*CP*CP*TP*GP*GP*TP*CP*AP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	19	Total	C	N	O	P	21	0	0
			387	185	67	116	19			

- Molecule 2 is a DNA chain called 5'-D(*AP*AP*GP*TP*AP*CP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	7	Total	C	N	O	P	20	0	0
			141	69	27	39	6			

- Molecule 3 is a RNA chain called 5'-R(*AP*AP*GP*AP*CP*CP*AP*GP*GP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	10	Total	C	N	O	P	0	0	0
			214	97	44	64	9			

- Molecule 4 is a protein called DNA-directed RNA polymerase II largest subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	1416	Total	C	N	O	S	0	0	0
			11140	7021	1946	2111	62			

- Molecule 5 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	1112	Total	C	N	O	S	0	0	0
			8836	5594	1548	1639	55			

- Molecule 6 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	266	Total	C	N	O	S	0	0	0
			2095	1317	348	417	13			

- Molecule 7 is a protein called DNA-directed RNA polymerase II 32 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	D	177	Total	C	N	O	S	0	0	0
			1356	840	241	273	2			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	E	214	Total	C	N	O	S	0	0	0
			1752	1111	309	321	11			

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	F	84	Total	C	N	O	S	0	0	0
			679	434	115	127	3			

- Molecule 10 is a protein called DNA-directed RNA polymerase II 19 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	G	171	Total	C	N	O	S	0	0	0
			1340	861	222	249	8			

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	H	133	Total	C	N	O	S	0	0	0
			1068	673	180	211	4			

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	I	119	Total	C	N	O	S	0	0	0
			971	596	179	186	10			

- Molecule 13 is a protein called DNA-directed RNA polymerases I/II/III subunit 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 14 is a protein called DNA-directed RNA polymerase II 13.6 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	K	114	Total	C	N	O	S	0	0	0
			919	590	156	171	2			

- Molecule 15 is a protein called DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	L	46	Total	C	N	O	S	0	0	0
			363	224	72	63	4			

- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	2	Total	Zn	0	0
			2	2		
16	B	1	Total	Zn	0	0
			1	1		
16	C	1	Total	Zn	0	0
			1	1		
16	I	2	Total	Zn	0	0
			2	2		
16	J	1	Total	Zn	0	0
			1	1		
16	L	1	Total	Zn	0	0
			1	1		

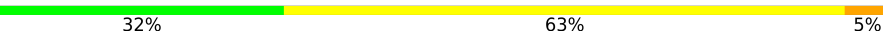
- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

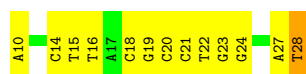
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

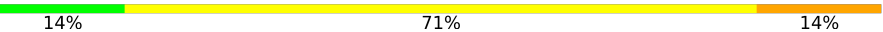
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

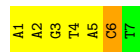
- Molecule 1: 5'-D(P*AP*GP*TP*AP*CP*TP*TP*AP*CP*GP*CP*CP*TP*GP*GP*TP*CP*AP*T)-3'

Chain T: 



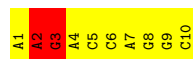
- Molecule 2: 5'-D(*AP*AP*GP*TP*AP*CP*T)-3'

Chain N: 

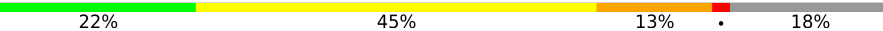


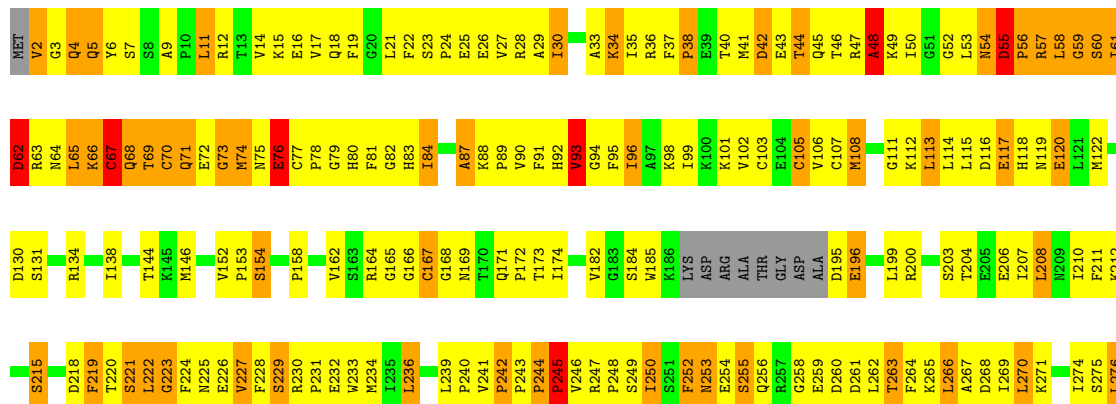
- Molecule 3: 5'-R(*AP*AP*GP*AP*CP*CP*AP*GP*GP*C)-3'

Chain P: 

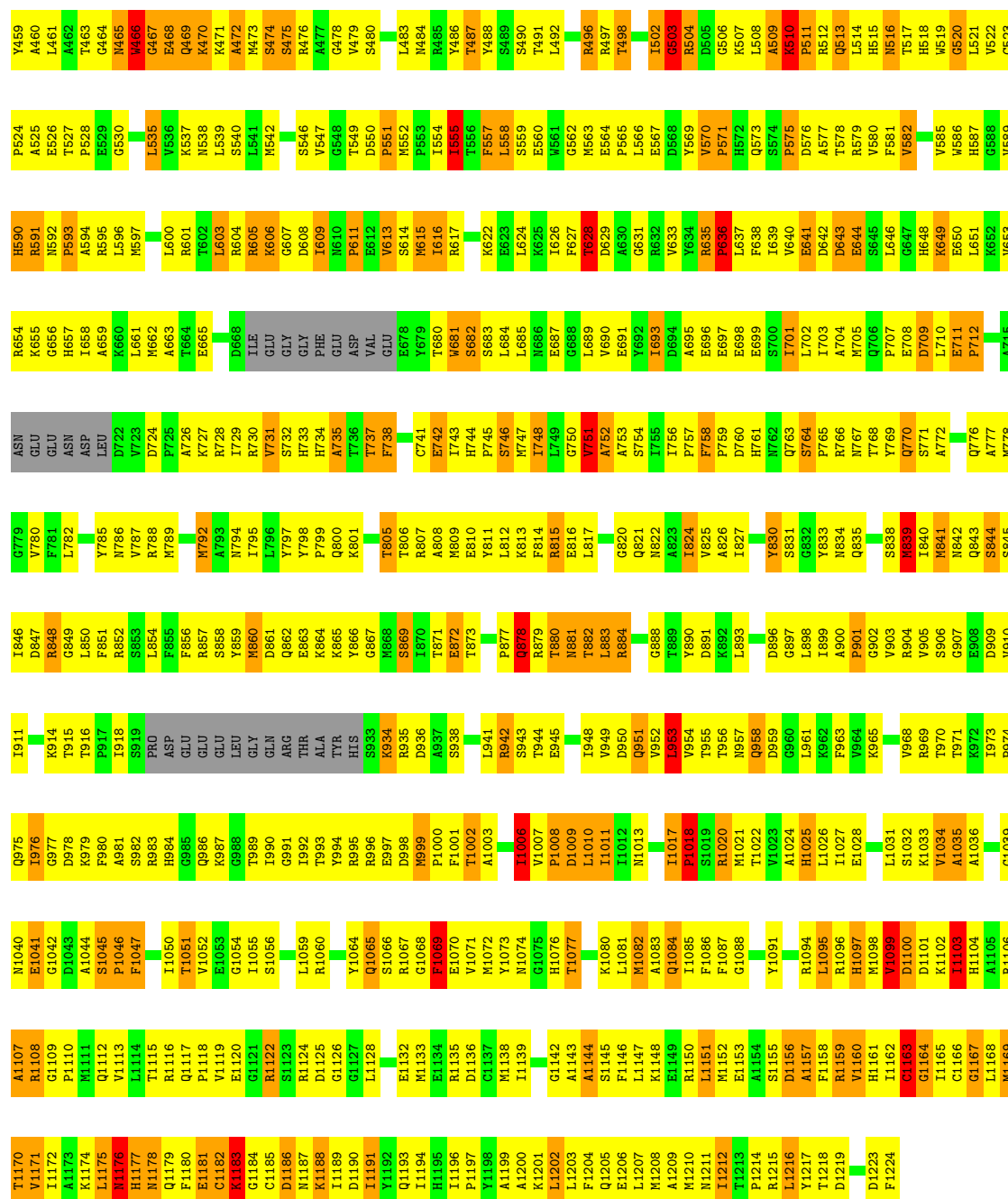


- Molecule 4: DNA-directed RNA polymerase II largest subunit

Chain A: 

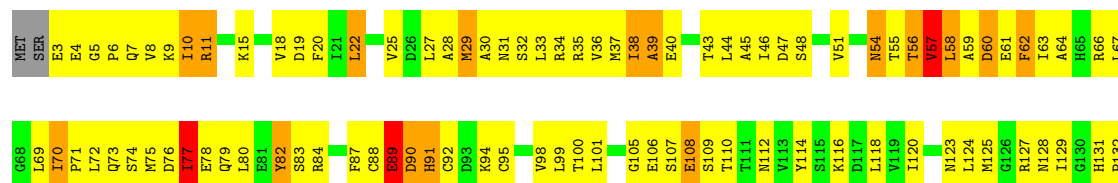


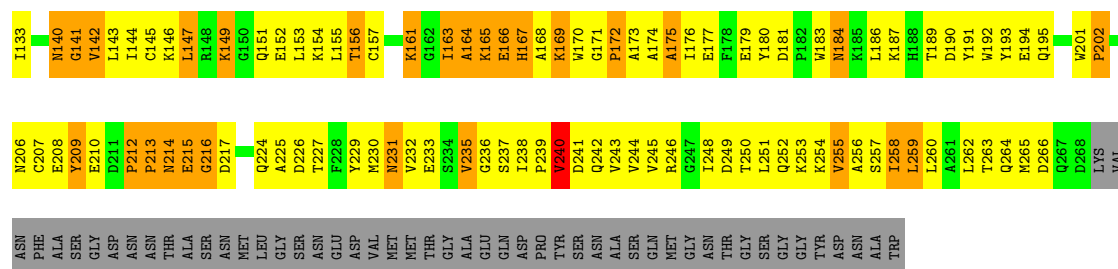
G1188	S1189	A1125	M1063	L1000	V863	V933	V863	E801	L737	D668	P600	T539	V474	I413	G338	E277
S1189	P1190	A1126	V1064	R1001	I864	G934	I864	M802	K738	T689	K601	F540	T475	D414	N339	T278
W1191	W1192	D1127	G1065	G1002	Q865	Q935	Q865	S803	D739	A671	D602	E542	S476	L415	L340	L279
L1192	L1192	L1067	V1066	N1004	I867	Q935	I867	Y804	N741	G672	G604	I543	P477	R416	M341	E280
L1193	Q1130	L1068	L1067	E1005	Y868	D939	Y868	R806	N742	G673	M605	D544	N478	S418	K342	H281
R1194	A1069	A1069	Q1070	I1006	C869	R940	C869	C807	V743	P674	L606	Q545	A480	K419	R344	G283
L1195	K1132	S1071	Q1070	I1007	D871	R941	D871	L808	K744	T675	I607	V546	D481	R420	V345	A284
L1196	L1133	L1072	F942	M1009	C872	F942	C872	T809	K745	M676	L608	N548	P482	A421	D346	P285
L1197	L1134	G1073	L943	A1010	M873	L943	M873	P810	M746		D609	N549	G484	D423	F347	H286
R1199				Q1011	Q811		Q811	E810	V747		G610	M549	G422	G422	S348	H287
A1200				R1012	E812	Y946	E812	F813	G750	T680	G611	L550	D485	I424	A349	A288
A1201				D1013	F814	F947	F814	F814	S751	T682	I612	Y551	E486	Q425	R350	I289
M1202				A1014	H877	F948	H877	F815	K752	L683	F614	V553	M487	L436	T351	E290
K1205				V1015	I878	Y948	I878	H816	G753	A684	G615	P554	N488	Q427	V352	E291
D1206						G950		A817	S754	G685	V616	D555	H489	Y428	I353	A292
L1207				L1017	Q881		Q881	M818	F755	A686	V617	W556	H490	G429	S354	S294
T1207				F1018	S882	R953	S882	C819	I756	K687	E618	D557	P492	K431	D356	L295
T1208				C1019	L883	Y954	L883	C820	N757	K688	K619	G558	Q493	V432	P357	L296
M1209				C1020	D884	Y955	D884	R821	I758	K689	K620	V559		E433	Q297	Q297
Q1210				L1021	T885	L956	T885	E822	A759	T690	T621	I560	T497	R434	F298	F298
Q1211				L1022	P887	P957	P887	C823	Q760	V622	V622	P561	R498	R435	H299	H299
V1212				R1023	C887	Y958	C887	L824	M761	D692	G623	T562	A499	H435	V364	
G1213				S1024	G888	R959	G888	R825	S762	V693	S624	P563	E500		G365	V300
E1214				R1025	S889	I960	S889	R826	A763	T694	S625	A564		D438	V366	A301
R1215				A1026	D890	R961	D890	T827	G764	K695	M626	I565	Q503	M439		T302
I1216				L1027	A891	R962	A891	R828	V765	E696	G627	I566	L504	D440	S369	T303
K1217				T1028	R896	L963	R896	V829	G766	A697	G628	K667	C505	V442	K372	D305
Q1218				R1029	R897	L964	R897	K830	Q767	G698	L629	P568	A506	L443	N306	N306
T1219				R1030	Y897	Q965	Y897	T831	Q768	A699	T630	K569	V507	F444	Y376	D367
F1220				V1031	R898	R966	R898	A832	S769	N700	H631	P570	P508	M445		I308
K1221				L1032	E833	A967	E833	A832	W770	L701	V632	L571		R446	T381	A309
N1222				Q1033	D900	Q968	D900	T834	R774	T709	V633	W572	I511	Q447	P382	G310
D1223				E1034	L901	Q969	L901	C835	I775	L710	K637	S573	V512	P448	Y383	Q311
L1224				Y1035	L902	T970	L902	Y836	A776	R711		G574	P514	S449	N384	P312
				R1036	N903	F971	N903	I837	F777	E712	C642	K575	Q515	L450	I385	Q313
				L1037	T904	H972	T904	Q836	G778	S713		I577	S516	H451	D386	A314
				T1038	D905	L973	D905	R839	G779	F714	L645	L578	N517	M453	L388	Q316
				K1039	H906		H906	R840	F779	F715	L646	L579	K518	S454	V392	K317
				Q1040	T907	D980	T907	L841	W780	E715	F646	S579	P519	M455	V392	S318
				A1041	D781	L981	D781	V842	D716	G647	G647	V580	G520	M456	G401	I325
					R909	L981	R909	K843	R782	N717	M648	H587	T527	V462	A402	R326
				V1044	D910	T982	D910	A844	T783	V718	L649	L582	M521	I463	K403	A327
				V1045	S911	L983	S911	L845	L784	W719	Q650	F583		P464	Y404	R328
					L912	K984	L912	D846	F785	R720	K651	N584	V524	Y465	V405	G331
					E914	D985	E914	D847	W786	F721	V652	G585	Q525	S466	I406	K332
				E1050	E914	L986	E914	T848	F787	L722	V653	I586	D526	T467	R407	E333
						Y987		T848	S788	N723	M654	H588	L528	T463	D408	G334
						L988		Y852	K789	E724	L658	Q589	G529	P464	S409	G334
						Y988		D853	S790	A725	L658	R590	G529	Y465	G410	R336
						Y990		M854	D791	R726	H659	F591	G529	T463	D411	I335
								T855		K728	M660	D592	I531	S466	L470	L337
								T856	F794	D727	G661	D592	R532	T467	G409	
								R857	E795	F662	F662	K533	L534	R469	S409	
								M858	S796	G730	S663	T595	T535	F469	L470	
								S859	K797	R731	T664	T596	L536	L470	G410	
								L860	G798	L732	G665	L597	L536	M471	D411	
								G861	F799	L732	T666	L598	R537	L472	R412	
								H862	W800	N736	G667	S599	D538	S473		



● Molecule 6: DNA-directed RNA polymerase II 45 kDa polypeptide

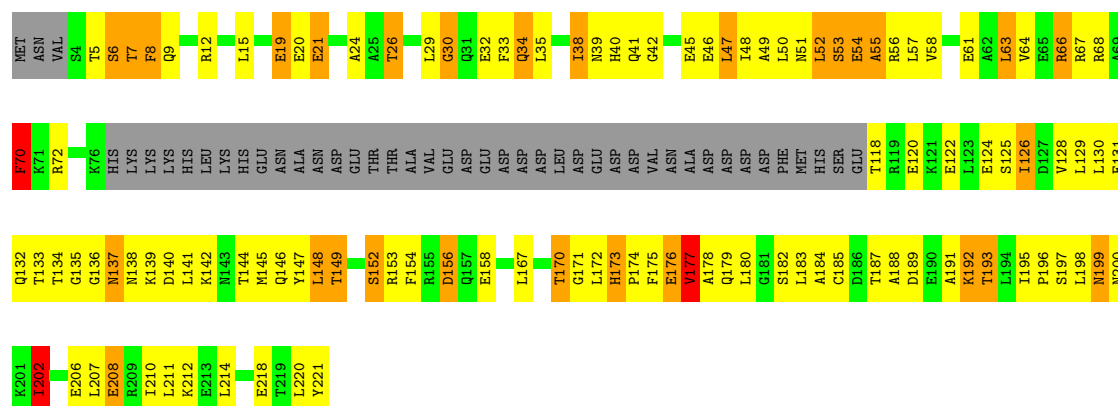
Chain C: 23% 46% 14% 16%





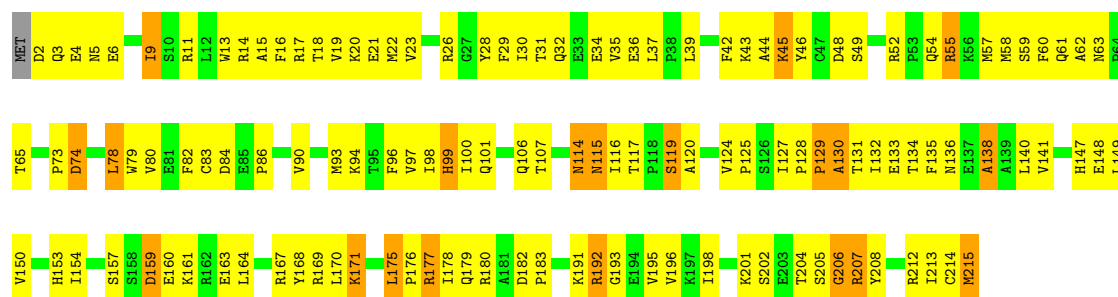
• Molecule 7: DNA-directed RNA polymerase II 32 kDa polypeptide

Chain D: 28% 38% 13% 20%



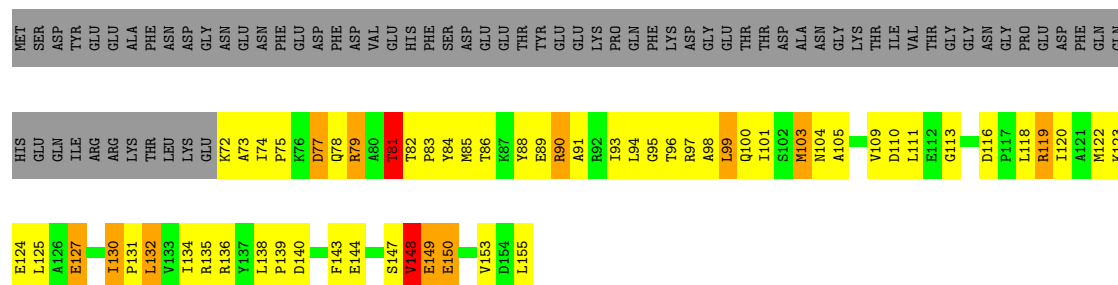
• Molecule 8: DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide

Chain E: 39% 51% 9%

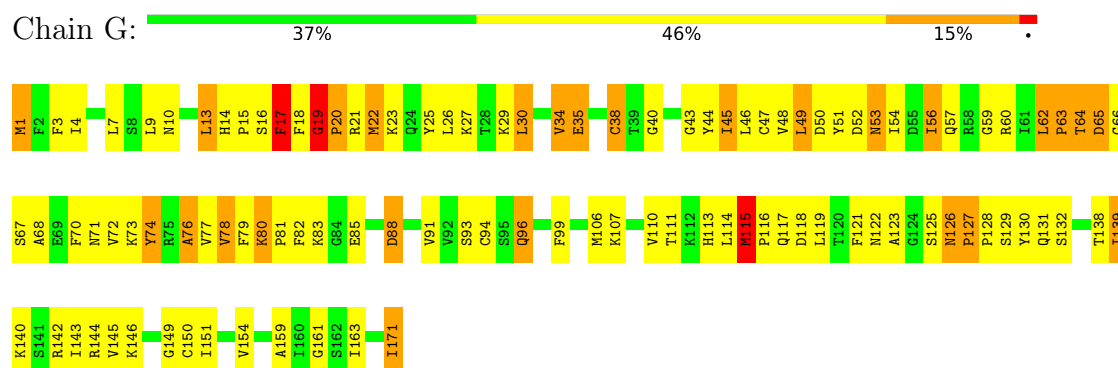


• Molecule 9: DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide

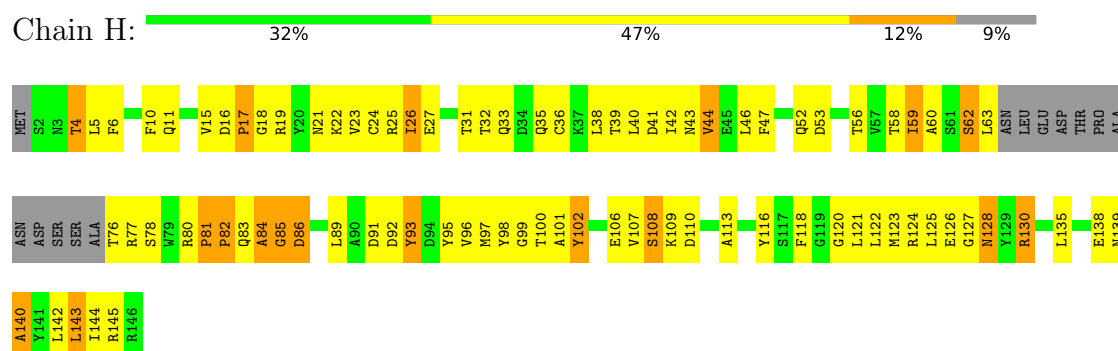
Chain F: 16% 30% 7% 46%



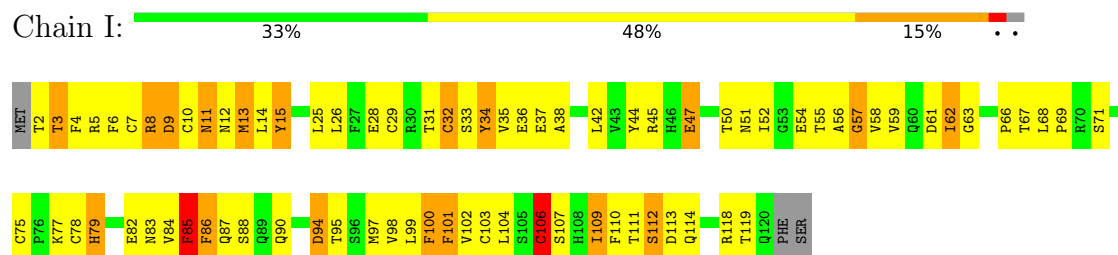
- Molecule 10: DNA-directed RNA polymerase II 19 kDa polypeptide



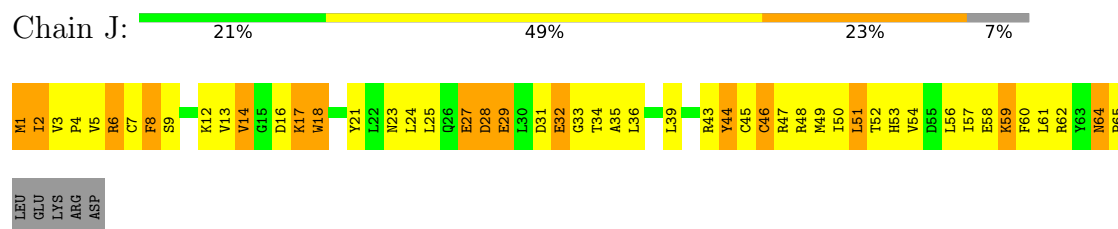
- Molecule 11: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide



- Molecule 12: DNA-directed RNA polymerase II subunit 9



- Molecule 13: DNA-directed RNA polymerases I/II/III subunit 10

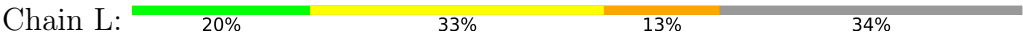


- Molecule 14: DNA-directed RNA polymerase II 13.6 kDa polypeptide





• Molecule 15: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	221.37Å 392.50Å 283.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.00 50.00 – 4.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-4.00) 94.4 (50.00-4.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 3.77Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.253 , 0.276 0.260 , 0.274	Depositor DCC
R_{free} test set	2439 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	77.4	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 114.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.28$, $\langle L^2 \rangle = 0.12$	Xtriage
Estimated twinning fraction	0.207 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.206 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	31802	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.51% 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 ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	T	0.67	1/432 (0.2%)	1.05	1/664 (0.2%)
2	N	1.08	1/158 (0.6%)	0.97	0/242
3	P	0.79	1/240 (0.4%)	1.07	3/373 (0.8%)
4	A	0.63	2/11339 (0.0%)	1.13	88/15334 (0.6%)
5	B	0.63	6/9008 (0.1%)	1.09	68/12146 (0.6%)
6	C	0.69	2/2133 (0.1%)	1.14	18/2891 (0.6%)
7	D	0.55	0/1365	1.18	16/1837 (0.9%)
8	E	0.52	0/1788	1.03	15/2406 (0.6%)
9	F	0.71	0/691	1.20	6/933 (0.6%)
10	G	0.63	0/1368	1.16	16/1844 (0.9%)
11	H	0.45	0/1086	1.01	6/1470 (0.4%)
12	I	0.52	0/989	1.07	5/1331 (0.4%)
13	J	0.60	0/541	1.05	1/727 (0.1%)
14	K	0.57	0/937	1.08	7/1265 (0.6%)
15	L	0.54	0/365	0.97	0/485
All	All	0.62	13/32440 (0.0%)	1.10	250/43948 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	B	0	1
6	C	0	1
All	All	0	2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	469	GLN	CA-C	7.52	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	10	DA	O3'-P	-7.29	1.50	1.61
5	B	504	ARG	N-CA	7.09	1.55	1.46
5	B	503	GLY	CA-C	6.81	1.61	1.51
6	C	89	GLU	N-CA	-6.39	1.38	1.46
4	A	120	GLU	N-CA	5.96	1.53	1.46
2	N	6	DC	O3'-P	5.69	1.69	1.61
5	B	473	MET	C-O	5.59	1.31	1.24
5	B	472	ALA	C-O	5.54	1.30	1.23
6	C	90	ASP	CA-C	5.32	1.60	1.52
4	A	1443	VAL	CA-CB	-5.17	1.48	1.54
3	P	3	G	P-OP1	-5.12	1.38	1.49
5	B	364	ILE	CA-CB	-5.04	1.47	1.54

All (250) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1185	CYS	N-CA-C	-15.47	94.17	113.97
4	A	452	LYS	N-CA-C	-14.08	95.94	111.14
7	D	54	GLU	N-CA-C	-11.61	99.64	114.04
4	A	466	SER	N-CA-C	10.56	124.75	112.72
7	D	26	THR	N-CA-C	-10.21	98.54	112.94
4	A	320	ARG	CA-C-N	9.68	131.93	119.84
4	A	320	ARG	C-N-CA	9.68	131.93	119.84
4	A	1261	LYS	N-CA-C	-9.16	104.18	114.62
4	A	982	THR	N-CA-C	-9.11	97.66	110.50
4	A	242	PRO	CA-C-N	9.05	129.70	120.38
4	A	242	PRO	C-N-CA	9.05	129.70	120.38
4	A	567	LYS	CA-C-N	-8.83	108.80	119.84
4	A	567	LYS	C-N-CA	-8.83	108.80	119.84
7	D	171	GLY	N-CA-C	-8.48	103.62	115.32
4	A	266	LEU	N-CA-C	-8.43	101.78	110.97
4	A	81	PHE	N-CA-C	8.38	121.13	110.24
9	F	127	GLU	N-CA-C	-8.24	102.24	112.88
10	G	62	LEU	CA-C-N	-8.05	109.77	119.84
10	G	62	LEU	C-N-CA	-8.05	109.77	119.84
10	G	22	MET	N-CA-C	-7.88	102.45	112.93
5	B	363	HIS	N-CA-C	-7.87	99.49	110.35
4	A	425	GLN	N-CA-C	-7.81	97.02	109.59
5	B	510	LYS	CA-C-N	-7.80	110.08	119.84
5	B	510	LYS	C-N-CA	-7.80	110.08	119.84
7	D	38	ILE	N-CA-C	7.80	119.09	108.17
5	B	296	GLU	N-CA-C	-7.79	102.42	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1009	ASP	N-CA-C	-7.73	104.07	113.97
4	A	454	SER	N-CA-C	-7.66	103.91	113.18
9	F	77	ASP	N-CA-C	-7.65	98.61	110.17
6	C	39	ALA	N-CA-C	7.62	123.25	113.88
5	B	882	THR	N-CA-C	7.58	120.26	111.02
4	A	158	PRO	N-CA-C	-7.57	104.72	114.03
6	C	38	ILE	N-CA-C	7.52	117.60	110.53
5	B	503	GLY	CA-C-N	7.45	135.77	121.54
5	B	503	GLY	C-N-CA	7.45	135.77	121.54
5	B	1177	HIS	N-CA-C	-7.45	104.59	112.93
5	B	395	GLN	N-CA-C	-7.43	100.72	110.53
3	P	2	A	C2'-C3'-O3'	7.41	124.82	113.70
4	A	1422	ARG	N-CA-C	-7.37	103.88	114.12
10	G	129	SER	N-CA-C	7.37	118.91	108.74
4	A	928	LEU	N-CA-C	-7.36	103.19	111.14
8	E	5	ASN	N-CA-C	-7.35	105.22	114.56
5	B	1020	ARG	N-CA-C	-7.35	103.29	111.82
4	A	1275	GLY	N-CA-C	7.23	119.94	111.63
8	E	63	ASN	CA-C-N	7.18	127.15	119.76
8	E	63	ASN	C-N-CA	7.18	127.15	119.76
11	H	80	ARG	CA-C-N	7.14	127.73	120.38
11	H	80	ARG	C-N-CA	7.14	127.73	120.38
4	A	288	ALA	N-CA-C	-7.11	102.42	113.02
6	C	11	ARG	N-CA-C	-7.10	102.95	108.78
7	D	7	THR	N-CA-C	7.08	122.47	107.67
6	C	235	VAL	N-CA-C	-7.05	104.98	111.67
4	A	582	ILE	CA-C-N	7.00	126.99	119.78
4	A	582	ILE	C-N-CA	7.00	126.99	119.78
5	B	208	SER	N-CA-C	6.94	119.78	110.35
7	D	173	HIS	CA-C-N	6.92	128.49	119.84
7	D	173	HIS	C-N-CA	6.92	128.49	119.84
4	A	564	ALA	N-CA-C	-6.90	103.69	111.14
4	A	729	ALA	N-CA-C	-6.88	103.86	111.36
4	A	950	GLY	N-CA-C	-6.82	105.18	115.00
4	A	415	LEU	N-CA-C	6.80	121.18	112.34
7	D	55	ALA	N-CA-C	-6.74	103.08	112.45
6	C	225	ALA	N-CA-C	6.71	118.38	107.32
8	E	171	LYS	N-CA-C	-6.62	99.50	110.17
4	A	1262	LYS	N-CA-C	-6.62	104.10	111.71
4	A	472	LEU	N-CA-C	6.60	118.26	111.14
4	A	291	GLU	N-CA-C	-6.59	105.15	113.72
5	B	616	ILE	N-CA-C	6.59	117.61	108.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1291	VAL	CA-C-N	6.59	128.08	119.84
4	A	1291	VAL	C-N-CA	6.59	128.08	119.84
5	B	872	GLU	N-CA-C	-6.58	102.04	110.53
4	A	311	GLN	N-CA-C	6.57	124.34	109.81
4	A	1098	VAL	CB-CA-C	-6.57	107.46	113.70
4	A	344	ARG	N-CA-C	-6.55	99.91	110.32
5	B	506	GLY	O-C-N	6.51	128.50	122.77
5	B	66	ASP	N-CA-C	-6.43	104.74	112.59
5	B	558	LEU	N-CA-C	6.41	117.96	110.97
7	D	72	ARG	N-CA-C	-6.41	105.32	113.01
8	E	149	LEU	N-CA-C	6.39	118.12	111.03
10	G	127	PRO	CA-C-N	6.35	126.38	119.90
10	G	127	PRO	C-N-CA	6.35	126.38	119.90
4	A	60	SER	N-CA-C	6.34	116.37	108.19
10	G	64	THR	N-CA-C	-6.29	104.81	113.18
6	C	70	ILE	CA-C-N	6.29	126.31	119.89
6	C	70	ILE	C-N-CA	6.29	126.31	119.89
10	G	56	ILE	CB-CA-C	-6.25	105.56	111.06
5	B	555	ILE	N-CA-C	-6.24	104.77	110.82
5	B	535	LEU	N-CA-C	-6.24	105.80	113.41
4	A	750	GLY	N-CA-C	-6.23	106.54	115.64
5	B	361	LEU	CA-C-N	6.23	127.62	119.84
5	B	361	LEU	C-N-CA	6.23	127.62	119.84
6	C	40	GLU	N-CA-C	6.21	120.89	112.88
4	A	252	PHE	N-CA-C	-6.18	102.86	110.65
5	B	1052	VAL	N-CA-C	-6.18	104.27	111.00
5	B	609	ILE	N-CA-C	-6.16	98.86	107.80
5	B	473	MET	CA-C-N	6.16	133.30	121.54
5	B	473	MET	C-N-CA	6.16	133.30	121.54
14	K	75	ILE	N-CA-C	6.12	116.93	108.12
5	B	1151	LEU	N-CA-C	6.12	118.92	111.82
5	B	606	LYS	N-CA-C	-6.08	106.41	113.88
7	D	34	GLN	N-CA-C	-6.05	102.55	110.53
5	B	292	ILE	CB-CA-C	-6.03	107.96	114.35
10	G	19	GLY	CA-C-N	6.02	127.36	119.84
10	G	19	GLY	C-N-CA	6.02	127.36	119.84
5	B	693	ILE	N-CA-C	6.00	116.45	107.51
4	A	476	SER	CA-C-N	-5.99	112.36	119.84
4	A	476	SER	C-N-CA	-5.99	112.36	119.84
5	B	681	TRP	N-CA-C	-5.98	102.40	111.56
14	K	82	ASP	CA-C-N	5.97	125.68	119.05
14	K	82	ASP	C-N-CA	5.97	125.68	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	68	GLN	N-CA-C	-5.97	103.02	111.56
8	E	6	GLU	N-CA-C	-5.96	105.11	112.38
5	B	291	ILE	CA-C-N	5.96	123.99	120.24
5	B	291	ILE	C-N-CA	5.96	123.99	120.24
5	B	976	ILE	N-CA-C	5.93	117.46	111.00
10	G	76	ALA	N-CA-C	5.93	117.97	109.14
4	A	1039	LYS	N-CA-C	-5.93	104.95	111.82
4	A	998	LEU	N-CA-C	5.92	119.17	109.76
4	A	590	ARG	N-CA-C	5.92	118.25	108.48
4	A	1104	ILE	N-CA-C	5.92	116.10	110.42
7	D	66	ARG	N-CA-C	-5.89	103.64	111.24
3	P	3	G	N9-C1'-C2'	5.88	120.81	112.00
4	A	87	ALA	N-CA-C	-5.87	105.12	112.93
4	A	1391	ARG	N-CA-C	-5.87	107.11	114.56
14	K	31	VAL	N-CA-C	5.85	117.13	108.65
5	B	934	LYS	N-CA-C	5.83	118.78	108.24
12	I	109	ILE	N-CA-C	5.82	114.74	106.53
4	A	1403	GLU	N-CA-C	5.81	123.17	110.80
4	A	776	ALA	N-CA-C	5.80	118.92	110.17
4	A	539	THR	N-CA-C	5.79	118.11	109.25
6	C	165	LYS	N-CA-C	-5.79	103.70	112.04
5	B	469	GLN	O-C-N	-5.76	116.96	123.13
12	I	85	PHE	N-CA-C	5.76	118.94	110.59
5	B	195	CYS	CA-C-N	5.75	124.95	118.97
5	B	195	CYS	C-N-CA	5.75	124.95	118.97
4	A	983	ILE	N-CA-C	-5.75	103.87	111.05
5	B	392	ARG	N-CA-C	-5.75	106.92	114.04
8	E	55	ARG	N-CA-C	5.73	117.21	111.07
4	A	467	THR	N-CA-C	5.71	118.77	109.24
1	T	28	DT	C2'-C3'-O3'	5.70	120.04	111.50
4	A	663	SER	N-CA-C	5.69	115.75	108.24
4	A	1376	THR	N-CA-C	5.68	120.71	113.55
11	H	16	ASP	N-CA-C	5.67	119.54	107.91
4	A	689	LYS	N-CA-C	-5.67	106.21	113.01
5	B	428	ILE	N-CA-C	-5.67	104.01	111.09
9	F	130	ILE	CA-C-N	5.67	126.92	119.84
9	F	130	ILE	C-N-CA	5.67	126.92	119.84
4	A	293	GLU	N-CA-C	-5.64	106.40	113.28
3	P	2	A	C3'-C2'-O2'	5.63	119.15	110.70
10	G	65	ASP	N-CA-C	-5.62	101.89	110.14
4	A	222	LEU	N-CA-C	-5.61	101.40	110.32
4	A	227	VAL	N-CA-C	5.59	116.62	111.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	57	VAL	N-CA-C	-5.58	105.43	113.07
13	J	59	LYS	N-CA-C	-5.57	105.11	111.07
7	D	188	ALA	N-CA-C	-5.55	105.23	112.23
4	A	424	ILE	N-CA-C	5.53	120.85	109.34
5	B	473	MET	N-CA-C	-5.53	106.30	113.16
5	B	1104	HIS	N-CA-C	5.53	117.38	108.32
4	A	55	ASP	N-CA-C	5.52	122.02	109.81
4	A	294	SER	N-CA-C	-5.50	105.30	112.23
14	K	58	PHE	N-CA-C	5.50	117.46	108.76
5	B	378	LEU	N-CA-C	-5.50	104.71	111.75
14	K	112	GLN	N-CA-C	5.49	118.93	110.42
4	A	1424	VAL	N-CA-C	-5.49	104.52	110.23
5	B	1025	HIS	N-CA-C	-5.48	105.20	111.07
5	B	1113	VAL	CB-CA-C	-5.48	106.04	111.30
5	B	1045	SER	CA-C-N	5.48	126.69	119.84
5	B	1045	SER	C-N-CA	5.48	126.69	119.84
4	A	781	ASP	N-CA-C	5.48	118.95	111.39
5	B	475	SER	N-CA-C	5.47	117.82	109.95
4	A	1413	GLY	N-CA-C	-5.45	107.90	114.66
4	A	1333	ILE	N-CA-C	-5.44	104.65	110.36
5	B	805	THR	N-CA-C	5.44	116.53	108.86
10	G	40	GLY	N-CA-C	-5.44	107.91	114.66
10	G	30	LEU	N-CA-C	-5.43	104.39	111.02
5	B	841	MET	N-CA-C	5.43	117.37	108.52
4	A	173	THR	N-CA-C	-5.43	103.37	110.53
12	I	119	THR	N-CA-C	-5.42	107.03	113.97
4	A	440	ASP	N-CA-C	-5.42	100.81	109.04
5	B	293	PRO	N-CA-C	5.40	120.56	111.32
6	C	51	VAL	N-CA-C	5.40	115.97	108.84
8	E	65	THR	N-CA-C	-5.39	102.90	110.50
4	A	56	PRO	N-CA-C	-5.37	101.40	112.47
6	C	38	ILE	CB-CA-C	-5.35	105.01	112.02
11	H	109	LYS	CB-CA-C	-5.35	109.42	115.79
4	A	923	LEU	N-CA-C	5.35	118.27	111.69
8	E	32	GLN	N-CA-C	-5.33	106.28	112.89
6	C	193	TYR	N-CA-C	5.33	115.32	108.34
4	A	1010	ALA	N-CA-C	-5.32	105.65	111.82
8	E	177	ARG	N-CA-C	5.31	118.37	110.14
4	A	778	GLY	N-CA-C	-5.30	105.90	113.86
4	A	398	GLU	N-CA-C	-5.30	103.53	110.53
9	F	105	ALA	N-CA-C	-5.30	102.44	110.39
4	A	30	ILE	N-CA-C	5.29	115.92	110.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	I	112	SER	N-CA-C	-5.29	105.28	112.26
5	B	69	LEU	N-CA-C	5.29	116.69	109.18
6	C	62	PHE	N-CA-C	-5.29	104.42	111.24
5	B	1163	CYS	N-CA-C	-5.28	100.58	109.07
14	K	20	LYS	N-CA-C	-5.26	99.25	107.93
5	B	172	ILE	N-CA-C	5.26	116.81	109.55
4	A	1138	ILE	CB-CA-C	-5.26	107.24	111.71
4	A	229	SER	N-CA-C	5.25	115.99	107.32
7	D	70	PHE	N-CA-C	-5.25	106.55	113.17
10	G	45	ILE	N-CA-C	-5.25	99.54	107.73
4	A	1102	LYS	N-CA-C	-5.25	105.46	111.07
8	E	52	ARG	CA-C-N	5.23	124.99	119.76
8	E	52	ARG	C-N-CA	5.23	124.99	119.76
5	B	201	GLY	N-CA-C	-5.22	107.85	115.63
5	B	112	LEU	N-CA-C	5.22	118.62	110.32
4	A	1299	VAL	N-CA-C	5.21	117.55	108.95
4	A	76	GLU	CB-CA-C	-5.21	100.05	110.42
6	C	129	ILE	N-CA-C	5.21	114.06	107.70
6	C	163	ILE	N-CA-C	5.21	117.55	108.95
7	D	212	LYS	N-CA-C	-5.20	105.52	111.14
9	F	148	VAL	N-CA-C	-5.20	104.69	110.62
8	E	119	SER	N-CA-C	-5.19	105.69	112.23
12	I	11	ASN	N-CA-C	5.18	121.84	110.80
4	A	491	VAL	N-CA-C	5.17	115.88	107.71
5	B	650	GLU	N-CA-C	5.17	116.38	108.52
5	B	277	LYS	N-CA-C	5.17	117.65	111.71
6	C	89	GLU	O-C-N	-5.17	115.72	122.59
4	A	227	VAL	CB-CA-C	-5.16	105.62	111.55
5	B	628	THR	N-CA-C	-5.16	107.65	114.31
5	B	292	ILE	N-CA-C	5.16	120.08	112.61
5	B	213	ILE	N-CA-C	5.15	116.39	108.71
4	A	337	ARG	N-CA-C	5.15	116.97	111.36
5	B	839	MET	N-CA-C	5.15	118.40	110.42
5	B	1164	GLY	N-CA-C	-5.14	109.01	114.67
7	D	8	PHE	N-CA-C	5.14	121.74	110.80
4	A	637	LYS	N-CA-C	5.13	117.78	111.82
4	A	1434	ALA	N-CA-C	5.11	116.51	110.07
4	A	724	GLU	N-CA-C	-5.11	105.22	111.75
5	B	1008	PRO	N-CA-C	5.11	119.07	111.41
5	B	99	LYS	CA-C-N	5.08	126.19	119.84
5	B	99	LYS	C-N-CA	5.08	126.19	119.84
8	E	9	ILE	N-CA-C	-5.08	106.85	111.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1445	ILE	CB-CA-C	-5.08	104.20	111.31
4	A	48	ALA	N-CA-C	-5.07	99.99	110.80
6	C	258	ILE	N-CA-C	-5.07	106.21	111.58
5	B	294	ASP	N-CA-C	-5.06	100.02	110.80
10	G	140	LYS	N-CA-C	5.06	118.71	112.54
8	E	159	ASP	N-CA-C	-5.05	105.97	112.68
11	H	4	THR	N-CA-C	-5.05	101.87	109.85
4	A	990	VAL	N-CA-C	-5.05	105.47	110.62
4	A	67	CYS	N-CA-C	-5.04	100.06	110.80
4	A	289	ILE	N-CA-C	-5.03	106.77	111.45
11	H	85	GLY	N-CA-C	-5.03	108.82	114.40
7	D	176	GLU	N-CA-C	-5.02	105.46	111.03
4	A	459	ARG	N-CA-C	-5.01	101.54	109.96
5	B	1107	ALA	N-CA-C	-5.01	97.77	107.44

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	B	503	GLY	Mainchain
6	C	82	TYR	Sidechain

5.2 Too-close contacts [i](#)

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	T	387	0	216	24	0
2	N	141	0	81	8	0
3	P	214	0	111	13	0
4	A	11140	0	11217	1407	0
5	B	8836	0	8871	1076	0
6	C	2095	0	2051	273	0
7	D	1356	0	1319	128	0
8	E	1752	0	1776	156	0
9	F	679	0	701	91	0
10	G	1340	0	1357	166	0
11	H	1068	0	1040	113	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	I	971	0	930	116	0
13	J	532	0	542	95	0
14	K	919	0	929	103	0
15	L	363	0	387	46	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	1	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	L	1	0	0	0	0
17	A	1	0	0	0	0
All	All	31802	0	31528	3486	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 55.

All (3486) 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)
7:D:40:HIS:HB3	10:G:73:LYS:NZ	1.61	1.14
14:K:47:ARG:HB3	14:K:47:ARG:HH11	1.00	1.14
4:A:53:LEU:HD23	4:A:54:ASN:H	1.08	1.12
4:A:76:GLU:HG3	4:A:76:GLU:O	1.53	1.08
4:A:53:LEU:HD23	4:A:54:ASN:N	1.70	1.07
7:D:48:ILE:HG21	10:G:4:ILE:HB	1.33	1.07
5:B:273:LEU:HB2	5:B:276:ILE:HD12	1.33	1.06
5:B:467:GLY:H	5:B:475:SER:HB3	1.18	1.06
5:B:824:ILE:HG22	5:B:1087:PHE:HE2	1.21	1.05
1:T:20:DC:H4'	4:A:447:GLN:NE2	1.70	1.05
4:A:56:PRO:O	4:A:57:ARG:HG3	1.55	1.05
4:A:779:PHE:HE1	4:A:785:PRO:HD3	1.21	1.04
6:C:43:THR:HG22	6:C:44:LEU:H	1.18	1.04
5:B:217:ARG:HE	5:B:405:ARG:HB2	1.20	1.04
4:A:1094:VAL:HG13	4:A:1113:THR:HG21	1.34	1.03
4:A:399:HIS:HB3	4:A:400:PRO:HD3	1.35	1.03
5:B:1072:MET:HE3	5:B:1085:ILE:HB	1.38	1.02
5:B:23:ALA:HB1	5:B:24:PRO:HD2	1.40	1.02
11:H:100:THR:HG23	11:H:138:GLU:HA	1.41	1.02
4:A:1017:LEU:HB2	8:E:206:GLY:H	1.25	1.01
4:A:1161:THR:HG22	4:A:1163:ILE:H	1.23	1.01
4:A:1444:MET:HE1	9:F:135:ARG:HB2	1.42	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:855:THR:HG21	4:A:857:ARG:HE	1.22	1.00
6:C:142:VAL:H	13:J:16:ASP:HB3	1.28	0.99
4:A:963:ILE:HD11	4:A:1048:ASN:HB3	1.43	0.99
12:I:85:PHE:H	12:I:85:PHE:HD2	1.06	0.99
4:A:1424:VAL:HG13	4:A:1436:ILE:HD11	1.44	0.98
7:D:40:HIS:HB3	10:G:73:LYS:HZ3	1.13	0.97
4:A:901:LEU:H	4:A:926:GLN:NE2	1.63	0.97
5:B:467:GLY:N	5:B:475:SER:HB3	1.78	0.97
5:B:589:VAL:HG12	5:B:590:HIS:H	1.25	0.97
14:K:47:ARG:HB3	14:K:47:ARG:NH1	1.80	0.96
4:A:84:ILE:HD11	4:A:270:LEU:HD13	1.47	0.96
8:E:19:VAL:O	8:E:23:VAL:HG23	1.66	0.96
4:A:40:THR:HG22	4:A:41:MET:HG3	1.48	0.96
11:H:4:THR:HA	11:H:60:ALA:HB2	1.45	0.96
13:J:5:VAL:HG12	13:J:6:ARG:HG3	1.47	0.96
1:T:22:DT:H2"	1:T:23:DG:H5"	1.48	0.95
7:D:47:LEU:HD13	7:D:48:ILE:H	1.30	0.95
6:C:166:GLU:HG3	14:K:10:PHE:HZ	1.31	0.95
10:G:15:PRO:HA	10:G:18:PHE:CD1	2.01	0.95
4:A:1329:THR:H	4:A:1335:ILE:HD11	1.30	0.95
10:G:1:MET:SD	10:G:79:PHE:HD1	1.89	0.95
6:C:39:ALA:HA	6:C:164:ALA:HB3	1.49	0.94
4:A:563:PRO:HG3	4:A:572:TRP:CZ2	2.02	0.94
5:B:1065:GLN:HE21	5:B:1067:ARG:H	1.08	0.94
4:A:244:PRO:HB2	4:A:245:PRO:HD3	1.48	0.94
5:B:1072:MET:CE	5:B:1085:ILE:HB	1.98	0.94
6:C:45:ALA:HA	6:C:72:LEU:HD12	1.50	0.93
4:A:535:THR:HG21	4:A:616:VAL:HA	1.50	0.93
4:A:541:ILE:HD13	4:A:549:MET:HE1	1.47	0.93
14:K:65:HIS:HD2	14:K:67:PHE:H	1.17	0.93
5:B:65:GLU:HG3	5:B:66:ASP:H	1.33	0.93
5:B:847:ASP:HB3	6:C:167:HIS:NE2	1.84	0.93
4:A:754:SER:H	4:A:757:ASN:HD22	1.08	0.92
14:K:47:ARG:HH11	14:K:47:ARG:CB	1.82	0.92
4:A:829:VAL:HG21	5:B:508:LEU:HD13	1.50	0.92
5:B:189:LEU:HA	5:B:192:LEU:HD12	1.52	0.92
5:B:46:GLN:HG3	5:B:47:GLN:H	1.33	0.92
4:A:768:GLN:HG2	4:A:816:HIS:HA	1.51	0.92
10:G:138:THR:HG22	10:G:139:ILE:H	1.32	0.92
4:A:779:PHE:CE1	4:A:785:PRO:HD3	2.05	0.91
6:C:262:LEU:HD11	14:K:87:LEU:HD23	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:198:ILE:HD11	8:E:212:ARG:HG3	1.52	0.91
5:B:1224:PHE:HE2	8:E:171:LYS:HG3	1.33	0.91
5:B:1065:GLN:HE21	5:B:1067:ARG:N	1.68	0.91
4:A:1445:ILE:H	4:A:1445:ILE:HD12	1.36	0.90
4:A:903:ASN:ND2	4:A:905:ASP:H	1.68	0.90
5:B:999:MET:HG3	5:B:1000:PRO:HD2	1.54	0.90
3:P:2:A:H2'	3:P:3:G:C8	2.05	0.90
6:C:57:VAL:HG11	13:J:60:PHE:HB3	1.52	0.90
4:A:567:LYS:CG	4:A:568:PRO:HD2	2.02	0.89
6:C:47:ASP:HA	15:L:69:ALA:HB3	1.50	0.89
8:E:180:ARG:HH21	8:E:192:ARG:HB2	1.34	0.89
10:G:1:MET:SD	10:G:79:PHE:CD1	2.66	0.89
13:J:64:ASN:HB3	13:J:65:PRO:CD	2.03	0.89
8:E:94:LYS:HE2	8:E:98:ILE:HD11	1.54	0.89
13:J:36:LEU:HD12	13:J:47:ARG:NH1	1.88	0.89
5:B:918:ILE:HB	5:B:935:ARG:HD2	1.54	0.88
5:B:1007:VAL:HG22	5:B:1008:PRO:HD2	1.53	0.88
5:B:778:MET:CE	5:B:1094:ARG:HD3	2.03	0.88
3:P:2:A:H2'	3:P:3:G:H8	1.37	0.88
4:A:858:ASN:ND2	4:A:860:LEU:H	1.72	0.88
5:B:579:ARG:HB2	5:B:586:TRP:HE1	1.39	0.88
6:C:44:LEU:HB2	6:C:77:ILE:HD11	1.54	0.88
10:G:23:LYS:HG3	10:G:56:ILE:HD11	1.54	0.88
4:A:1189:SER:O	4:A:1241:ARG:HD3	1.74	0.88
4:A:1409:LEU:HD13	5:B:1207:LEU:HD21	1.52	0.88
4:A:335:ARG:NH1	5:B:1202:LEU:HD13	1.89	0.87
4:A:901:LEU:HG	4:A:926:GLN:HE21	1.40	0.87
4:A:356:ASP:HB2	4:A:469:ARG:NH1	1.90	0.87
7:D:144:THR:O	7:D:148:LEU:HB2	1.75	0.87
4:A:392:VAL:HG13	4:A:415:LEU:HD11	1.56	0.86
5:B:999:MET:HA	5:B:999:MET:HE3	1.57	0.86
5:B:847:ASP:HB3	6:C:167:HIS:HE2	1.34	0.86
4:A:541:ILE:HG22	4:A:546:VAL:HG23	1.56	0.86
5:B:211:VAL:O	5:B:480:SER:HA	1.75	0.86
5:B:579:ARG:HB2	5:B:586:TRP:NE1	1.91	0.86
1:T:20:DC:H4'	4:A:447:GLN:HE22	1.40	0.86
6:C:43:THR:HG22	6:C:44:LEU:N	1.88	0.86
10:G:7:LEU:HB2	10:G:74:TYR:CE2	2.10	0.86
4:A:709:THR:HG23	12:I:94:ASP:HA	1.57	0.86
5:B:549:THR:HG22	5:B:550:ASP:H	1.40	0.86
4:A:55:ASP:C	4:A:57:ARG:H	1.78	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:115:LEU:HB2	4:A:122:MET:HE2	1.55	0.85
4:A:1341:ILE:HG23	4:A:1342:GLU:N	1.90	0.85
4:A:709:THR:HG22	4:A:711:ARG:H	1.38	0.85
4:A:825:ILE:HG22	5:B:508:LEU:HD11	1.59	0.85
5:B:466:TRP:O	5:B:468:GLU:N	2.08	0.85
6:C:32:SER:O	6:C:36:VAL:HG23	1.76	0.85
4:A:1329:THR:HG22	4:A:1331:SER:H	1.41	0.85
4:A:829:VAL:C	4:A:831:THR:H	1.82	0.85
9:F:93:ILE:HD11	9:F:134:ILE:HD11	1.58	0.85
4:A:1312:ASN:O	4:A:1316:VAL:HG23	1.77	0.85
5:B:1197:PRO:HG2	5:B:1200:ALA:HB2	1.59	0.84
7:D:153:ARG:NH2	7:D:184:ALA:HA	1.92	0.84
5:B:800:GLN:HB3	13:J:52:THR:HG21	1.55	0.84
11:H:81:PRO:HB2	11:H:82:PRO:HD2	1.58	0.84
4:A:503:GLN:HE21	9:F:90:ARG:HH21	1.21	0.84
6:C:213:PRO:O	6:C:214:ASN:HB2	1.77	0.84
12:I:8:ARG:HG3	12:I:34:TYR:HE1	1.40	0.84
4:A:1329:THR:CG2	4:A:1331:SER:H	1.90	0.84
4:A:1242:VAL:HG12	4:A:1243:VAL:H	1.41	0.84
6:C:241:ASP:O	6:C:245:VAL:HG23	1.77	0.83
4:A:828:ALA:CB	5:B:530:GLY:HA2	2.08	0.83
5:B:168:GLY:H	5:B:450:ALA:HB1	1.40	0.83
4:A:528:LEU:O	4:A:531:ILE:HG22	1.78	0.83
4:A:903:ASN:C	4:A:903:ASN:HD22	1.86	0.83
4:A:567:LYS:HG3	4:A:568:PRO:HD2	1.57	0.83
4:A:808:LEU:HD23	4:A:813:PHE:HA	1.60	0.83
5:B:521:LEU:HB3	5:B:633:VAL:HG11	1.60	0.83
6:C:56:THR:HG22	6:C:57:VAL:H	1.43	0.83
4:A:340:LEU:HD13	4:A:1429:ILE:HG23	1.61	0.83
8:E:213:ILE:HG12	8:E:214:CYS:H	1.44	0.83
6:C:47:ASP:HA	15:L:69:ALA:CB	2.07	0.83
4:A:442:VAL:HB	4:A:489:LEU:HD11	1.61	0.83
4:A:741:ASN:HD22	4:A:744:LYS:H	1.27	0.82
5:B:882:THR:HG22	5:B:884:ARG:H	1.41	0.82
5:B:25:ILE:HD11	5:B:653:VAL:O	1.77	0.82
5:B:507:LYS:O	5:B:512:ARG:NE	2.10	0.82
5:B:806:THR:HG22	5:B:808:ALA:H	1.42	0.82
5:B:1096:ARG:O	5:B:1097:HIS:HB2	1.77	0.82
13:J:57:ILE:HA	13:J:60:PHE:HD2	1.44	0.82
4:A:475:THR:HG23	4:A:476:SER:H	1.42	0.82
5:B:770:GLN:OE1	5:B:983:ARG:HA	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:8:ARG:HG3	12:I:34:TYR:CE1	2.13	0.82
4:A:351:THR:HB	5:B:1103:ILE:HD12	1.62	0.82
6:C:232:VAL:HG21	6:C:244:VAL:HG22	1.60	0.82
5:B:217:ARG:NE	5:B:405:ARG:HB2	1.94	0.82
13:J:16:ASP:OD1	13:J:17:LYS:HD2	1.80	0.82
4:A:1329:THR:HG22	4:A:1331:SER:N	1.94	0.82
5:B:172:ILE:HD13	5:B:178:ASN:HB3	1.60	0.82
5:B:955:THR:HG22	5:B:956:THR:H	1.44	0.82
4:A:1444:MET:CE	9:F:135:ARG:HB2	2.08	0.82
5:B:955:THR:HG22	5:B:956:THR:N	1.95	0.82
4:A:794:PRO:HG2	4:A:795:GLU:OE2	1.80	0.81
8:E:175:LEU:HD23	8:E:176:PRO:HD2	1.60	0.81
11:H:102:TYR:OH	11:H:122:LEU:HD22	1.78	0.81
13:J:3:VAL:HG21	13:J:18:TRP:HB2	1.61	0.81
4:A:746:MET:HE3	5:B:1018:PRO:HG2	1.59	0.81
5:B:467:GLY:O	5:B:468:GLU:HB2	1.81	0.81
4:A:560:ILE:HG13	11:H:78:SER:HB2	1.62	0.81
4:A:1341:ILE:HG23	4:A:1342:GLU:H	1.45	0.81
4:A:1420:ASP:HB3	4:A:1422:ARG:HG3	1.62	0.81
5:B:521:LEU:HD22	5:B:633:VAL:HG12	1.63	0.81
5:B:955:THR:HG23	15:L:54:ARG:O	1.80	0.81
4:A:567:LYS:HB3	11:H:96:VAL:H	1.46	0.81
6:C:244:VAL:O	6:C:248:ILE:HG13	1.79	0.81
13:J:64:ASN:HB3	13:J:65:PRO:HD3	1.60	0.81
5:B:1065:GLN:NE2	5:B:1067:ARG:H	1.78	0.81
8:E:2:ASP:O	8:E:3:GLN:HG2	1.81	0.81
4:A:70:CYS:O	4:A:72:GLU:HG2	1.80	0.81
5:B:516:ASN:HD22	5:B:516:ASN:N	1.76	0.80
5:B:899:ILE:HD11	5:B:911:ILE:HA	1.61	0.80
4:A:106:VAL:HG13	4:A:112:LYS:O	1.81	0.80
5:B:515:HIS:HD2	5:B:517:THR:H	1.29	0.80
5:B:233:PRO:HG2	5:B:234:ILE:HD12	1.61	0.80
8:E:16:PHE:CZ	8:E:20:LYS:HE2	2.17	0.80
8:E:22:MET:HE3	8:E:26:ARG:HE	1.47	0.80
4:A:78:PRO:HB3	5:B:1201:LYS:HE3	1.62	0.80
5:B:98:THR:O	5:B:126:SER:HB2	1.81	0.80
6:C:184:ASN:ND2	6:C:187:LYS:HA	1.97	0.80
4:A:310:GLY:O	4:A:312:PRO:HD2	1.81	0.80
4:A:567:LYS:NZ	11:H:46:LEU:HB2	1.97	0.80
4:A:868:TYR:CE1	4:A:1064:VAL:HG11	2.17	0.80
5:B:1159:ARG:HB3	5:B:1159:ARG:HH11	1.47	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:49:LYS:HZ1	4:A:61:ILE:HG13	1.47	0.80
5:B:952:VAL:HG12	5:B:953:LEU:H	1.46	0.80
10:G:1:MET:HE1	10:G:80:LYS:N	1.97	0.80
12:I:71:SER:OG	12:I:83:ASN:HB2	1.82	0.80
4:A:768:GLN:CG	4:A:816:HIS:HA	2.11	0.80
5:B:824:ILE:HG22	5:B:1087:PHE:CE2	2.13	0.80
10:G:1:MET:HE1	10:G:80:LYS:H	1.44	0.79
9:F:86:THR:HG23	9:F:89:GLU:OE1	1.82	0.79
11:H:123:MET:HE1	11:H:142:LEU:HD11	1.63	0.79
12:I:26:LEU:HD23	12:I:37:GLU:HA	1.62	0.79
14:K:21:ILE:HG12	14:K:33:ILE:HG12	1.65	0.79
5:B:1099:VAL:O	5:B:1101:ASP:N	2.16	0.79
5:B:705:MET:H	5:B:710:LEU:HD12	1.47	0.79
6:C:186:LEU:HD21	6:C:224:GLN:O	1.82	0.79
11:H:59:ILE:HG22	11:H:60:ALA:N	1.97	0.79
13:J:12:LYS:O	13:J:14:VAL:HG23	1.83	0.79
4:A:76:GLU:O	4:A:76:GLU:CG	2.29	0.79
14:K:113:THR:O	14:K:114:LEU:HB2	1.81	0.79
10:G:13:LEU:HD21	10:G:17:PHE:HB2	1.61	0.79
4:A:253:ASN:HB3	5:B:935:ARG:NH2	1.98	0.79
11:H:4:THR:HA	11:H:60:ALA:CB	2.13	0.79
11:H:93:TYR:HB3	11:H:144:ILE:O	1.83	0.79
4:A:475:THR:HG23	4:A:476:SER:N	1.96	0.78
10:G:34:VAL:HG12	10:G:45:ILE:HG21	1.64	0.78
6:C:212:PRO:HB3	6:C:213:PRO:HD2	1.63	0.78
5:B:37:PHE:HE2	5:B:542:MET:HA	1.47	0.78
4:A:858:ASN:C	4:A:858:ASN:HD22	1.89	0.78
10:G:128:PRO:O	10:G:138:THR:HG23	1.83	0.78
5:B:401:PHE:HA	5:B:404:LYS:HG3	1.65	0.78
5:B:508:LEU:O	5:B:509:ALA:HB2	1.82	0.78
4:A:1336:MET:HE3	4:A:1381:LEU:HG	1.63	0.78
11:H:23:VAL:HG22	11:H:43:ASN:HA	1.66	0.78
4:A:35:ILE:HG22	4:A:35:ILE:O	1.84	0.78
4:A:1422:ARG:HH22	5:B:1224:PHE:C	1.91	0.78
5:B:1183:LYS:N	5:B:1183:LYS:HE3	1.99	0.77
4:A:115:LEU:CB	4:A:122:MET:HE2	2.13	0.77
5:B:953:LEU:HD21	5:B:965:LYS:HB2	1.65	0.77
4:A:524:VAL:HG12	4:A:525:GLN:H	1.49	0.77
5:B:863:GLU:OE2	5:B:873:THR:HA	1.84	0.77
6:C:166:GLU:HG3	14:K:10:PHE:CZ	2.19	0.77
4:A:588:LEU:O	4:A:606:LEU:HA	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:798:GLY:HA2	4:A:815:PHE:CD1	2.19	0.77
5:B:483:LEU:HD11	5:B:491:THR:HG23	1.67	0.77
8:E:117:THR:HG22	8:E:119:SER:H	1.47	0.77
4:A:754:SER:H	4:A:757:ASN:ND2	1.83	0.77
4:A:1424:VAL:HG11	5:B:1139:ILE:HD13	1.66	0.77
5:B:1159:ARG:HD3	5:B:1193:GLN:CG	2.13	0.77
4:A:321:PRO:O	4:A:322:VAL:HB	1.85	0.77
5:B:1162:ILE:HG22	5:B:1163:CYS:H	1.49	0.77
6:C:70:ILE:HG12	6:C:142:VAL:HG11	1.66	0.77
4:A:590:ARG:NH2	4:A:620:LYS:HB3	1.99	0.77
14:K:65:HIS:CD2	14:K:67:PHE:H	2.02	0.77
4:A:567:LYS:HB3	11:H:95:TYR:HA	1.67	0.77
4:A:836:TYR:CE2	4:A:840:ARG:HD2	2.19	0.77
4:A:1116:LEU:HB2	4:A:1329:THR:OG1	1.83	0.77
5:B:859:TYR:OH	5:B:941:LEU:HD12	1.85	0.76
5:B:102:VAL:HG23	5:B:112:LEU:HB2	1.66	0.76
5:B:1201:LYS:HE2	5:B:1205:GLN:OE1	1.85	0.76
6:C:98:VAL:C	6:C:99:LEU:HD23	2.09	0.76
8:E:22:MET:HE3	8:E:26:ARG:NE	2.00	0.76
4:A:399:HIS:CB	4:A:400:PRO:HD3	2.15	0.76
5:B:503:GLY:HA3	5:B:507:LYS:HE3	1.67	0.76
8:E:29:PHE:O	8:E:30:ILE:HG13	1.85	0.76
4:A:886:ILE:HD11	4:A:943:LEU:HB3	1.66	0.76
5:B:39:ARG:NH2	5:B:665:GLU:HG2	2.01	0.76
5:B:53:GLN:HG2	5:B:547:VAL:HG22	1.66	0.76
5:B:1034:VAL:HG12	5:B:1035:ALA:N	1.99	0.76
6:C:43:THR:CG2	6:C:44:LEU:H	1.96	0.76
5:B:254:LEU:HD23	5:B:381:MET:HE1	1.66	0.76
5:B:778:MET:HE1	5:B:1094:ARG:HD3	1.67	0.76
11:H:42:ILE:HG23	11:H:95:TYR:HE1	1.50	0.76
4:A:1291:VAL:HG13	4:A:1292:PRO:HD2	1.66	0.76
5:B:798:TYR:HE2	6:C:62:PHE:CE2	2.03	0.76
7:D:48:ILE:CG2	10:G:4:ILE:HB	2.12	0.76
12:I:8:ARG:CG	12:I:34:TYR:HE1	1.99	0.76
4:A:87:ALA:HB3	4:A:276:LEU:HD23	1.67	0.75
4:A:534:LEU:O	4:A:574:GLY:HA3	1.85	0.75
5:B:363:HIS:O	5:B:364:ILE:HB	1.85	0.75
5:B:1007:VAL:CG2	5:B:1008:PRO:HD2	2.16	0.75
4:A:152:VAL:CG1	4:A:153:PRO:HD2	2.17	0.75
4:A:225:ASN:HD22	4:A:228:PHE:H	1.32	0.75
5:B:1159:ARG:HB3	5:B:1159:ARG:NH1	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:179:GLU:HG2	6:C:180:TYR:N	1.99	0.75
4:A:1424:VAL:HG13	4:A:1436:ILE:CD1	2.15	0.75
5:B:200:GLY:HA2	5:B:202:TYR:CE2	2.22	0.75
4:A:1343:ALA:HB2	8:E:150:VAL:HG22	1.66	0.75
5:B:794:ASN:C	5:B:795:ILE:HD12	2.11	0.75
7:D:40:HIS:CB	10:G:73:LYS:NZ	2.46	0.75
4:A:353:ILE:CD1	4:A:487:MET:HE2	2.17	0.75
4:A:590:ARG:HG3	4:A:590:ARG:NH1	2.02	0.75
5:B:37:PHE:CD1	5:B:41:LYS:HG3	2.22	0.75
5:B:995:ARG:HH12	6:C:165:LYS:HG2	1.52	0.75
4:A:855:THR:CG2	4:A:857:ARG:HE	1.99	0.75
5:B:351:TYR:CE1	5:B:355:ILE:HD11	2.21	0.75
5:B:577:ALA:HB1	5:B:589:VAL:HG11	1.68	0.75
5:B:613:VAL:HG13	5:B:627:PHE:O	1.87	0.75
7:D:170:THR:CG2	7:D:172:LEU:HG	2.17	0.75
1:T:15:DT:H5"	4:A:1407:GLU:OE2	1.87	0.75
4:A:899:VAL:HB	4:A:929:LEU:CD1	2.17	0.75
5:B:37:PHE:CE1	5:B:41:LYS:HG3	2.22	0.75
5:B:615:MET:C	5:B:616:ILE:HD12	2.11	0.75
4:A:388:LEU:O	4:A:392:VAL:HG23	1.87	0.74
4:A:741:ASN:HD21	4:A:743:VAL:HB	1.50	0.74
4:A:92:HIS:O	4:A:94:GLY:N	2.19	0.74
4:A:670:ILE:HG23	4:A:805:LEU:HD21	1.68	0.74
4:A:1004:ASN:ND2	8:E:167:ARG:HD2	2.02	0.74
4:A:993:LEU:HD23	4:A:1022:LEU:HD21	1.70	0.74
4:A:1116:LEU:N	4:A:1308:THR:HG22	2.02	0.74
7:D:130:LEU:C	7:D:132:GLN:H	1.95	0.74
4:A:93:VAL:HG13	4:A:301:ALA:HB1	1.67	0.74
5:B:604:ARG:NH2	5:B:613:VAL:O	2.20	0.74
6:C:66:ARG:NH2	13:J:5:VAL:HG23	2.01	0.74
4:A:438:ASP:O	4:A:439:ASN:HB2	1.87	0.74
5:B:1099:VAL:CG1	5:B:1100:ASP:N	2.50	0.74
4:A:1332:PHE:HD2	4:A:1332:PHE:N	1.85	0.74
4:A:87:ALA:CB	4:A:276:LEU:HD23	2.18	0.74
5:B:359:GLU:O	5:B:362:PRO:HD3	1.87	0.74
5:B:378:LEU:HD12	5:B:378:LEU:O	1.86	0.74
5:B:847:ASP:C	5:B:849:GLY:H	1.93	0.74
4:A:1161:THR:HG22	4:A:1163:ILE:N	2.02	0.74
5:B:223:VAL:HG11	5:B:381:MET:HG2	1.68	0.74
5:B:801:LYS:O	13:J:52:THR:HG23	1.88	0.74
5:B:642:ASP:O	5:B:644:GLU:N	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:81:THR:HG21	9:F:136:ARG:HD3	1.70	0.74
4:A:107:CYS:SG	4:A:171:GLN:HG2	2.28	0.74
4:A:646:PHE:O	4:A:650:GLN:HG3	1.88	0.74
5:B:996:ARG:NH1	6:C:38:ILE:HG23	2.01	0.74
4:A:69:THR:O	4:A:71:GLN:N	2.21	0.73
5:B:902:GLY:O	15:L:65:VAL:HG11	1.87	0.73
14:K:12:LEU:H	14:K:12:LEU:HD12	1.52	0.73
4:A:248:PRO:O	4:A:260:ASP:HB2	1.87	0.73
4:A:335:ARG:HA	4:A:339:ASN:HB2	1.68	0.73
10:G:80:LYS:N	10:G:80:LYS:HD3	2.03	0.73
4:A:239:LEU:HD12	4:A:240:PRO:HD2	1.69	0.73
5:B:906:SER:O	5:B:941:LEU:HD23	1.87	0.73
5:B:1224:PHE:CE2	8:E:171:LYS:HG3	2.20	0.73
6:C:263:THR:C	6:C:265:MET:H	1.96	0.73
7:D:40:HIS:HB3	10:G:73:LYS:HZ2	1.51	0.73
4:A:49:LYS:NZ	4:A:61:ILE:HG13	2.03	0.73
4:A:1121:GLU:HG2	4:A:1122:PRO:HD2	1.68	0.73
14:K:45:LEU:HG	14:K:94:ILE:HD13	1.69	0.73
4:A:783:THR:HG21	4:A:815:PHE:CZ	2.23	0.73
4:A:164:ARG:HG3	4:A:165:GLY:N	2.02	0.73
4:A:384:ASN:OD1	4:A:388:LEU:HD12	1.89	0.73
5:B:370:PHE:HE2	5:B:373:ARG:HH11	1.36	0.73
4:A:855:THR:HG21	4:A:857:ARG:NE	2.01	0.73
7:D:138:ASN:OD1	7:D:141:LEU:HB2	1.89	0.73
12:I:7:CYS:HB3	12:I:14:LEU:HD21	1.71	0.73
4:A:856:THR:HB	4:A:865:GLN:HB2	1.69	0.73
10:G:23:LYS:HG3	10:G:56:ILE:CD1	2.18	0.73
4:A:1348:LEU:HG	4:A:1372:VAL:CG2	2.18	0.73
5:B:295:GLY:H	5:B:298:LEU:HD23	1.53	0.73
4:A:903:ASN:HD22	4:A:904:THR:N	1.87	0.72
5:B:615:MET:HB3	5:B:626:ILE:HG12	1.71	0.72
5:B:975:GLN:O	5:B:990:ILE:HD12	1.89	0.72
6:C:22:LEU:HD13	6:C:230:MET:HE3	1.71	0.72
7:D:29:LEU:HD22	10:G:82:PHE:CE2	2.24	0.72
4:A:302:THR:HA	4:A:305:ASP:O	1.89	0.72
4:A:382:PRO:HB3	4:A:428:TYR:HE2	1.53	0.72
4:A:567:LYS:CD	4:A:568:PRO:HD2	2.19	0.72
5:B:507:LYS:H	5:B:512:ARG:HH21	1.35	0.72
5:B:603:LEU:HD13	5:B:608:ASP:HB2	1.71	0.72
5:B:1017:ILE:HB	5:B:1018:PRO:HD3	1.71	0.72
4:A:347:PHE:H	5:B:1107:ALA:HA	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:171:PRO:HD2	5:B:457:LEU:HD13	1.71	0.72
6:C:165:LYS:O	14:K:6:ARG:NH1	2.22	0.72
7:D:176:GLU:O	7:D:178:ALA:N	2.18	0.72
9:F:119:ARG:HH11	9:F:119:ARG:HG3	1.53	0.72
4:A:873:MET:HE3	4:A:957:PRO:HG3	1.71	0.72
4:A:1239:ARG:HH22	4:A:1241:ARG:NH2	1.87	0.72
5:B:281:PRO:HG2	5:B:284:ILE:HG13	1.69	0.72
5:B:879:ARG:HH11	5:B:883:LEU:HD22	1.54	0.72
5:B:1001:PHE:CE1	5:B:1073:TYR:HB2	2.24	0.72
5:B:365:THR:HG23	5:B:367:LEU:H	1.55	0.72
5:B:502:ILE:HG12	5:B:535:LEU:HD13	1.71	0.72
10:G:74:TYR:H	10:G:74:TYR:HD2	1.35	0.72
5:B:361:LEU:HD21	5:B:377:PHE:CD2	2.24	0.72
5:B:594:ALA:HA	5:B:617:ARG:NH1	2.05	0.72
7:D:134:THR:HG22	7:D:136:GLY:H	1.52	0.72
15:L:30:ILE:O	15:L:56:LEU:HA	1.88	0.72
5:B:589:VAL:HG12	5:B:590:HIS:N	2.04	0.72
5:B:112:LEU:HD12	5:B:113:TYR:H	1.54	0.72
5:B:953:LEU:HD23	5:B:953:LEU:O	1.89	0.72
4:A:55:ASP:CG	4:A:55:ASP:O	2.31	0.72
4:A:67:CYS:O	4:A:70:CYS:HB3	1.90	0.72
5:B:847:ASP:HB3	6:C:167:HIS:CD2	2.24	0.72
5:B:1095:LEU:H	5:B:1095:LEU:HD12	1.54	0.72
11:H:40:LEU:HD13	11:H:123:MET:HB2	1.70	0.72
4:A:844:ALA:C	4:A:845:LEU:HD23	2.15	0.71
5:B:223:VAL:CG1	5:B:381:MET:HG2	2.19	0.71
5:B:601:ARG:O	5:B:605:ARG:HG3	1.89	0.71
5:B:1099:VAL:HG12	5:B:1100:ASP:H	1.53	0.71
7:D:33:PHE:CE1	10:G:80:LYS:HE3	2.24	0.71
12:I:50:THR:HG22	12:I:52:ILE:H	1.55	0.71
4:A:69:THR:C	4:A:71:GLN:H	1.95	0.71
4:A:567:LYS:HZ1	11:H:46:LEU:HB2	1.53	0.71
4:A:1437:GLY:O	4:A:1439:GLY:N	2.23	0.71
5:B:23:ALA:HB1	5:B:24:PRO:CD	2.19	0.71
6:C:45:ALA:HA	6:C:72:LEU:CD1	2.19	0.71
4:A:897:TYR:HD2	4:A:936:LEU:HD13	1.55	0.71
5:B:562:GLY:HA3	5:B:590:HIS:CE1	2.26	0.71
5:B:411:PRO:O	5:B:414:ALA:HB3	1.89	0.71
5:B:800:GLN:HB3	13:J:52:THR:CG2	2.20	0.71
4:A:590:ARG:HB3	4:A:605:MET:N	2.05	0.71
6:C:183:TRP:CZ2	6:C:207:CYS:HB3	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:14:VAL:CG1	13:J:50:ILE:HD11	2.20	0.71
4:A:164:ARG:HG3	4:A:165:GLY:H	1.52	0.71
4:A:341:MET:HE2	4:A:843:LYS:HZ1	1.55	0.71
4:A:598:LEU:HA	11:H:122:LEU:HD13	1.71	0.71
4:A:800:VAL:HG22	4:A:812:GLU:HB3	1.73	0.71
5:B:364:ILE:HG12	5:B:585:VAL:HG13	1.72	0.71
8:E:48:ASP:CG	8:E:49:SER:H	1.99	0.71
10:G:119:LEU:HD12	10:G:131:GLN:O	1.91	0.71
4:A:1239:ARG:HH22	4:A:1241:ARG:HH22	1.39	0.71
5:B:542:MET:HE2	5:B:743:ILE:HG13	1.73	0.71
4:A:503:GLN:C	4:A:504:LEU:HD12	2.16	0.71
4:A:1094:VAL:HG13	4:A:1113:THR:CG2	2.16	0.71
5:B:35:SER:HA	5:B:811:TYR:HE2	1.56	0.71
5:B:1069:PHE:H	5:B:1069:PHE:HD1	1.37	0.71
5:B:1085:ILE:N	5:B:1085:ILE:HD12	2.06	0.71
10:G:30:LEU:HD13	10:G:72:VAL:HG11	1.72	0.71
5:B:728:ARG:HH12	5:B:1047:PHE:HB3	1.56	0.71
5:B:737:THR:HG21	12:I:66:PRO:HA	1.73	0.71
11:H:126:GLU:C	11:H:130:ARG:HH22	1.98	0.71
12:I:34:TYR:CD2	12:I:35:VAL:N	2.59	0.71
14:K:7:PHE:HA	14:K:10:PHE:CE2	2.26	0.71
4:A:1006:ILE:HD12	8:E:163:GLU:HG3	1.73	0.70
5:B:710:LEU:HA	5:B:733:HIS:HB3	1.74	0.70
1:T:20:DC:H4'	4:A:447:GLN:CD	2.16	0.70
4:A:1151:GLU:OE2	12:I:45:ARG:HD2	1.90	0.70
4:A:1191:TRP:CD1	4:A:1256:GLU:HB2	2.27	0.70
5:B:882:THR:HG22	5:B:884:ARG:N	2.05	0.70
8:E:124:VAL:HG13	8:E:132:ILE:HB	1.71	0.70
4:A:250:ILE:O	4:A:258:GLY:HA3	1.91	0.70
4:A:1332:PHE:N	4:A:1332:PHE:CD2	2.58	0.70
5:B:871:THR:HG22	5:B:872:GLU:O	1.90	0.70
11:H:81:PRO:CB	11:H:82:PRO:HD2	2.20	0.70
4:A:63:ARG:HA	4:A:74:MET:SD	2.32	0.70
4:A:244:PRO:HB2	4:A:245:PRO:CD	2.20	0.70
5:B:1163:CYS:SG	5:B:1165:ILE:HB	2.30	0.70
11:H:36:CYS:HA	11:H:126:GLU:O	1.91	0.70
5:B:365:THR:HG23	5:B:367:LEU:HG	1.74	0.70
5:B:827:ILE:HD12	5:B:1086:PHE:HD2	1.55	0.70
5:B:852:ARG:HH22	15:L:70:ARG:C	1.99	0.70
5:B:1073:TYR:CE2	5:B:1080:LYS:HG2	2.27	0.70
6:C:20:PHE:HE1	6:C:22:LEU:HD12	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2:VAL:HG21	5:B:1157:ALA:C	2.17	0.70
4:A:341:MET:HE1	5:B:1135:ARG:NH1	2.07	0.70
4:A:346:ASP:HB3	5:B:1108:ARG:H	1.56	0.70
4:A:903:ASN:HD22	4:A:905:ASP:H	1.37	0.70
4:A:382:PRO:HD3	4:A:428:TYR:CD2	2.26	0.70
6:C:66:ARG:NH1	13:J:2:ILE:HG21	2.07	0.70
14:K:50:LEU:HD11	14:K:75:ILE:HD13	1.72	0.70
4:A:1155:ASP:OD2	4:A:1161:THR:HG23	1.91	0.70
4:A:1341:ILE:CG2	4:A:1342:GLU:H	2.04	0.70
4:A:1394:THR:HG21	4:A:1398:MET:SD	2.32	0.70
10:G:15:PRO:HA	10:G:18:PHE:CE1	2.27	0.70
13:J:8:PHE:H	13:J:49:MET:CE	2.05	0.70
4:A:68:GLN:C	4:A:70:CYS:H	2.00	0.69
5:B:557:PHE:C	5:B:557:PHE:CD2	2.69	0.69
7:D:66:ARG:HD2	7:D:133:THR:HB	1.74	0.69
15:L:48:CYS:HB3	15:L:51:CYS:O	1.91	0.69
4:A:56:PRO:O	4:A:57:ARG:CG	2.38	0.69
4:A:1450:LEU:O	4:A:1450:LEU:HG	1.92	0.69
6:C:177:GLU:HB2	6:C:231:ASN:HB3	1.74	0.69
5:B:1002:THR:HG21	5:B:1006:ILE:HD12	1.74	0.69
14:K:31:VAL:HG12	14:K:32:VAL:N	2.07	0.69
4:A:79:GLY:HA3	4:A:243:PRO:CG	2.21	0.69
4:A:254:GLU:HB2	5:B:935:ARG:HH12	1.56	0.69
5:B:948:ILE:HG22	5:B:949:VAL:O	1.92	0.69
9:F:103:MET:O	9:F:104:ASN:HB2	1.91	0.69
9:F:125:LEU:HG	9:F:125:LEU:O	1.91	0.69
4:A:450:LEU:HD12	4:A:450:LEU:N	2.07	0.69
4:A:722:LEU:O	4:A:725:ALA:HB3	1.91	0.69
4:A:816:HIS:CD2	5:B:764:SER:HB2	2.27	0.69
5:B:708:GLU:O	5:B:710:LEU:N	2.26	0.69
8:E:135:PHE:HD2	8:E:140:LEU:HD21	1.55	0.69
4:A:49:LYS:HE2	4:A:61:ILE:HD12	1.73	0.69
4:A:427:GLN:HG3	4:A:430:TRP:CZ2	2.27	0.69
5:B:701:ILE:HD11	5:B:703:ILE:HD11	1.74	0.69
11:H:59:ILE:HG22	11:H:60:ALA:H	1.58	0.69
4:A:1293:SER:OG	4:A:1294:PRO:HD2	1.93	0.69
5:B:1099:VAL:HG12	5:B:1100:ASP:N	2.07	0.69
12:I:111:THR:HG22	12:I:112:SER:N	2.06	0.69
13:J:48:ARG:HD2	13:J:49:MET:N	2.08	0.69
4:A:107:CYS:N	4:A:114:LEU:HD21	2.08	0.69
4:A:154:SER:HB3	4:A:162:VAL:HG21	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:463:ILE:HB	4:A:464:PRO:HD2	1.75	0.69
4:A:665:GLY:O	4:A:667:GLY:N	2.26	0.69
4:A:1030:ARG:HG3	4:A:1034:GLU:OE2	1.92	0.69
5:B:496:ARG:HB3	5:B:496:ARG:HH11	1.57	0.69
7:D:34:GLN:O	7:D:47:LEU:HD23	1.92	0.69
7:D:47:LEU:HD13	7:D:48:ILE:N	2.05	0.69
15:L:38:LEU:O	15:L:39:SER:HB3	1.91	0.69
15:L:58:LYS:O	15:L:58:LYS:HG2	1.92	0.69
3:P:10:C:H4'	4:A:485:ASP:OD1	1.92	0.69
4:A:853:ASP:OD1	4:A:855:THR:N	2.26	0.69
4:A:857:ARG:HD3	4:A:861:GLY:O	1.92	0.69
4:A:901:LEU:HG	4:A:926:GLN:NE2	2.08	0.69
6:C:5:GLY:O	6:C:7:GLN:HG3	1.93	0.69
6:C:239:PRO:HB2	6:C:241:ASP:OD1	1.92	0.69
8:E:135:PHE:HB3	8:E:140:LEU:HD11	1.75	0.69
4:A:503:GLN:HE21	9:F:90:ARG:NH2	1.91	0.69
4:A:694:THR:O	4:A:698:GLN:HG3	1.90	0.69
4:A:886:ILE:HG22	4:A:887:GLY:N	2.08	0.69
4:A:107:CYS:H	4:A:114:LEU:HD21	1.56	0.68
5:B:831:SER:HB3	5:B:994:TYR:OH	1.93	0.68
7:D:52:LEU:HD21	7:D:147:TYR:HE2	1.57	0.68
14:K:46:ILE:O	14:K:50:LEU:HB2	1.92	0.68
1:T:15:DT:H1'	4:A:1386:ARG:NH1	2.09	0.68
4:A:88:LYS:HE3	4:A:280:GLU:OE2	1.94	0.68
4:A:853:ASP:O	4:A:854:ASN:HB2	1.92	0.68
5:B:806:THR:HG22	5:B:808:ALA:N	2.08	0.68
5:B:1115:THR:O	5:B:1116:ARG:HB2	1.92	0.68
10:G:7:LEU:HD11	10:G:45:ILE:HD11	1.76	0.68
4:A:285:PRO:HG2	4:A:288:ALA:HB3	1.74	0.68
4:A:591:PHE:HA	4:A:595:THR:HG21	1.76	0.68
4:A:672:ASP:HB2	4:A:736:ASN:OD1	1.92	0.68
4:A:866:PHE:O	4:A:867:ILE:HG13	1.94	0.68
4:A:885:THR:O	4:A:940:ARG:HD2	1.92	0.68
4:A:1332:PHE:HD2	4:A:1332:PHE:H	1.40	0.68
5:B:282:ILE:HD12	5:B:382:ILE:HD13	1.75	0.68
5:B:1165:ILE:HG22	5:B:1166:CYS:N	2.07	0.68
4:A:567:LYS:HD3	11:H:95:TYR:CD2	2.28	0.68
4:A:666:ILE:HD12	4:A:667:GLY:H	1.57	0.68
5:B:1180:PHE:HB3	5:B:1191:ILE:HD12	1.76	0.68
5:B:1223:ASP:O	5:B:1224:PHE:HB2	1.92	0.68
9:F:82:THR:HG22	9:F:84:TYR:H	1.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:99:GLY:HA3	11:H:118:PHE:HA	1.75	0.68
4:A:547:LEU:HD22	14:K:58:PHE:CD1	2.29	0.68
4:A:1348:LEU:HG	4:A:1372:VAL:HG23	1.74	0.68
5:B:293:PRO:HG2	5:B:296:GLU:HB3	1.75	0.68
5:B:824:ILE:CG2	5:B:1087:PHE:HE2	2.03	0.68
6:C:114:TYR:HB3	6:C:140:ASN:O	1.93	0.68
6:C:167:HIS:CE1	15:L:70:ARG:HB3	2.29	0.68
3:P:1:A:H2'	3:P:2:A:C8	2.28	0.68
4:A:325:ILE:HG21	5:B:1210:MET:HG3	1.76	0.68
4:A:763:ALA:O	4:A:803:SER:HB3	1.93	0.68
4:A:1152:ILE:HG13	12:I:44:TYR:HB3	1.76	0.68
13:J:44:TYR:HA	13:J:47:ARG:HB2	1.74	0.68
6:C:56:THR:HG22	6:C:57:VAL:N	2.09	0.68
15:L:40:LEU:HD13	15:L:44:ASP:HB3	1.76	0.68
4:A:152:VAL:HG12	4:A:153:PRO:HD2	1.75	0.68
8:E:198:ILE:CD1	8:E:212:ARG:HG3	2.23	0.68
5:B:502:ILE:HG22	5:B:507:LYS:HD2	1.76	0.68
5:B:745:PRO:O	5:B:748:ILE:HG12	1.94	0.68
9:F:130:ILE:O	9:F:148:VAL:HG21	1.93	0.68
4:A:1445:ILE:HD12	4:A:1445:ILE:N	2.06	0.67
7:D:176:GLU:C	7:D:178:ALA:H	2.02	0.67
4:A:475:THR:CG2	4:A:476:SER:H	2.07	0.67
4:A:800:VAL:HG13	4:A:812:GLU:OE1	1.94	0.67
4:A:829:VAL:C	4:A:831:THR:N	2.50	0.67
6:C:73:GLN:NE2	6:C:74:SER:H	1.92	0.67
6:C:253:LYS:O	6:C:256:ALA:HB3	1.95	0.67
4:A:567:LYS:CE	11:H:46:LEU:HB2	2.25	0.67
5:B:1208:MET:O	5:B:1211:ASN:N	2.23	0.67
6:C:179:GLU:HG2	6:C:180:TYR:H	1.59	0.67
2:N:3:DG:H2''	2:N:4:DT:OP2	1.93	0.67
4:A:3:GLY:O	4:A:4:GLN:HB2	1.94	0.67
4:A:458:HIS:CE1	4:A:507:VAL:HG21	2.30	0.67
4:A:503:GLN:NE2	9:F:90:ARG:HH21	1.92	0.67
4:A:1341:ILE:CG2	4:A:1342:GLU:N	2.57	0.67
5:B:653:VAL:CG2	5:B:689:LEU:HB3	2.24	0.67
7:D:170:THR:HG21	7:D:172:LEU:HG	1.75	0.67
1:T:23:DG:H2'	1:T:24:DG:C8	2.29	0.67
4:A:71:GLN:C	4:A:73:GLY:H	2.02	0.67
5:B:393:LYS:HA	5:B:393:LYS:HE3	1.77	0.67
7:D:198:LEU:O	7:D:200:ASN:N	2.27	0.67
13:J:44:TYR:HA	13:J:47:ARG:CB	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:356:ASP:HB2	4:A:469:ARG:HH11	1.56	0.67
5:B:1045:SER:O	5:B:1046:PRO:O	2.12	0.67
10:G:138:THR:HG22	10:G:139:ILE:N	2.09	0.67
4:A:79:GLY:HA3	4:A:243:PRO:HG2	1.77	0.67
4:A:399:HIS:HB3	4:A:400:PRO:CD	2.17	0.67
4:A:590:ARG:HG3	4:A:590:ARG:HH11	1.59	0.67
4:A:869:GLY:O	8:E:204:THR:HG21	1.94	0.67
4:A:1007:ILE:C	4:A:1009:ASN:H	2.03	0.67
4:A:1017:LEU:HB2	8:E:206:GLY:N	2.06	0.67
7:D:40:HIS:CB	10:G:73:LYS:HZ2	2.07	0.67
5:B:108:VAL:HG12	5:B:109:THR:H	1.58	0.67
5:B:746:SER:HB2	5:B:1046:PRO:HG2	1.76	0.67
5:B:758:PHE:CE1	5:B:1027:ILE:HG22	2.29	0.67
5:B:955:THR:CG2	5:B:956:THR:H	2.08	0.67
8:E:90:VAL:HG23	8:E:120:ALA:HA	1.76	0.67
8:E:157:SER:C	8:E:159:ASP:H	2.03	0.67
12:I:55:THR:CG2	12:I:58:VAL:HG21	2.25	0.67
4:A:450:LEU:HD12	4:A:450:LEU:H	1.60	0.67
5:B:860:MET:HG2	5:B:861:ASP:N	2.10	0.67
8:E:157:SER:OG	8:E:160:GLU:HG3	1.94	0.67
4:A:19:PHE:O	4:A:1416:ALA:HA	1.95	0.66
4:A:874:ASP:N	4:A:1058:VAL:HG22	2.10	0.66
4:A:1336:MET:CE	4:A:1381:LEU:HG	2.26	0.66
4:A:55:ASP:C	4:A:57:ARG:N	2.47	0.66
5:B:125:SER:HA	5:B:171:PRO:HA	1.77	0.66
5:B:244:LEU:HD21	5:B:366:GLN:NE2	2.09	0.66
5:B:515:HIS:CD2	5:B:517:THR:H	2.12	0.66
5:B:563:MET:HE3	5:B:580:VAL:HB	1.76	0.66
5:B:1065:GLN:NE2	5:B:1066:SER:N	2.42	0.66
4:A:351:THR:HG22	5:B:1103:ILE:HA	1.76	0.66
4:A:384:ASN:CG	4:A:388:LEU:HD12	2.21	0.66
4:A:1261:LYS:O	4:A:1264:GLU:HB3	1.95	0.66
5:B:95:ILE:HG13	5:B:130:VAL:HG22	1.77	0.66
5:B:899:ILE:CD1	5:B:911:ILE:HA	2.26	0.66
5:B:975:GLN:HG2	5:B:976:ILE:H	1.60	0.66
11:H:17:PRO:HB3	11:H:24:CYS:SG	2.35	0.66
13:J:8:PHE:H	13:J:49:MET:HE3	1.59	0.66
4:A:12:ARG:HD2	5:B:1218:THR:HB	1.76	0.66
4:A:349:ALA:C	5:B:1128:LEU:HD11	2.20	0.66
4:A:567:LYS:HE3	11:H:46:LEU:HB2	1.78	0.66
4:A:1444:MET:HG2	10:G:60:ARG:HA	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:376:PHE:CE2	5:B:569:TYR:HD2	2.12	0.66
5:B:508:LEU:O	5:B:509:ALA:CB	2.43	0.66
5:B:770:GLN:CD	5:B:983:ARG:HA	2.20	0.66
10:G:143:ILE:HG22	10:G:144:ARG:N	2.10	0.66
11:H:89:LEU:C	11:H:91:ASP:H	2.04	0.66
4:A:335:ARG:HH12	5:B:1202:LEU:HD13	1.58	0.66
5:B:192:LEU:O	5:B:193:LYS:HB2	1.95	0.66
5:B:516:ASN:N	5:B:516:ASN:ND2	2.43	0.66
5:B:642:ASP:HB3	5:B:649:LYS:CD	2.26	0.66
6:C:39:ALA:CA	6:C:164:ALA:HB3	2.22	0.66
4:A:899:VAL:HB	4:A:929:LEU:HD11	1.77	0.66
6:C:66:ARG:HH21	13:J:5:VAL:HG23	1.61	0.66
8:E:213:ILE:HG12	8:E:214:CYS:N	2.06	0.66
4:A:666:ILE:HD11	5:B:1067:ARG:O	1.95	0.66
5:B:503:GLY:HA3	5:B:507:LYS:CE	2.25	0.66
5:B:952:VAL:HG12	5:B:953:LEU:N	2.11	0.66
12:I:32:CYS:SG	12:I:33:SER:N	2.69	0.66
4:A:23:SER:HA	4:A:233:TRP:CD1	2.31	0.66
4:A:701:LEU:HD21	12:I:114:GLN:HB2	1.78	0.66
4:A:1291:VAL:HG13	4:A:1292:PRO:CD	2.26	0.66
5:B:859:TYR:CZ	5:B:941:LEU:HD12	2.31	0.66
4:A:590:ARG:HH21	4:A:620:LYS:HB3	1.60	0.66
5:B:39:ARG:HH21	5:B:665:GLU:HG2	1.60	0.66
5:B:229:ALA:HB1	5:B:231:PRO:HD2	1.77	0.66
5:B:357:GLN:O	5:B:366:GLN:HA	1.96	0.66
11:H:81:PRO:CB	11:H:82:PRO:CD	2.73	0.66
4:A:868:TYR:HD2	4:A:1058:VAL:HG21	1.59	0.65
5:B:46:GLN:HG3	5:B:47:GLN:N	2.10	0.65
5:B:1182:CYS:O	5:B:1182:CYS:SG	2.54	0.65
8:E:153:HIS:HB3	8:E:196:VAL:HG11	1.78	0.65
10:G:43:GLY:HA3	10:G:80:LYS:HB3	1.76	0.65
4:A:269:ILE:HD13	4:A:300:VAL:HG22	1.78	0.65
4:A:535:THR:CG2	4:A:616:VAL:HA	2.26	0.65
4:A:567:LYS:CB	11:H:95:TYR:HA	2.25	0.65
4:A:1120:LEU:O	4:A:1323:ASP:HB2	1.96	0.65
5:B:821:GLN:HE22	5:B:851:PHE:HA	1.60	0.65
6:C:147:LEU:HB2	6:C:151:GLN:HB2	1.78	0.65
7:D:56:ARG:HD3	7:D:149:THR:HA	1.77	0.65
9:F:79:ARG:HG3	9:F:144:GLU:OE1	1.96	0.65
10:G:59:GLY:HA3	10:G:70:PHE:CD2	2.32	0.65
5:B:995:ARG:NH1	6:C:165:LYS:HG2	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:111:LEU:C	9:F:113:GLY:H	2.04	0.65
11:H:100:THR:OG1	11:H:138:GLU:HG3	1.97	0.65
4:A:108:MET:N	4:A:108:MET:SD	2.69	0.65
4:A:384:ASN:O	4:A:385:ILE:C	2.40	0.65
4:A:548:ASN:OD1	14:K:60:ALA:HB1	1.97	0.65
5:B:978:ASP:OD2	5:B:1098:MET:HG2	1.95	0.65
10:G:1:MET:SD	10:G:1:MET:C	2.80	0.65
4:A:1115:SER:O	4:A:1116:LEU:HB3	1.94	0.65
5:B:179:CYS:SG	5:B:181:LEU:HB2	2.37	0.65
5:B:465:ASN:HD22	5:B:465:ASN:N	1.95	0.65
6:C:177:GLU:HG3	6:C:231:ASN:HD22	1.62	0.65
4:A:907:THR:CG2	4:A:908:LEU:N	2.58	0.65
7:D:134:THR:HG22	7:D:135:GLY:N	2.12	0.65
4:A:1195:LEU:HD11	4:A:1267:MET:HE1	1.78	0.65
5:B:121:ASN:HA	5:B:207:GLY:HA2	1.79	0.65
8:E:176:PRO:O	8:E:212:ARG:HA	1.96	0.65
8:E:202:SER:OG	8:E:204:THR:HG22	1.97	0.65
9:F:90:ARG:HG3	9:F:91:ALA:N	2.09	0.65
5:B:172:ILE:HD13	5:B:178:ASN:CB	2.27	0.65
5:B:642:ASP:HA	5:B:649:LYS:HA	1.77	0.65
5:B:766:ARG:HH22	5:B:1020:ARG:HH11	1.42	0.65
11:H:56:THR:HB	11:H:145:ARG:HG2	1.79	0.65
4:A:353:ILE:HD12	4:A:487:MET:HE2	1.78	0.65
4:A:385:ILE:HG22	4:A:386:ASP:N	2.11	0.65
4:A:1224:LEU:HD12	4:A:1241:ARG:O	1.97	0.65
6:C:252:GLN:HG3	14:K:95:ILE:HG23	1.79	0.65
4:A:18:GLN:HB2	5:B:1215:ARG:HB2	1.80	0.65
5:B:840:ILE:HB	5:B:1011:ILE:HB	1.77	0.65
2:N:1:DA:H1'	2:N:2:DA:O5'	1.96	0.64
3:P:9:G:H5''	5:B:776:GLN:HE22	1.62	0.64
5:B:118:ARG:HH22	5:B:194:GLU:CD	2.05	0.64
5:B:190:TYR:CE2	13:J:62:ARG:HB3	2.31	0.64
6:C:77:ILE:HG23	6:C:161:LYS:HE3	1.79	0.64
6:C:80:LEU:HD11	6:C:95:CYS:CA	2.28	0.64
7:D:130:LEU:O	7:D:132:GLN:N	2.29	0.64
7:D:202:ILE:HG21	7:D:207:LEU:HB2	1.78	0.64
4:A:1438:THR:HB	5:B:1144:ALA:HB3	1.80	0.64
7:D:5:THR:O	7:D:6:SER:O	2.15	0.64
4:A:332:LYS:HG3	4:A:333:GLU:HG2	1.77	0.64
4:A:618:GLU:O	4:A:620:LYS:N	2.30	0.64
4:A:630:ILE:HD13	4:A:646:PHE:CZ	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:604:ARG:HH22	5:B:614:SER:HA	1.63	0.64
5:B:616:ILE:HD12	5:B:616:ILE:N	2.11	0.64
8:E:84:ASP:O	8:E:86:PRO:HD3	1.97	0.64
4:A:33:ALA:O	4:A:83:HIS:HD2	1.81	0.64
4:A:289:ILE:C	4:A:291:GLU:H	2.05	0.64
4:A:605:MET:HE2	4:A:607:ILE:HG13	1.80	0.64
4:A:901:LEU:CG	4:A:926:GLN:HE21	2.10	0.64
4:A:979:SER:OG	4:A:980:ASP:N	2.30	0.64
4:A:1402:PHE:CE1	4:A:1403:GLU:HG3	2.33	0.64
5:B:515:HIS:O	5:B:518:HIS:HB2	1.97	0.64
10:G:81:PRO:HG3	10:G:106:MET:SD	2.36	0.64
11:H:4:THR:CA	11:H:60:ALA:HB2	2.22	0.64
14:K:61:TYR:C	14:K:61:TYR:CD2	2.76	0.64
4:A:262:LEU:C	4:A:264:PHE:H	2.05	0.64
4:A:1206:ASP:HB3	4:A:1274:ARG:HH12	1.61	0.64
6:C:238:ILE:CG2	6:C:242:GLN:HB2	2.27	0.64
8:E:179:GLN:HB2	8:E:182:ASP:HB2	1.78	0.64
10:G:34:VAL:CG1	10:G:45:ILE:HG21	2.26	0.64
4:A:798:GLY:HA2	4:A:815:PHE:HD1	1.60	0.64
5:B:295:GLY:N	5:B:298:LEU:HD23	2.13	0.64
5:B:705:MET:H	5:B:710:LEU:CD1	2.11	0.64
8:E:93:MET:SD	8:E:97:VAL:HG23	2.37	0.64
8:E:192:ARG:HH11	8:E:192:ARG:HG3	1.62	0.64
11:H:99:GLY:N	11:H:118:PHE:HD2	1.96	0.64
4:A:1428:VAL:HG13	5:B:1151:LEU:CD2	2.27	0.64
5:B:777:ALA:HA	5:B:1095:LEU:HA	1.78	0.64
12:I:6:PHE:HB3	12:I:12:ASN:O	1.97	0.64
4:A:901:LEU:O	4:A:921:GLY:N	2.30	0.64
7:D:122:GLU:HA	7:D:125:SER:OG	1.98	0.64
8:E:15:ALA:O	8:E:19:VAL:HG23	1.98	0.64
4:A:863:VAL:HG11	4:A:866:PHE:CD2	2.33	0.64
4:A:1072:ILE:O	4:A:1075:PRO:HD2	1.98	0.64
5:B:911:ILE:HD11	5:B:941:LEU:HD13	1.78	0.64
6:C:172:PRO:O	6:C:235:VAL:HG23	1.97	0.64
10:G:88:ASP:HB3	10:G:144:ARG:HA	1.80	0.64
4:A:69:THR:C	4:A:71:GLN:N	2.55	0.63
4:A:518:LYS:HE2	4:A:624:SER:O	1.97	0.63
4:A:1107:VAL:HG12	4:A:1107:VAL:O	1.98	0.63
4:A:1116:LEU:HD11	4:A:1118:VAL:HG13	1.80	0.63
4:A:1166:ASP:OD2	4:A:1239:ARG:HD2	1.97	0.63
5:B:778:MET:HE2	5:B:1094:ARG:HD3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1183:LYS:N	5:B:1183:LYS:CE	2.61	0.63
7:D:56:ARG:HB2	7:D:148:LEU:HD22	1.79	0.63
8:E:14:ARG:HH21	8:E:141:VAL:CG1	2.11	0.63
9:F:77:ASP:C	9:F:79:ARG:H	2.05	0.63
10:G:9:LEU:HD12	10:G:10:ASN:H	1.62	0.63
12:I:99:LEU:C	12:I:100:PHE:HD1	2.06	0.63
13:J:36:LEU:HD12	13:J:47:ARG:HH12	1.61	0.63
4:A:467:THR:O	4:A:469:ARG:HG3	1.99	0.63
5:B:635:ARG:NH2	5:B:742:GLU:OE2	2.32	0.63
6:C:22:LEU:HD13	6:C:230:MET:CE	2.28	0.63
11:H:91:ASP:C	11:H:93:TYR:H	2.06	0.63
4:A:547:LEU:HB3	14:K:58:PHE:HE1	1.63	0.63
4:A:1323:ASP:OD1	4:A:1325:THR:HB	1.98	0.63
5:B:880:THR:O	5:B:881:ASN:HB2	1.97	0.63
6:C:191:TYR:HD2	6:C:201:TRP:CD1	2.16	0.63
4:A:901:LEU:HD22	4:A:919:ILE:CG2	2.28	0.63
4:A:902:LEU:HG	4:A:926:GLN:HG3	1.81	0.63
4:A:1341:ILE:HD12	4:A:1379:GLY:O	1.98	0.63
5:B:212:LEU:HD23	5:B:480:SER:HB2	1.80	0.63
5:B:798:TYR:HE2	6:C:62:PHE:CZ	2.17	0.63
4:A:1325:THR:O	8:E:148:GLU:HB2	1.98	0.63
5:B:549:THR:H	5:B:628:THR:HG23	1.63	0.63
5:B:1087:PHE:HD2	5:B:1088:GLY:N	1.97	0.63
4:A:84:ILE:O	4:A:84:ILE:HG23	1.97	0.63
5:B:121:ASN:HA	5:B:207:GLY:CA	2.28	0.63
5:B:622:LYS:HE2	12:I:59:VAL:HG22	1.79	0.63
7:D:173:HIS:O	7:D:177:VAL:HG23	1.98	0.63
4:A:265:LYS:NZ	4:A:322:VAL:HG22	2.14	0.63
4:A:353:ILE:HD13	4:A:487:MET:HE2	1.81	0.63
4:A:567:LYS:HB3	11:H:96:VAL:N	2.12	0.63
4:A:1364:ASN:O	4:A:1365:TYR:C	2.42	0.63
10:G:1:MET:SD	10:G:1:MET:O	2.56	0.63
4:A:18:GLN:O	5:B:1215:ARG:HG2	1.98	0.63
4:A:265:LYS:HE2	4:A:322:VAL:CG1	2.29	0.63
4:A:728:LYS:O	4:A:732:LEU:HG	1.97	0.63
13:J:44:TYR:H	13:J:44:TYR:HD2	1.47	0.63
4:A:504:LEU:HD11	9:F:91:ALA:HB1	1.79	0.63
4:A:552:TRP:HE3	4:A:651:LYS:HB3	1.64	0.63
4:A:613:ILE:O	4:A:614:PHE:HB3	1.97	0.63
4:A:828:ALA:HB2	5:B:530:GLY:HA2	1.79	0.63
5:B:284:ILE:HD13	5:B:333:PHE:HD2	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:857:ARG:HD2	5:B:945:GLU:OE1	1.97	0.63
6:C:164:ALA:HA	6:C:167:HIS:O	1.98	0.63
4:A:50:ILE:C	4:A:52:GLY:H	2.06	0.62
4:A:782:ARG:NH2	5:B:699:GLU:O	2.31	0.62
5:B:65:GLU:HG3	5:B:66:ASP:N	2.11	0.62
5:B:237:VAL:HG22	5:B:257:LYS:HA	1.81	0.62
5:B:597:MET:HA	5:B:597:MET:HE3	1.80	0.62
5:B:604:ARG:NH1	5:B:691:GLU:OE2	2.31	0.62
6:C:73:GLN:HB3	6:C:131:HIS:H	1.62	0.62
4:A:404:TYR:HB2	4:A:433:GLU:HB2	1.80	0.62
4:A:606:LEU:HB3	4:A:614:PHE:CE2	2.33	0.62
4:A:720:ARG:O	4:A:724:GLU:HB2	1.98	0.62
4:A:853:ASP:OD1	4:A:855:THR:HG22	1.98	0.62
5:B:205:ILE:O	5:B:207:GLY:N	2.33	0.62
5:B:1034:VAL:HG23	5:B:1059:LEU:HD13	1.81	0.62
6:C:73:GLN:HE21	6:C:74:SER:H	1.45	0.62
10:G:18:PHE:HA	10:G:22:MET:CE	2.28	0.62
15:L:40:LEU:HD22	15:L:44:ASP:CG	2.24	0.62
15:L:53:HIS:O	15:L:55:ILE:HG12	1.99	0.62
4:A:665:GLY:HA2	5:B:1026:LEU:HD21	1.79	0.62
4:A:809:THR:OG1	4:A:812:GLU:HG3	1.98	0.62
5:B:642:ASP:HB3	5:B:649:LYS:HG3	1.80	0.62
5:B:1159:ARG:HD3	5:B:1193:GLN:HG3	1.79	0.62
4:A:75:ASN:O	4:A:76:GLU:HB3	1.98	0.62
4:A:408:ASP:C	4:A:410:GLY:H	2.07	0.62
4:A:767:GLN:OE1	4:A:799:PHE:HB2	2.00	0.62
4:A:901:LEU:N	4:A:926:GLN:NE2	2.41	0.62
5:B:233:PRO:HG2	5:B:234:ILE:CD1	2.28	0.62
5:B:293:PRO:HG2	5:B:296:GLU:CB	2.30	0.62
5:B:827:ILE:HD12	5:B:1086:PHE:CD2	2.34	0.62
14:K:10:PHE:N	14:K:10:PHE:CD2	2.68	0.62
4:A:93:VAL:HG22	4:A:301:ALA:HA	1.82	0.62
4:A:1214:GLU:O	4:A:1218:GLN:HG2	1.99	0.62
5:B:36:ALA:HA	5:B:39:ARG:HD2	1.81	0.62
5:B:1082:MET:O	6:C:189:THR:HG23	1.99	0.62
5:B:1099:VAL:C	5:B:1101:ASP:H	2.06	0.62
6:C:133:ILE:CD1	6:C:237:SER:HA	2.30	0.62
6:C:152:GLU:OE2	6:C:154:LYS:HE3	1.99	0.62
12:I:62:ILE:O	12:I:62:ILE:HG12	2.00	0.62
4:A:14:VAL:H	4:A:1432:GLN:HE22	1.48	0.62
4:A:23:SER:HB3	4:A:233:TRP:CE2	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:699:ALA:HB3	4:A:701:LEU:HG	1.81	0.62
4:A:714:PHE:O	4:A:718:VAL:HG23	2.00	0.62
4:A:783:THR:HG21	4:A:815:PHE:CE2	2.35	0.62
4:A:899:VAL:HB	4:A:929:LEU:HD12	1.82	0.62
4:A:1019:CYS:O	4:A:1022:LEU:N	2.32	0.62
5:B:758:PHE:CE2	5:B:1044:ALA:HA	2.35	0.62
5:B:1107:ALA:O	5:B:1108:ARG:HG2	1.99	0.62
5:B:1215:ARG:C	5:B:1216:LEU:HD23	2.24	0.62
4:A:308:ILE:HG22	4:A:309:ALA:H	1.64	0.62
4:A:590:ARG:HB2	4:A:605:MET:HB3	1.81	0.62
4:A:855:THR:HG23	4:A:857:ARG:HG3	1.80	0.62
5:B:515:HIS:H	5:B:518:HIS:HD2	1.47	0.62
8:E:207:ARG:CB	8:E:207:ARG:HH11	2.12	0.62
4:A:675:THR:O	4:A:679:ILE:HG13	1.98	0.62
4:A:897:TYR:CD2	4:A:936:LEU:HD13	2.35	0.62
5:B:1102:LYS:O	5:B:1103:ILE:C	2.41	0.62
11:H:113:ALA:HB2	11:H:126:GLU:HG3	1.81	0.62
13:J:2:ILE:H	13:J:57:ILE:CG2	2.13	0.62
4:A:1017:LEU:HB3	8:E:205:SER:HA	1.80	0.62
5:B:43:LEU:HD11	5:B:811:TYR:O	2.00	0.62
7:D:53:SER:HB3	7:D:152:SER:CA	2.30	0.62
4:A:262:LEU:O	4:A:264:PHE:N	2.33	0.62
4:A:1063:MET:CG	4:A:1436:ILE:HG23	2.30	0.62
4:A:1120:LEU:HD13	4:A:1304:TRP:O	2.00	0.62
5:B:611:PRO:HB3	5:B:685:LEU:HD11	1.80	0.62
5:B:737:THR:CG2	12:I:66:PRO:HA	2.30	0.62
5:B:1040:ASN:O	5:B:1041:GLU:C	2.43	0.62
7:D:134:THR:CG2	7:D:135:GLY:N	2.62	0.62
11:H:44:VAL:O	11:H:44:VAL:HG12	1.99	0.62
4:A:1057:VAL:HG12	4:A:1058:VAL:H	1.64	0.61
4:A:1227:ILE:HG22	4:A:1228:TRP:N	2.14	0.61
5:B:189:LEU:O	5:B:192:LEU:N	2.29	0.61
5:B:1162:ILE:HD11	5:B:1194:ILE:HD13	1.82	0.61
6:C:212:PRO:CB	6:C:213:PRO:HD2	2.30	0.61
7:D:53:SER:HB3	7:D:152:SER:HA	1.82	0.61
13:J:57:ILE:HA	13:J:60:PHE:CD2	2.32	0.61
4:A:340:LEU:HD21	5:B:1200:ALA:N	2.15	0.61
4:A:463:ILE:HD12	4:A:469:ARG:HD2	1.82	0.61
4:A:825:ILE:CG2	5:B:508:LEU:HD11	2.30	0.61
5:B:842:ASN:ND2	5:B:845:SER:H	1.98	0.61
8:E:23:VAL:HG13	8:E:78:LEU:HD13	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:14:VAL:O	13:J:14:VAL:HG12	2.00	0.61
4:A:263:THR:HG22	4:A:263:THR:O	2.00	0.61
4:A:319:GLY:HA3	5:B:471:LYS:HA	1.82	0.61
4:A:471:ASN:OD1	4:A:472:LEU:N	2.34	0.61
4:A:730:GLY:C	4:A:732:LEU:H	2.08	0.61
4:A:738:LYS:HB2	4:A:740:LEU:HG	1.83	0.61
4:A:765:VAL:HG12	4:A:766:GLY:N	2.15	0.61
4:A:1155:ASP:OD1	4:A:1161:THR:HA	2.00	0.61
5:B:1065:GLN:HE21	5:B:1066:SER:N	1.97	0.61
7:D:47:LEU:HD11	10:G:3:PHE:CD2	2.35	0.61
4:A:337:ARG:HD3	5:B:1132:GLU:OE1	2.01	0.61
4:A:1127:ASP:HB3	4:A:1130:GLN:CB	2.30	0.61
4:A:1305:VAL:HG12	4:A:1306:LEU:N	2.16	0.61
5:B:705:MET:N	5:B:710:LEU:HD12	2.13	0.61
5:B:763:GLN:HG2	5:B:765:PRO:HD2	1.82	0.61
5:B:865:LYS:HE2	5:B:871:THR:OG1	2.01	0.61
6:C:98:VAL:O	6:C:99:LEU:HD23	2.00	0.61
10:G:1:MET:HG3	10:G:85:GLU:OE2	2.01	0.61
10:G:51:TYR:C	10:G:51:TYR:CD2	2.79	0.61
4:A:40:THR:HG22	4:A:41:MET:CG	2.28	0.61
4:A:730:GLY:O	4:A:732:LEU:N	2.34	0.61
5:B:496:ARG:NH1	5:B:539:LEU:HB2	2.16	0.61
5:B:825:VAL:CG1	5:B:826:ALA:N	2.63	0.61
9:F:89:GLU:OE2	9:F:134:ILE:HG21	2.01	0.61
14:K:65:HIS:HD2	14:K:67:PHE:N	1.94	0.61
4:A:299:HIS:C	4:A:301:ALA:H	2.09	0.61
4:A:666:ILE:CD1	4:A:667:GLY:H	2.14	0.61
5:B:114:PRO:HG2	5:B:115:GLN:H	1.65	0.61
5:B:227:LYS:HB2	5:B:395:GLN:OE1	2.00	0.61
5:B:569:TYR:CE1	5:B:589:VAL:HG21	2.35	0.61
5:B:1006:ILE:HD13	13:J:44:TYR:CE2	2.35	0.61
4:A:311:GLN:O	4:A:312:PRO:C	2.44	0.61
8:E:180:ARG:HH21	8:E:192:ARG:CB	2.10	0.61
10:G:18:PHE:HA	10:G:22:MET:HE3	1.83	0.61
4:A:244:PRO:O	4:A:246:VAL:N	2.33	0.61
4:A:321:PRO:O	4:A:322:VAL:CB	2.49	0.61
4:A:351:THR:HB	5:B:1103:ILE:CD1	2.30	0.61
4:A:981:LEU:CD2	4:A:1039:LYS:HA	2.31	0.61
9:F:101:ILE:HD11	9:F:124:GLU:OE1	2.01	0.61
3:P:8:G:O2'	3:P:9:G:H5'	2.00	0.61
4:A:1410:PHE:HA	5:B:1212:ILE:HD11	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:496:ARG:HB3	5:B:496:ARG:NH1	2.15	0.61
4:A:416:ARG:C	4:A:417:TYR:HD2	2.09	0.61
4:A:1114:PRO:O	4:A:1115:SER:O	2.19	0.61
4:A:1149:ALA:HB2	12:I:47:GLU:HA	1.83	0.61
4:A:1198:ASP:O	4:A:1202:MET:HG2	2.01	0.61
5:B:217:ARG:HD2	5:B:217:ARG:C	2.26	0.61
6:C:76:ASP:OD2	6:C:128:ASN:N	2.34	0.61
3:P:9:G:H5'	5:B:776:GLN:NE2	2.16	0.60
4:A:50:ILE:O	4:A:52:GLY:N	2.31	0.60
4:A:1002:GLY:HA3	4:A:1007:ILE:HG21	1.82	0.60
4:A:1364:ASN:HD22	4:A:1364:ASN:C	2.09	0.60
12:I:101:PHE:N	12:I:101:PHE:CD1	2.67	0.60
4:A:466:SER:O	5:B:1103:ILE:HD11	2.01	0.60
4:A:481:ASP:OD1	4:A:485:ASP:OD2	2.19	0.60
4:A:598:LEU:HD22	11:H:25:ARG:NH1	2.16	0.60
4:A:1313:LEU:O	4:A:1315:GLU:N	2.34	0.60
5:B:794:ASN:O	5:B:795:ILE:HD12	2.00	0.60
5:B:822:ASN:O	13:J:48:ARG:NH1	2.34	0.60
5:B:846:ILE:HG23	5:B:974:PRO:HG2	1.83	0.60
5:B:955:THR:CG2	5:B:956:THR:N	2.63	0.60
9:F:135:ARG:HD3	9:F:143:PHE:CD2	2.36	0.60
10:G:14:HIS:ND1	10:G:15:PRO:HD2	2.16	0.60
4:A:265:LYS:N	4:A:265:LYS:HD2	2.16	0.60
4:A:504:LEU:HD11	9:F:91:ALA:CB	2.31	0.60
4:A:1057:VAL:HG12	4:A:1058:VAL:N	2.16	0.60
5:B:1197:PRO:HG2	5:B:1200:ALA:CB	2.29	0.60
6:C:112:ASN:HB2	6:C:114:TYR:CE1	2.36	0.60
4:A:1076:ALA:HA	4:A:1079:MET:HE2	1.83	0.60
5:B:213:ILE:HD12	5:B:497:ARG:HB3	1.83	0.60
5:B:230:ALA:N	5:B:231:PRO:HD2	2.16	0.60
5:B:744:HIS:CG	5:B:745:PRO:HD2	2.36	0.60
5:B:850:LEU:HD12	5:B:851:PHE:N	2.16	0.60
6:C:124:LEU:O	6:C:127:ARG:HG2	2.02	0.60
12:I:2:THR:O	12:I:3:THR:C	2.43	0.60
4:A:114:LEU:HD13	4:A:171:GLN:OE1	2.02	0.60
4:A:979:SER:OG	4:A:981:LEU:HG	2.01	0.60
4:A:1097:GLY:O	4:A:1100:ARG:HB3	2.01	0.60
4:A:1436:ILE:O	4:A:1437:GLY:C	2.42	0.60
6:C:66:ARG:NH2	13:J:3:VAL:O	2.34	0.60
11:H:89:LEU:HB3	11:H:91:ASP:OD1	2.02	0.60
1:T:18:DC:H5'	4:A:832:ALA:O	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:366:VAL:HG21	4:A:460:VAL:HG22	1.84	0.60
4:A:475:THR:CG2	4:A:476:SER:N	2.64	0.60
4:A:1364:ASN:HD22	4:A:1365:TYR:N	1.99	0.60
4:A:108:MET:SD	4:A:210:ILE:HD13	2.41	0.60
4:A:605:MET:HE2	4:A:607:ILE:CG1	2.32	0.60
4:A:818:MET:HA	5:B:514:LEU:HB3	1.84	0.60
5:B:696:GLU:O	5:B:699:GLU:HB2	2.00	0.60
5:B:705:MET:HA	5:B:705:MET:HE3	1.83	0.60
5:B:1034:VAL:C	5:B:1036:ALA:H	2.09	0.60
6:C:67:LEU:HD11	6:C:155:LEU:CD1	2.32	0.60
6:C:80:LEU:CD1	6:C:95:CYS:HA	2.32	0.60
4:A:783:THR:HG22	4:A:784:LEU:HG	1.82	0.60
4:A:1362:TYR:CD1	4:A:1363:VAL:N	2.70	0.60
5:B:225:VAL:HG11	5:B:385:LEU:HA	1.84	0.60
14:K:49:GLU:HG3	14:K:94:ILE:CG1	2.32	0.60
4:A:90:VAL:HG13	4:A:297:GLN:HA	1.82	0.60
4:A:341:MET:HE2	4:A:843:LYS:NZ	2.17	0.60
4:A:598:LEU:O	4:A:599:SER:C	2.45	0.60
4:A:858:ASN:ND2	4:A:858:ASN:C	2.55	0.60
4:A:965:GLN:O	4:A:968:GLN:HB2	2.02	0.60
4:A:1121:GLU:CG	4:A:1122:PRO:HD2	2.31	0.60
4:A:1373:ASP:HA	4:A:1376:THR:HG22	1.82	0.60
12:I:13:MET:HG3	12:I:14:LEU:N	2.16	0.60
4:A:998:LEU:H	4:A:998:LEU:HD12	1.66	0.59
5:B:763:GLN:C	5:B:765:PRO:HD2	2.27	0.59
6:C:69:LEU:N	6:C:69:LEU:HD12	2.16	0.59
8:E:35:VAL:C	8:E:37:LEU:H	2.10	0.59
9:F:96:THR:O	9:F:99:LEU:HB3	2.02	0.59
13:J:23:ASN:C	13:J:25:LEU:H	2.10	0.59
4:A:207:ILE:O	4:A:208:LEU:C	2.45	0.59
4:A:265:LYS:HE2	4:A:322:VAL:HG13	1.83	0.59
5:B:378:LEU:O	5:B:382:ILE:HG13	2.00	0.59
5:B:515:HIS:H	5:B:518:HIS:CD2	2.19	0.59
5:B:637:LEU:HD12	5:B:693:ILE:HD12	1.84	0.59
5:B:816:GLU:O	5:B:817:LEU:HD23	2.02	0.59
5:B:1166:CYS:SG	5:B:1166:CYS:O	2.59	0.59
6:C:18:VAL:HG12	6:C:18:VAL:O	2.02	0.59
6:C:31:ASN:O	6:C:32:SER:C	2.42	0.59
12:I:111:THR:HG22	12:I:112:SER:H	1.67	0.59
13:J:1:MET:H2	13:J:56:LEU:N	1.99	0.59
4:A:49:LYS:HZ1	4:A:61:ILE:CG1	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:230:ARG:H	4:A:233:TRP:HE3	1.42	0.59
4:A:714:PHE:HB2	12:I:97:MET:HE1	1.85	0.59
4:A:741:ASN:ND2	4:A:743:VAL:HB	2.18	0.59
4:A:834:THR:HG22	4:A:835:GLY:N	2.17	0.59
5:B:642:ASP:HB3	5:B:649:LYS:CG	2.33	0.59
5:B:843:GLN:O	5:B:844:SER:C	2.45	0.59
7:D:54:GLU:O	7:D:58:VAL:HG23	2.01	0.59
11:H:123:MET:HE1	11:H:142:LEU:CD1	2.33	0.59
12:I:52:ILE:HG13	12:I:52:ILE:O	2.01	0.59
4:A:341:MET:HE1	5:B:1135:ARG:HH12	1.67	0.59
4:A:1027:ALA:O	4:A:1028:THR:C	2.43	0.59
5:B:834:ASN:HA	5:B:838:SER:O	2.01	0.59
5:B:1162:ILE:HG22	5:B:1163:CYS:N	2.16	0.59
6:C:35:ARG:NH1	14:K:41:THR:OG1	2.34	0.59
10:G:15:PRO:O	10:G:16:SER:C	2.46	0.59
4:A:663:SER:OG	4:A:664:THR:N	2.34	0.59
4:A:1299:VAL:HG12	4:A:1300:LYS:N	2.16	0.59
5:B:521:LEU:HB3	5:B:633:VAL:CG1	2.31	0.59
5:B:616:ILE:HG13	5:B:697:GLU:HG3	1.84	0.59
6:C:18:VAL:CG2	6:C:240:VAL:HB	2.32	0.59
7:D:130:LEU:C	7:D:132:GLN:N	2.61	0.59
8:E:157:SER:C	8:E:159:ASP:N	2.61	0.59
4:A:78:PRO:CB	5:B:1201:LYS:HE3	2.32	0.59
5:B:46:GLN:CG	5:B:47:GLN:H	2.11	0.59
6:C:18:VAL:HG23	6:C:240:VAL:HB	1.84	0.59
1:T:24:DG:OP1	5:B:857:ARG:NH2	2.35	0.59
4:A:264:PHE:O	4:A:267:ALA:HB3	2.01	0.59
4:A:785:PRO:HG2	4:A:786:HIS:HD2	1.67	0.59
4:A:971:PHE:CE2	4:A:1040:GLN:HG2	2.37	0.59
5:B:287:ARG:HG2	5:B:292:ILE:HA	1.83	0.59
5:B:552:MET:HA	5:B:555:ILE:HB	1.84	0.59
9:F:86:THR:OG1	9:F:89:GLU:HG3	2.03	0.59
11:H:27:GLU:HA	11:H:38:LEU:O	2.03	0.59
11:H:81:PRO:HB2	11:H:82:PRO:CD	2.31	0.59
12:I:82:GLU:HB3	12:I:104:LEU:HD12	1.84	0.59
13:J:47:ARG:HG2	13:J:47:ARG:HH11	1.66	0.59
4:A:23:SER:HB3	4:A:233:TRP:CZ2	2.38	0.59
4:A:47:ARG:HH12	4:A:254:GLU:HG2	1.68	0.59
5:B:408:LEU:HG	5:B:409:ALA:H	1.66	0.59
5:B:830:TYR:O	5:B:831:SER:C	2.44	0.59
5:B:997:GLU:CD	5:B:997:GLU:H	2.11	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:7:CYS:HB2	13:J:46:CYS:HB3	1.84	0.59
4:A:61:ILE:HG22	4:A:62:ASP:H	1.68	0.59
4:A:407:ARG:HG2	4:A:430:TRP:CH2	2.37	0.59
4:A:408:ASP:O	4:A:410:GLY:N	2.34	0.59
4:A:829:VAL:O	4:A:831:THR:N	2.36	0.59
5:B:294:ASP:O	5:B:296:GLU:N	2.32	0.59
5:B:376:PHE:HE2	5:B:569:TYR:HD2	1.50	0.59
5:B:1001:PHE:CE2	6:C:34:ARG:CZ	2.85	0.59
6:C:166:GLU:O	6:C:167:HIS:HB2	2.02	0.59
6:C:254:LYS:O	6:C:256:ALA:N	2.35	0.59
7:D:51:ASN:O	7:D:54:GLU:HB3	2.03	0.59
4:A:852:TYR:CE2	4:A:1060:PRO:HB2	2.38	0.59
5:B:114:PRO:HG3	5:B:181:LEU:HD11	1.85	0.59
5:B:522:VAL:HG11	5:B:537:LYS:HB3	1.85	0.59
5:B:850:LEU:HD12	5:B:851:PHE:H	1.67	0.59
5:B:1084:GLN:N	5:B:1084:GLN:NE2	2.51	0.59
6:C:263:THR:C	6:C:265:MET:N	2.61	0.59
8:E:178:ILE:HG22	8:E:213:ILE:O	2.02	0.59
14:K:69:ALA:O	14:K:70:ARG:HB3	2.03	0.59
4:A:364:VAL:O	4:A:364:VAL:HG13	2.03	0.58
4:A:537:ARG:NH1	11:H:120:GLY:O	2.36	0.58
4:A:981:LEU:HD21	4:A:1038:THR:C	2.28	0.58
4:A:1010:ALA:HA	4:A:1013:ASP:OD2	2.02	0.58
5:B:1162:ILE:O	5:B:1171:VAL:HG21	2.03	0.58
6:C:18:VAL:O	6:C:20:PHE:HD2	1.85	0.58
6:C:238:ILE:HG23	6:C:242:GLN:HB2	1.85	0.58
11:H:143:LEU:HD12	11:H:143:LEU:N	2.18	0.58
4:A:224:PHE:CE2	4:A:231:PRO:HG3	2.37	0.58
5:B:731:VAL:HG12	5:B:732:SER:N	2.18	0.58
6:C:242:GLN:C	6:C:244:VAL:H	2.09	0.58
7:D:47:LEU:HD11	10:G:3:PHE:HD2	1.68	0.58
8:E:90:VAL:HA	8:E:120:ALA:HB2	1.84	0.58
8:E:169:ARG:HH12	9:F:74:ILE:HD11	1.68	0.58
13:J:21:TYR:HB2	13:J:39:LEU:HD13	1.85	0.58
4:A:225:ASN:ND2	4:A:228:PHE:H	2.00	0.58
4:A:567:LYS:CG	4:A:568:PRO:CD	2.79	0.58
4:A:1070:GLN:O	4:A:1072:ILE:N	2.37	0.58
6:C:107:SER:C	6:C:109:SER:H	2.10	0.58
10:G:1:MET:O	10:G:1:MET:HE2	2.02	0.58
10:G:1:MET:O	10:G:3:PHE:CE1	2.57	0.58
11:H:100:THR:HG22	11:H:101:ALA:N	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:119:ASN:O	4:A:122:MET:HB3	2.03	0.58
4:A:218:ASP:HA	4:A:221:SER:OG	2.03	0.58
4:A:269:ILE:HD11	4:A:300:VAL:HA	1.86	0.58
4:A:1299:VAL:HG12	4:A:1300:LYS:H	1.69	0.58
4:A:1454:MET:O	4:A:1454:MET:HG3	2.03	0.58
5:B:842:ASN:HD22	5:B:845:SER:CB	2.16	0.58
5:B:999:MET:HA	5:B:999:MET:CE	2.31	0.58
6:C:80:LEU:HD11	6:C:95:CYS:C	2.28	0.58
4:A:774:ARG:O	4:A:775:ILE:C	2.46	0.58
7:D:51:ASN:O	7:D:52:LEU:O	2.22	0.58
11:H:18:GLY:O	11:H:19:ARG:HB2	2.04	0.58
4:A:843:LYS:HD3	4:A:846:GLU:OE2	2.04	0.58
4:A:1197:LEU:HD12	4:A:1209:MET:HE1	1.85	0.58
4:A:1435:PRO:O	4:A:1436:ILE:HG13	2.03	0.58
5:B:446:LEU:O	5:B:447:ALA:HB3	2.03	0.58
5:B:466:TRP:C	5:B:468:GLU:H	2.09	0.58
7:D:56:ARG:NH2	7:D:57:LEU:HD21	2.18	0.58
9:F:73:ALA:HA	9:F:143:PHE:CE1	2.38	0.58
4:A:1035:TYR:O	4:A:1037:LEU:N	2.36	0.58
4:A:1445:ILE:HG12	10:G:18:PHE:CE2	2.38	0.58
7:D:47:LEU:CD1	7:D:48:ILE:H	2.11	0.58
9:F:90:ARG:HD3	9:F:155:LEU:CD1	2.33	0.58
10:G:17:PHE:N	10:G:17:PHE:CD2	2.69	0.58
4:A:35:ILE:HD12	4:A:241:VAL:HG21	1.86	0.58
4:A:382:PRO:HD3	4:A:428:TYR:HD2	1.67	0.58
4:A:401:GLY:C	4:A:435:HIS:CD2	2.82	0.58
4:A:658:LEU:HD23	4:A:659:HIS:CE1	2.38	0.58
4:A:982:THR:HB	4:A:985:ASP:H	1.68	0.58
5:B:57:TYR:CD1	5:B:57:TYR:N	2.70	0.58
5:B:606:LYS:HD2	5:B:608:ASP:OD2	2.04	0.58
5:B:1051:THR:HB	5:B:1054:GLY:H	1.68	0.58
4:A:401:GLY:C	4:A:435:HIS:HD2	2.12	0.58
4:A:541:ILE:CG2	4:A:546:VAL:HG23	2.32	0.58
5:B:118:ARG:HH11	5:B:204:ILE:HD11	1.68	0.58
5:B:750:GLY:O	5:B:751:VAL:C	2.46	0.58
5:B:798:TYR:CE2	6:C:62:PHE:CE2	2.90	0.58
4:A:353:ILE:HG21	4:A:487:MET:HE3	1.85	0.58
4:A:1007:ILE:C	4:A:1009:ASN:N	2.59	0.58
4:A:1116:LEU:C	4:A:1116:LEU:HD12	2.29	0.58
5:B:653:VAL:HG22	5:B:689:LEU:HB3	1.85	0.58
5:B:797:TYR:HE1	5:B:854:LEU:CD2	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:36:VAL:HG21	6:C:251:LEU:HD22	1.85	0.58
7:D:7:THR:O	7:D:9:GLN:N	2.37	0.58
7:D:175:PHE:HZ	10:G:85:GLU:HG3	1.69	0.58
11:H:38:LEU:HD12	11:H:124:ARG:O	2.04	0.58
4:A:23:SER:HA	4:A:233:TRP:NE1	2.18	0.57
4:A:774:ARG:NH2	4:A:797:LYS:HB2	2.18	0.57
5:B:377:PHE:O	5:B:380:TYR:N	2.37	0.57
5:B:707:PRO:O	5:B:711:GLU:HG3	2.04	0.57
11:H:83:GLN:C	11:H:85:GLY:H	2.12	0.57
1:T:16:DT:H4'	4:A:1403:GLU:OE2	2.04	0.57
4:A:299:HIS:O	4:A:301:ALA:N	2.37	0.57
4:A:665:GLY:C	4:A:666:ILE:HD12	2.29	0.57
5:B:981:ALA:HB2	5:B:987:LYS:HA	1.86	0.57
5:B:990:ILE:HG22	5:B:991:GLY:N	2.19	0.57
6:C:100:THR:HG22	6:C:101:LEU:N	2.18	0.57
6:C:112:ASN:HD22	6:C:112:ASN:N	2.02	0.57
8:E:114:ASN:O	8:E:115:ASN:HB3	2.03	0.57
4:A:254:GLU:O	4:A:256:GLN:N	2.37	0.57
4:A:500:GLU:OE2	5:B:1145:SER:HB2	2.04	0.57
6:C:66:ARG:NH2	13:J:5:VAL:CG2	2.68	0.57
7:D:35:LEU:HD23	7:D:174:PRO:HD2	1.86	0.57
9:F:140:ASP:C	9:F:140:ASP:OD1	2.48	0.57
4:A:670:ILE:HG23	4:A:805:LEU:CD2	2.35	0.57
4:A:1434:ALA:HB3	4:A:1436:ILE:HD12	1.86	0.57
5:B:351:TYR:O	5:B:355:ILE:HG13	2.04	0.57
5:B:862:GLN:HG2	5:B:963:PHE:HD1	1.70	0.57
5:B:879:ARG:NH1	5:B:883:LEU:HD22	2.18	0.57
5:B:558:LEU:C	5:B:560:GLU:H	2.13	0.57
5:B:640:VAL:O	5:B:641:GLU:C	2.47	0.57
8:E:29:PHE:C	8:E:30:ILE:HG13	2.28	0.57
4:A:836:TYR:O	4:A:839:ARG:N	2.38	0.57
5:B:63:ILE:O	5:B:67:SER:HB3	2.04	0.57
5:B:731:VAL:HG12	5:B:732:SER:H	1.69	0.57
13:J:1:MET:N	13:J:56:LEU:N	2.53	0.57
15:L:52:GLY:O	15:L:53:HIS:C	2.48	0.57
4:A:185:TRP:CZ3	4:A:200:ARG:HG2	2.39	0.57
4:A:743:VAL:O	4:A:747:VAL:HG23	2.04	0.57
4:A:1242:VAL:HG12	4:A:1243:VAL:N	2.18	0.57
5:B:838:SER:HB2	5:B:989:THR:O	2.04	0.57
5:B:841:MET:HE1	5:B:980:PHE:CE1	2.40	0.57
5:B:957:ASN:O	5:B:959:ASP:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:146:LYS:C	6:C:147:LEU:HD23	2.29	0.57
4:A:42:ASP:HB3	4:A:45:GLN:H	1.68	0.57
4:A:244:PRO:CB	4:A:245:PRO:CD	2.83	0.57
4:A:469:ARG:NH2	5:B:991:GLY:O	2.38	0.57
4:A:1164:PRO:HG2	4:A:1165:GLU:H	1.68	0.57
4:A:1365:TYR:O	4:A:1367:HIS:N	2.38	0.57
5:B:167:ILE:HG22	5:B:453:ILE:HD12	1.86	0.57
5:B:321:GLY:O	5:B:323:VAL:N	2.37	0.57
5:B:745:PRO:C	5:B:747:MET:H	2.12	0.57
5:B:953:LEU:CD2	5:B:965:LYS:HB2	2.35	0.57
5:B:999:MET:HB3	5:B:1007:VAL:HG21	1.87	0.57
5:B:1011:ILE:O	5:B:1011:ILE:HG22	2.04	0.57
5:B:1107:ALA:O	5:B:1108:ARG:O	2.23	0.57
5:B:1115:THR:HG22	5:B:1117:GLN:HG3	1.87	0.57
5:B:1169:MET:HE1	5:B:1201:LYS:HA	1.86	0.57
4:A:55:ASP:N	4:A:56:PRO:HD3	2.20	0.57
4:A:982:THR:O	4:A:985:ASP:HB2	2.04	0.57
5:B:782:LEU:HD12	5:B:788:ARG:HH11	1.70	0.57
5:B:847:ASP:C	5:B:849:GLY:N	2.60	0.57
10:G:26:LEU:O	10:G:27:LYS:C	2.47	0.57
11:H:82:PRO:C	11:H:84:ALA:H	2.13	0.57
12:I:61:ASP:C	12:I:63:GLY:H	2.13	0.57
4:A:63:ARG:HA	4:A:74:MET:CE	2.34	0.57
4:A:1441:PHE:CZ	9:F:89:GLU:HA	2.40	0.57
5:B:234:ILE:HD12	5:B:234:ILE:N	2.20	0.57
5:B:310:MET:O	5:B:313:MET:HB2	2.04	0.57
5:B:821:GLN:NE2	5:B:851:PHE:HA	2.19	0.57
6:C:22:LEU:HD23	6:C:25:VAL:HG21	1.85	0.57
4:A:95:PHE:O	4:A:96:ILE:C	2.48	0.56
4:A:600:PRO:C	4:A:602:ASP:H	2.12	0.56
5:B:39:ARG:HG2	5:B:39:ARG:HH11	1.70	0.56
5:B:44:VAL:O	5:B:45:SER:C	2.48	0.56
5:B:950:ASP:O	5:B:951:GLN:HB2	2.05	0.56
6:C:258:ILE:HD12	6:C:258:ILE:N	2.19	0.56
8:E:94:LYS:CE	8:E:98:ILE:HD11	2.30	0.56
11:H:116:TYR:HB2	11:H:123:MET:HB3	1.85	0.56
14:K:6:ARG:O	14:K:9:LEU:HG	2.05	0.56
14:K:31:VAL:CG1	14:K:32:VAL:N	2.68	0.56
1:T:27:DA:C2	3:P:3:G:N2	2.74	0.56
4:A:316:GLN:O	4:A:317:LYS:C	2.48	0.56
4:A:540:PHE:HB3	4:A:571:LEU:HD23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1199:ARG:O	4:A:1202:MET:HB2	2.05	0.56
4:A:1242:VAL:O	4:A:1243:VAL:HB	2.05	0.56
4:A:1308:THR:HG23	4:A:1309:ASP:N	2.19	0.56
7:D:153:ARG:HH22	7:D:184:ALA:HA	1.67	0.56
8:E:78:LEU:HD23	8:E:78:LEU:C	2.29	0.56
11:H:15:VAL:HG22	11:H:26:ILE:HD11	1.86	0.56
12:I:111:THR:HG22	12:I:113:ASP:N	2.20	0.56
13:J:14:VAL:HG12	13:J:50:ILE:HD11	1.85	0.56
4:A:35:ILE:CD1	4:A:241:VAL:HG21	2.35	0.56
4:A:47:ARG:HH12	4:A:254:GLU:CG	2.18	0.56
4:A:265:LYS:HD2	4:A:265:LYS:H	1.71	0.56
4:A:789:LYS:HE3	12:I:67:THR:CB	2.35	0.56
4:A:840:ARG:O	4:A:841:LEU:C	2.48	0.56
4:A:874:ASP:CA	4:A:1058:VAL:HG22	2.36	0.56
5:B:27:ALA:O	5:B:29:ASP:N	2.38	0.56
5:B:315:LYS:N	5:B:316:PRO:HD2	2.21	0.56
5:B:582:VAL:HG23	5:B:626:ILE:HB	1.87	0.56
5:B:654:ARG:H	5:B:657:HIS:HD2	1.52	0.56
5:B:980:PHE:HE2	5:B:1094:ARG:HG3	1.70	0.56
5:B:1152:MET:SD	5:B:1197:PRO:HD3	2.45	0.56
6:C:3:GLU:HB3	14:K:104:ASN:HD21	1.70	0.56
6:C:123:ASN:HD22	6:C:125:MET:HG2	1.68	0.56
8:E:39:LEU:O	8:E:42:PHE:HB3	2.05	0.56
10:G:1:MET:O	10:G:1:MET:CE	2.53	0.56
12:I:34:TYR:HD2	12:I:35:VAL:N	2.03	0.56
4:A:331:GLY:O	4:A:332:LYS:HB3	2.04	0.56
5:B:557:PHE:C	5:B:557:PHE:HD2	2.12	0.56
5:B:811:TYR:N	5:B:811:TYR:CD1	2.72	0.56
6:C:38:ILE:HA	6:C:173:ALA:HB2	1.88	0.56
13:J:43:ARG:HG3	13:J:45:CYS:SG	2.45	0.56
4:A:590:ARG:HH11	4:A:590:ARG:CG	2.18	0.56
4:A:648:ASN:O	4:A:649:ILE:C	2.48	0.56
4:A:730:GLY:C	4:A:732:LEU:N	2.62	0.56
4:A:901:LEU:H	4:A:926:GLN:HE21	1.48	0.56
4:A:909:ASP:O	4:A:911:SER:N	2.39	0.56
4:A:1349:TYR:CE1	4:A:1368:MET:HE3	2.40	0.56
5:B:195:CYS:SG	5:B:197:PHE:HB2	2.46	0.56
9:F:75:PRO:HG2	9:F:78:GLN:HB2	1.87	0.56
10:G:79:PHE:CZ	10:G:106:MET:HE2	2.40	0.56
12:I:98:VAL:C	12:I:99:LEU:HD23	2.31	0.56
15:L:43:THR:HG22	15:L:43:THR:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:466:SER:HB2	5:B:1099:VAL:HG11	1.87	0.56
4:A:1007:ILE:O	4:A:1009:ASN:N	2.38	0.56
4:A:1319:VAL:HG13	4:A:1320:PRO:HD2	1.88	0.56
5:B:205:ILE:O	5:B:206:ASN:C	2.49	0.56
5:B:526:GLU:HG2	5:B:538:ASN:HD22	1.70	0.56
13:J:2:ILE:H	13:J:57:ILE:HG22	1.70	0.56
4:A:68:GLN:O	4:A:70:CYS:N	2.38	0.56
4:A:98:LYS:O	4:A:99:ILE:C	2.49	0.56
4:A:230:ARG:N	4:A:233:TRP:CE3	2.64	0.56
4:A:384:ASN:O	4:A:386:ASP:N	2.38	0.56
4:A:567:LYS:HD3	11:H:95:TYR:CG	2.40	0.56
4:A:1115:SER:C	4:A:1308:THR:HG22	2.31	0.56
4:A:1335:ILE:HG23	4:A:1339:LEU:HD12	1.87	0.56
5:B:661:LEU:C	5:B:663:ALA:H	2.13	0.56
9:F:109:VAL:HG21	9:F:124:GLU:HA	1.88	0.56
4:A:382:PRO:HD3	4:A:428:TYR:CE2	2.41	0.56
4:A:499:ALA:O	4:A:503:GLN:HB2	2.05	0.56
4:A:852:TYR:CD2	4:A:1060:PRO:HB2	2.41	0.56
4:A:871:ASP:OD1	4:A:1366:ARG:NH2	2.39	0.56
5:B:63:ILE:HD12	5:B:421:PHE:CE2	2.40	0.56
5:B:265:SER:O	5:B:266:ALA:HB3	2.05	0.56
5:B:785:TYR:CD1	5:B:785:TYR:C	2.83	0.56
5:B:842:ASN:HD22	5:B:845:SER:HB3	1.71	0.56
7:D:63:LEU:HD13	7:D:133:THR:OG1	2.05	0.56
4:A:75:ASN:O	4:A:76:GLU:CB	2.53	0.56
4:A:547:LEU:HD22	14:K:58:PHE:HD1	1.70	0.56
4:A:548:ASN:HA	14:K:60:ALA:HB1	1.87	0.56
4:A:1343:ALA:HB2	8:E:150:VAL:CG2	2.35	0.56
5:B:197:PHE:HZ	5:B:816:GLU:HG2	1.71	0.56
5:B:309:GLN:HG3	12:I:52:ILE:CD1	2.36	0.56
5:B:980:PHE:CD2	5:B:1094:ARG:HA	2.41	0.56
6:C:226:ASP:O	6:C:227:THR:HB	2.06	0.56
8:E:78:LEU:HD23	8:E:79:TRP:N	2.20	0.56
10:G:80:LYS:O	10:G:80:LYS:HG2	2.05	0.56
14:K:15:GLY:O	14:K:16:GLU:HG3	2.06	0.56
2:N:5:DA:H2"	2:N:6:DC:OP2	2.05	0.56
4:A:907:THR:HG22	4:A:908:LEU:N	2.18	0.56
4:A:1015:VAL:HG12	4:A:1019:CYS:SG	2.45	0.56
4:A:1283:VAL:HG12	4:A:1284:MET:H	1.71	0.56
4:A:1441:PHE:HB2	9:F:135:ARG:O	2.05	0.56
5:B:217:ARG:HE	5:B:405:ARG:CB	2.07	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:63:VAL:HG23	14:K:63:VAL:O	2.06	0.56
4:A:49:LYS:HZ1	4:A:61:ILE:N	2.04	0.55
4:A:546:VAL:O	4:A:550:LEU:HG	2.06	0.55
4:A:649:ILE:O	4:A:653:VAL:HG23	2.06	0.55
4:A:754:SER:N	4:A:757:ASN:HD22	1.92	0.55
4:A:757:ASN:HA	5:B:1021:MET:SD	2.46	0.55
4:A:913:LEU:HD12	4:A:914:GLU:N	2.21	0.55
4:A:1220:PHE:O	4:A:1221:LYS:HB2	2.05	0.55
4:A:1369:ALA:O	4:A:1372:VAL:HG12	2.06	0.55
6:C:252:GLN:CG	14:K:95:ILE:HG23	2.36	0.55
12:I:100:PHE:N	12:I:100:PHE:CD1	2.74	0.55
4:A:306:ASN:HB2	4:A:324:SER:HB3	1.88	0.55
4:A:929:LEU:CD2	4:A:983:ILE:HG21	2.36	0.55
4:A:1283:VAL:HG12	4:A:1284:MET:N	2.21	0.55
4:A:1430:LEU:HB2	4:A:1432:GLN:HG3	1.88	0.55
5:B:197:PHE:CZ	5:B:816:GLU:HG2	2.41	0.55
5:B:358:LYS:HA	5:B:366:GLN:HB3	1.89	0.55
5:B:523:CYS:SG	5:B:524:PRO:HD2	2.46	0.55
5:B:830:TYR:CE2	5:B:1000:PRO:HD3	2.42	0.55
5:B:1034:VAL:CG1	5:B:1035:ALA:N	2.69	0.55
6:C:215:GLU:O	6:C:216:GLY:C	2.48	0.55
7:D:52:LEU:C	7:D:54:GLU:H	2.14	0.55
14:K:49:GLU:HG3	14:K:94:ILE:HG12	1.88	0.55
4:A:71:GLN:C	4:A:73:GLY:N	2.65	0.55
4:A:356:ASP:O	4:A:358:ASN:N	2.39	0.55
4:A:673:GLY:O	4:A:676:MET:HB2	2.05	0.55
5:B:199:MET:HE2	5:B:492:LEU:HD23	1.88	0.55
5:B:542:MET:HG2	5:B:747:MET:HB3	1.88	0.55
5:B:702:LEU:HD12	5:B:703:ILE:H	1.71	0.55
6:C:48:SER:O	6:C:157:CYS:HA	2.06	0.55
10:G:91:VAL:HB	10:G:139:ILE:O	2.06	0.55
4:A:567:LYS:HZ2	11:H:47:PHE:HB2	1.71	0.55
4:A:628:GLY:O	4:A:632:VAL:HG23	2.06	0.55
5:B:872:GLU:CD	5:B:914:LYS:HE2	2.32	0.55
5:B:980:PHE:CE2	5:B:1094:ARG:HG3	2.41	0.55
10:G:20:PRO:HG2	10:G:21:ARG:H	1.70	0.55
4:A:24:PRO:HD2	4:A:233:TRP:CD1	2.40	0.55
4:A:43:GLU:O	4:A:44:THR:HB	2.07	0.55
4:A:632:VAL:O	4:A:633:VAL:C	2.49	0.55
4:A:685:GLU:HG3	4:A:686:ALA:N	2.20	0.55
4:A:714:PHE:CB	12:I:97:MET:HE1	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1372:VAL:O	4:A:1376:THR:HG22	2.07	0.55
5:B:57:TYR:N	5:B:57:TYR:HD1	2.04	0.55
5:B:108:VAL:HG12	5:B:109:THR:N	2.22	0.55
5:B:240:ILE:CG2	5:B:254:LEU:HB3	2.36	0.55
5:B:579:ARG:HG2	5:B:579:ARG:HH11	1.71	0.55
4:A:445:ASN:HB2	4:A:455:MET:HG2	1.89	0.55
4:A:1290:LYS:O	4:A:1291:VAL:HG23	2.06	0.55
4:A:1428:VAL:HG13	5:B:1151:LEU:HD21	1.88	0.55
5:B:778:MET:HE2	5:B:1094:ARG:HG2	1.88	0.55
5:B:918:ILE:HD12	5:B:935:ARG:HD3	1.89	0.55
5:B:1095:LEU:H	5:B:1095:LEU:CD1	2.14	0.55
5:B:1159:ARG:HD3	5:B:1193:GLN:HG2	1.87	0.55
9:F:116:ASP:C	9:F:116:ASP:OD1	2.49	0.55
4:A:667:GLY:HA3	6:C:192:TRP:CH2	2.41	0.55
4:A:828:ALA:HB1	5:B:530:GLY:HA2	1.85	0.55
4:A:1377:THR:O	4:A:1379:GLY:N	2.40	0.55
8:E:23:VAL:O	8:E:28:TYR:HB2	2.07	0.55
8:E:177:ARG:HD3	8:E:215:MET:HG3	1.89	0.55
13:J:27:GLU:C	13:J:29:GLU:H	2.14	0.55
4:A:35:ILE:HG22	4:A:84:ILE:HD12	1.88	0.55
4:A:500:GLU:OE1	5:B:1143:ALA:C	2.50	0.55
4:A:881:GLN:NE2	4:A:958:VAL:O	2.35	0.55
4:A:1345:ARG:NH1	4:A:1373:ASP:OD1	2.36	0.55
5:B:214:ALA:HB3	5:B:498:THR:HA	1.89	0.55
5:B:502:ILE:HG12	5:B:535:LEU:CD1	2.35	0.55
5:B:1180:PHE:O	5:B:1181:GLU:O	2.24	0.55
12:I:100:PHE:HD1	12:I:100:PHE:N	2.04	0.55
14:K:58:PHE:HB3	14:K:76:GLN:HB3	1.89	0.55
4:A:224:PHE:HD2	4:A:229:SER:O	1.90	0.55
4:A:524:VAL:HG12	4:A:525:GLN:N	2.19	0.55
4:A:528:LEU:HD23	4:A:751:SER:HA	1.89	0.55
4:A:1209:MET:CE	4:A:1236:LEU:HB3	2.36	0.55
5:B:973:ILE:HG23	5:B:974:PRO:HD2	1.89	0.55
10:G:51:TYR:O	10:G:54:ILE:HG13	2.06	0.55
4:A:414:ASP:OD1	4:A:416:ARG:HG3	2.07	0.55
4:A:779:PHE:O	4:A:780:VAL:C	2.50	0.55
4:A:870:GLU:HG2	8:E:208:TYR:CD2	2.42	0.55
5:B:520:GLY:HA2	5:B:748:ILE:HG22	1.89	0.55
7:D:156:ASP:C	7:D:158:GLU:N	2.65	0.55
9:F:130:ILE:O	9:F:148:VAL:CG2	2.55	0.55
12:I:56:ALA:O	12:I:57:GLY:O	2.25	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:53:HIS:C	13:J:53:HIS:CD2	2.84	0.55
4:A:90:VAL:HG12	4:A:91:PHE:N	2.21	0.54
4:A:420:ARG:O	4:A:421:ALA:C	2.50	0.54
4:A:679:ILE:O	4:A:682:THR:N	2.40	0.54
4:A:746:MET:CE	5:B:1018:PRO:HG2	2.34	0.54
4:A:789:LYS:HE3	12:I:67:THR:HB	1.89	0.54
4:A:1279:ILE:HD11	4:A:1316:VAL:HG21	1.89	0.54
4:A:1385:THR:HG22	4:A:1386:ARG:N	2.22	0.54
5:B:880:THR:HB	5:B:934:LYS:HD2	1.88	0.54
5:B:1197:PRO:O	5:B:1200:ALA:HB3	2.07	0.54
11:H:127:GLY:O	11:H:128:ASN:HB2	2.07	0.54
12:I:34:TYR:HE2	12:I:36:GLU:HB3	1.71	0.54
4:A:366:VAL:CG2	4:A:460:VAL:HG22	2.37	0.54
4:A:418:SER:O	4:A:420:ARG:N	2.40	0.54
4:A:446:ARG:HB2	4:A:487:MET:SD	2.48	0.54
7:D:53:SER:HB3	7:D:152:SER:CB	2.37	0.54
7:D:53:SER:CB	7:D:153:ARG:H	2.19	0.54
8:E:14:ARG:HH21	8:E:141:VAL:HG12	1.72	0.54
10:G:56:ILE:O	10:G:57:GLN:HB2	2.06	0.54
10:G:106:MET:CG	10:G:107:LYS:N	2.70	0.54
15:L:32:ALA:HB3	15:L:55:ILE:HD12	1.88	0.54
4:A:268:ASP:O	4:A:269:ILE:C	2.50	0.54
4:A:1032:LEU:O	4:A:1036:ARG:HD3	2.07	0.54
5:B:472:ALA:HB1	5:B:474:SER:HB3	1.88	0.54
5:B:769:TYR:O	5:B:771:SER:N	2.40	0.54
5:B:1002:THR:HG23	5:B:1006:ILE:HG13	1.88	0.54
5:B:1031:LEU:HD13	5:B:1055:ILE:HD11	1.89	0.54
6:C:145:CYS:HA	13:J:2:ILE:HD11	1.88	0.54
8:E:22:MET:HE3	8:E:26:ARG:CZ	2.37	0.54
8:E:124:VAL:HG13	8:E:132:ILE:HD12	1.88	0.54
9:F:81:THR:HB	9:F:136:ARG:NH1	2.23	0.54
10:G:13:LEU:HD22	10:G:14:HIS:O	2.07	0.54
13:J:8:PHE:N	13:J:49:MET:HE3	2.21	0.54
14:K:46:ILE:O	14:K:46:ILE:HG22	2.07	0.54
4:A:146:MET:HA	4:A:171:GLN:HB2	1.90	0.54
4:A:266:LEU:O	4:A:267:ALA:C	2.49	0.54
4:A:608:ILE:C	4:A:610:GLY:N	2.64	0.54
4:A:942:PHE:C	4:A:942:PHE:CD2	2.85	0.54
4:A:1100:ARG:HH21	4:A:1351:GLU:CG	2.21	0.54
4:A:1127:ASP:HB3	4:A:1130:GLN:HB3	1.87	0.54
4:A:1161:THR:OG1	4:A:1239:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1208:THR:HG22	4:A:1210:GLY:H	1.73	0.54
5:B:39:ARG:HG2	5:B:39:ARG:NH1	2.23	0.54
5:B:278:GLN:HG2	5:B:279:ASP:H	1.72	0.54
5:B:896:ASP:CG	15:L:58:LYS:HZ2	2.15	0.54
5:B:1166:CYS:O	5:B:1168:LEU:N	2.39	0.54
8:E:207:ARG:HH11	8:E:207:ARG:HB3	1.72	0.54
9:F:77:ASP:C	9:F:79:ARG:N	2.66	0.54
4:A:365:GLY:O	4:A:468:PHE:HA	2.08	0.54
4:A:590:ARG:HD2	4:A:605:MET:HB3	1.89	0.54
4:A:909:ASP:C	4:A:911:SER:H	2.16	0.54
4:A:1118:VAL:O	4:A:1305:VAL:HG13	2.07	0.54
7:D:156:ASP:C	7:D:158:GLU:H	2.13	0.54
7:D:170:THR:HB	7:D:172:LEU:H	1.73	0.54
8:E:161:LYS:HD2	8:E:195:VAL:HG23	1.88	0.54
10:G:145:VAL:HG12	10:G:146:LYS:N	2.23	0.54
4:A:61:ILE:O	4:A:63:ARG:N	2.41	0.54
4:A:742:ASN:O	4:A:745:GLN:HB2	2.07	0.54
4:A:1019:CYS:O	4:A:1020:CYS:C	2.50	0.54
4:A:1369:ALA:O	4:A:1370:LEU:C	2.49	0.54
5:B:35:SER:O	5:B:39:ARG:HG3	2.07	0.54
5:B:710:LEU:O	5:B:711:GLU:HG2	2.07	0.54
6:C:120:ILE:HD13	6:C:124:LEU:HD21	1.90	0.54
11:H:4:THR:O	11:H:5:LEU:HD23	2.08	0.54
11:H:142:LEU:C	11:H:143:LEU:HD12	2.32	0.54
15:L:39:SER:O	15:L:40:LEU:HG	2.08	0.54
4:A:64:ASN:O	4:A:65:LEU:C	2.50	0.54
4:A:341:MET:CE	4:A:843:LYS:NZ	2.71	0.54
4:A:986:ILE:HG22	4:A:987:VAL:N	2.23	0.54
4:A:1401:SER:O	4:A:1402:PHE:HB2	2.07	0.54
5:B:224:GLN:O	5:B:238:ALA:HA	2.08	0.54
5:B:1084:GLN:C	5:B:1085:ILE:HD12	2.33	0.54
10:G:7:LEU:O	10:G:73:LYS:HD2	2.08	0.54
14:K:21:ILE:HG23	14:K:31:VAL:CG1	2.38	0.54
4:A:252:PHE:O	4:A:256:GLN:NE2	2.40	0.54
6:C:147:LEU:HD12	6:C:151:GLN:O	2.07	0.54
10:G:122:ASN:ND2	10:G:125:SER:HB3	2.23	0.54
4:A:105:CYS:O	4:A:114:LEU:HG	2.07	0.54
4:A:866:PHE:C	4:A:867:ILE:HG13	2.30	0.54
4:A:1017:LEU:CB	8:E:205:SER:HA	2.38	0.54
4:A:1127:ASP:HB3	4:A:1130:GLN:HB2	1.90	0.54
4:A:1389:PHE:CD1	4:A:1389:PHE:C	2.85	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:604:ARG:NH2	5:B:614:SER:HA	2.22	0.54
6:C:214:ASN:HB3	6:C:217:ASP:OD2	2.08	0.54
6:C:239:PRO:O	6:C:241:ASP:N	2.41	0.54
7:D:52:LEU:O	7:D:54:GLU:N	2.40	0.54
13:J:21:TYR:HB2	13:J:39:LEU:CD1	2.38	0.54
13:J:34:THR:O	13:J:35:ALA:C	2.51	0.54
15:L:60:ARG:HG2	15:L:61:THR:H	1.73	0.54
4:A:134:ARG:O	4:A:138:ILE:HG13	2.07	0.54
4:A:244:PRO:CB	4:A:245:PRO:HD3	2.29	0.54
4:A:590:ARG:HD3	4:A:604:GLY:C	2.32	0.54
4:A:696:GLU:O	4:A:696:GLU:HG2	2.08	0.54
4:A:794:PRO:C	4:A:796:SER:H	2.14	0.54
5:B:1106:ARG:NH1	5:B:1110:PRO:HD2	2.23	0.54
8:E:29:PHE:O	8:E:30:ILE:CG1	2.55	0.54
8:E:55:ARG:C	8:E:57:MET:H	2.14	0.54
11:H:139:ASN:O	11:H:140:ALA:HB2	2.08	0.54
4:A:21:LEU:HG	4:A:1413:GLY:O	2.08	0.53
4:A:666:ILE:HD12	4:A:666:ILE:N	2.22	0.53
4:A:844:ALA:O	4:A:845:LEU:HD23	2.08	0.53
5:B:309:GLN:HG3	12:I:52:ILE:HD11	1.89	0.53
5:B:1159:ARG:HE	5:B:1193:GLN:HE21	1.56	0.53
6:C:256:ALA:O	6:C:259:LEU:N	2.41	0.53
10:G:81:PRO:HB3	10:G:106:MET:HE1	1.89	0.53
10:G:88:ASP:OD2	10:G:88:ASP:N	2.40	0.53
12:I:14:LEU:HA	12:I:28:GLU:O	2.08	0.53
12:I:106:CYS:O	12:I:107:SER:HB2	2.06	0.53
12:I:111:THR:HG22	12:I:113:ASP:H	1.73	0.53
4:A:42:ASP:HB3	4:A:45:GLN:HA	1.90	0.53
4:A:231:PRO:C	4:A:233:TRP:H	2.16	0.53
4:A:836:TYR:CD2	4:A:840:ARG:HD2	2.44	0.53
4:A:1156:PRO:HA	4:A:1190:PRO:CB	2.38	0.53
5:B:53:GLN:HG2	5:B:547:VAL:CG2	2.36	0.53
5:B:758:PHE:CE1	5:B:1027:ILE:CG2	2.91	0.53
6:C:254:LYS:C	6:C:256:ALA:N	2.64	0.53
6:C:254:LYS:C	6:C:256:ALA:H	2.16	0.53
8:E:3:GLN:HG3	8:E:4:GLU:N	2.22	0.53
8:E:134:THR:C	8:E:135:PHE:HD1	2.16	0.53
9:F:109:VAL:HG11	9:F:123:LYS:HG2	1.90	0.53
9:F:119:ARG:HG3	9:F:119:ARG:NH1	2.21	0.53
10:G:123:ALA:C	10:G:125:SER:H	2.16	0.53
14:K:58:PHE:HE2	14:K:74:ARG:HE	1.53	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:541:ILE:HD13	4:A:549:MET:CE	2.29	0.53
4:A:761:MET:HA	4:A:804:TYR:HB2	1.89	0.53
4:A:868:TYR:CE1	4:A:1064:VAL:CG1	2.88	0.53
5:B:371:GLU:CD	5:B:371:GLU:H	2.17	0.53
5:B:521:LEU:HD13	5:B:633:VAL:HB	1.90	0.53
5:B:661:LEU:C	5:B:663:ALA:N	2.67	0.53
5:B:980:PHE:HD2	5:B:1094:ARG:HA	1.72	0.53
5:B:1022:THR:HG23	5:B:1022:THR:O	2.08	0.53
6:C:174:ALA:O	6:C:175:ALA:HB2	2.07	0.53
6:C:242:GLN:C	6:C:244:VAL:N	2.65	0.53
7:D:35:LEU:H	7:D:35:LEU:HD12	1.72	0.53
7:D:49:ALA:HB2	7:D:174:PRO:HB3	1.90	0.53
10:G:110:VAL:HG22	10:G:161:GLY:O	2.08	0.53
10:G:150:CYS:C	10:G:151:ILE:HG13	2.33	0.53
4:A:265:LYS:HZ3	4:A:322:VAL:HG22	1.73	0.53
4:A:417:TYR:N	4:A:417:TYR:CD2	2.75	0.53
4:A:586:ILE:HG22	4:A:587:HIS:N	2.24	0.53
4:A:913:LEU:HD12	4:A:914:GLU:H	1.73	0.53
4:A:1001:ARG:O	4:A:1002:GLY:O	2.26	0.53
5:B:65:GLU:CG	5:B:66:ASP:H	2.16	0.53
5:B:196:PRO:HG2	5:B:197:PHE:H	1.73	0.53
5:B:205:ILE:N	5:B:205:ILE:HD12	2.23	0.53
5:B:798:TYR:CE2	6:C:62:PHE:HE2	2.24	0.53
5:B:952:VAL:O	5:B:953:LEU:HB3	2.08	0.53
5:B:986:GLN:OE1	5:B:986:GLN:HA	2.08	0.53
6:C:89:GLU:O	6:C:89:GLU:HG2	2.07	0.53
10:G:7:LEU:CD1	10:G:45:ILE:HD11	2.38	0.53
11:H:113:ALA:HB1	11:H:125:LEU:O	2.09	0.53
11:H:116:TYR:O	11:H:122:LEU:HA	2.08	0.53
4:A:218:ASP:HA	4:A:221:SER:HG	1.71	0.53
4:A:399:HIS:O	4:A:401:GLY:N	2.41	0.53
4:A:786:HIS:HE1	5:B:705:MET:HE1	1.73	0.53
5:B:168:GLY:N	5:B:450:ALA:HB1	2.18	0.53
5:B:225:VAL:HA	5:B:237:VAL:O	2.09	0.53
5:B:595:ARG:O	5:B:596:LEU:C	2.51	0.53
5:B:942:ARG:O	5:B:944:THR:N	2.42	0.53
5:B:1219:ASP:OD1	5:B:1219:ASP:O	2.27	0.53
6:C:39:ALA:HA	6:C:164:ALA:CB	2.29	0.53
6:C:189:THR:HG22	6:C:190:ASP:N	2.23	0.53
4:A:50:ILE:C	4:A:52:GLY:N	2.67	0.53
4:A:95:PHE:CD1	4:A:234:MET:HG2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:534:LEU:O	4:A:534:LEU:HG	2.08	0.53
4:A:608:ILE:C	4:A:610:GLY:H	2.16	0.53
4:A:847:ASP:OD1	4:A:848:ILE:HG13	2.08	0.53
4:A:1410:PHE:HA	5:B:1212:ILE:CD1	2.39	0.53
5:B:1001:PHE:CD2	6:C:34:ARG:NH2	2.77	0.53
12:I:50:THR:CG2	12:I:52:ILE:HG12	2.39	0.53
4:A:577:ILE:C	4:A:579:SER:N	2.64	0.53
4:A:1118:VAL:CG2	4:A:1306:LEU:HB2	2.39	0.53
4:A:1151:GLU:HA	12:I:44:TYR:O	2.09	0.53
5:B:470:LYS:C	5:B:472:ALA:H	2.15	0.53
5:B:479:VAL:O	5:B:480:SER:HB3	2.09	0.53
4:A:71:GLN:O	4:A:73:GLY:N	2.37	0.53
4:A:152:VAL:HG12	4:A:153:PRO:CD	2.37	0.53
4:A:427:GLN:HB2	4:A:430:TRP:CD1	2.44	0.53
5:B:872:GLU:HA	5:B:915:THR:O	2.09	0.53
5:B:1050:ILE:HG22	5:B:1051:THR:N	2.24	0.53
5:B:1138:MET:HE2	5:B:1146:PHE:HD2	1.74	0.53
6:C:168:ALA:O	6:C:170:TRP:N	2.42	0.53
9:F:103:MET:CE	10:G:66:GLY:H	2.22	0.53
9:F:131:PRO:C	9:F:132:LEU:HD23	2.34	0.53
10:G:14:HIS:CE1	10:G:15:PRO:HD2	2.43	0.53
4:A:497:THR:HG22	4:A:498:ARG:N	2.24	0.53
4:A:1030:ARG:NH1	4:A:1035:TYR:OH	2.41	0.53
4:A:1434:ALA:CB	4:A:1436:ILE:HD12	2.39	0.53
5:B:199:MET:HE2	5:B:492:LEU:CD2	2.39	0.53
5:B:637:LEU:O	5:B:690:VAL:HG13	2.09	0.53
5:B:843:GLN:O	5:B:846:ILE:HB	2.09	0.53
6:C:184:ASN:HD21	6:C:187:LYS:HA	1.69	0.53
7:D:40:HIS:CE1	7:D:41:GLN:HG3	2.43	0.53
10:G:14:HIS:CD2	10:G:16:SER:H	2.27	0.53
4:A:241:VAL:HG13	4:A:266:LEU:HD13	1.90	0.53
4:A:341:MET:CE	4:A:843:LYS:HZ1	2.20	0.53
4:A:601:LYS:HB2	4:A:603:ASN:ND2	2.24	0.53
5:B:118:ARG:HG2	5:B:204:ILE:HD13	1.91	0.53
5:B:360:PHE:O	5:B:361:LEU:C	2.52	0.53
6:C:20:PHE:CE1	6:C:22:LEU:HD12	2.42	0.53
6:C:175:ALA:O	6:C:176:ILE:HG13	2.09	0.53
7:D:185:CYS:HB2	7:D:211:LEU:HD22	1.89	0.53
10:G:1:MET:O	10:G:3:PHE:CD1	2.62	0.53
10:G:3:PHE:CE1	10:G:80:LYS:HE2	2.44	0.53
15:L:36:SER:O	15:L:37:LYS:C	2.51	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:18:GLN:O	5:B:1215:ARG:CG	2.57	0.52
4:A:299:HIS:C	4:A:301:ALA:N	2.66	0.52
5:B:216:GLU:HA	5:B:406:LEU:HD23	1.91	0.52
5:B:877:PRO:C	5:B:878:GLN:HG3	2.34	0.52
5:B:900:ALA:HB3	15:L:61:THR:OG1	2.09	0.52
5:B:1189:ILE:HG22	5:B:1190:ASP:N	2.23	0.52
5:B:1216:LEU:HD23	5:B:1216:LEU:N	2.24	0.52
10:G:49:LEU:HD21	10:G:77:VAL:HG23	1.89	0.52
10:G:111:THR:HB	10:G:114:LEU:HB2	1.91	0.52
11:H:95:TYR:HB3	11:H:144:ILE:HB	1.91	0.52
4:A:90:VAL:CG1	4:A:297:GLN:HA	2.39	0.52
4:A:382:PRO:CB	4:A:428:TYR:HE2	2.22	0.52
5:B:467:GLY:O	5:B:468:GLU:CB	2.56	0.52
5:B:918:ILE:HG21	5:B:935:ARG:NH1	2.25	0.52
5:B:1160:VAL:HG12	5:B:1161:HIS:H	1.72	0.52
6:C:235:VAL:HG13	13:J:13:VAL:CG2	2.40	0.52
6:C:263:THR:O	6:C:265:MET:N	2.42	0.52
7:D:33:PHE:CZ	10:G:80:LYS:HE3	2.44	0.52
8:E:22:MET:HE3	8:E:26:ARG:NH2	2.24	0.52
10:G:80:LYS:H	10:G:80:LYS:HD3	1.73	0.52
10:G:138:THR:CG2	10:G:139:ILE:H	2.13	0.52
11:H:62:SER:O	11:H:63:LEU:C	2.50	0.52
1:T:27:DA:H2"	1:T:28:DT:OP2	2.08	0.52
4:A:35:ILE:CG2	4:A:84:ILE:HD12	2.40	0.52
4:A:249:SER:O	4:A:250:ILE:HG13	2.09	0.52
4:A:1101:LEU:HB2	4:A:1355:VAL:HG11	1.91	0.52
5:B:113:TYR:HB3	5:B:114:PRO:HD2	1.91	0.52
5:B:758:PHE:HE1	5:B:1027:ILE:HG22	1.73	0.52
5:B:1115:THR:HG21	5:B:1117:GLN:NE2	2.23	0.52
6:C:73:GLN:HE21	6:C:74:SER:N	2.07	0.52
6:C:133:ILE:HD11	6:C:237:SER:HA	1.92	0.52
10:G:34:VAL:HG12	10:G:45:ILE:CG2	2.35	0.52
4:A:152:VAL:HG13	4:A:153:PRO:HD2	1.89	0.52
4:A:399:HIS:CB	4:A:400:PRO:CD	2.79	0.52
4:A:567:LYS:HB3	11:H:95:TYR:CA	2.38	0.52
4:A:765:VAL:HG23	4:A:802:ASN:O	2.10	0.52
4:A:946:VAL:HG22	8:E:201:LYS:HD2	1.90	0.52
4:A:1345:ARG:HG3	4:A:1376:THR:HG21	1.90	0.52
5:B:980:PHE:HE2	5:B:1094:ARG:CG	2.21	0.52
5:B:1138:MET:HE2	5:B:1146:PHE:CD2	2.45	0.52
5:B:1202:LEU:O	5:B:1206:GLU:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:47:CYS:O	10:G:76:ALA:HB1	2.08	0.52
4:A:621:THR:O	4:A:629:LEU:HB2	2.09	0.52
4:A:825:ILE:HG22	5:B:508:LEU:CD1	2.36	0.52
4:A:873:MET:C	4:A:1058:VAL:CG2	2.82	0.52
4:A:1004:ASN:O	4:A:1008:GLN:HB2	2.10	0.52
5:B:831:SER:CB	5:B:994:TYR:OH	2.58	0.52
6:C:31:ASN:O	6:C:34:ARG:N	2.42	0.52
8:E:55:ARG:HD2	8:E:83:CYS:O	2.09	0.52
9:F:147:SER:OG	9:F:150:GLU:HG3	2.09	0.52
10:G:96:GLN:HA	10:G:121:PHE:CE2	2.45	0.52
4:A:195:ASP:O	4:A:196:GLU:HB3	2.08	0.52
4:A:647:GLY:O	4:A:651:LYS:HG3	2.09	0.52
4:A:1153:TYR:CE1	12:I:42:LEU:HD13	2.45	0.52
5:B:288:ALA:HA	5:B:331:LEU:HD12	1.92	0.52
5:B:579:ARG:CB	5:B:586:TRP:HE1	2.16	0.52
5:B:758:PHE:N	5:B:759:PRO:CD	2.73	0.52
5:B:842:ASN:O	5:B:846:ILE:HG13	2.10	0.52
6:C:8:VAL:HG12	6:C:9:LYS:H	1.74	0.52
6:C:66:ARG:NH1	6:C:144:ILE:O	2.43	0.52
6:C:91:HIS:C	6:C:91:HIS:CD2	2.88	0.52
4:A:35:ILE:HA	4:A:52:GLY:O	2.10	0.52
4:A:91:PHE:HB2	4:A:297:GLN:HE22	1.74	0.52
4:A:92:HIS:HB2	4:A:236:LEU:HD21	1.90	0.52
4:A:817:ALA:O	4:A:818:MET:C	2.53	0.52
5:B:225:VAL:O	5:B:226:PHE:CD2	2.63	0.52
5:B:282:ILE:CD1	5:B:382:ILE:HD13	2.40	0.52
5:B:360:PHE:C	5:B:360:PHE:CD2	2.88	0.52
5:B:542:MET:HE3	5:B:636:PRO:HG3	1.91	0.52
7:D:153:ARG:HB3	7:D:154:PHE:CE1	2.45	0.52
8:E:90:VAL:O	8:E:90:VAL:HG22	2.09	0.52
10:G:115:MET:CB	10:G:116:PRO:HD2	2.40	0.52
12:I:55:THR:HG22	12:I:58:VAL:HG21	1.91	0.52
13:J:23:ASN:C	13:J:25:LEU:N	2.66	0.52
13:J:45:CYS:O	13:J:48:ARG:HG3	2.08	0.52
15:L:61:THR:CG2	15:L:63:ARG:HG2	2.39	0.52
3:P:3:G:H2'	3:P:4:A:C8	2.45	0.52
4:A:17:VAL:HA	5:B:1215:ARG:O	2.10	0.52
4:A:91:PHE:HB2	4:A:297:GLN:NE2	2.24	0.52
4:A:381:THR:CG2	4:A:383:TYR:H	2.23	0.52
4:A:698:GLN:HA	12:I:97:MET:O	2.08	0.52
4:A:840:ARG:NH2	4:A:1106:ASN:OD1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:847:ASP:O	5:B:849:GLY:N	2.43	0.52
5:B:1132:GLU:O	5:B:1135:ARG:HB3	2.09	0.52
6:C:80:LEU:HD11	6:C:95:CYS:HA	1.91	0.52
7:D:56:ARG:HD2	7:D:149:THR:OG1	2.09	0.52
7:D:176:GLU:C	7:D:178:ALA:N	2.64	0.52
10:G:66:GLY:O	10:G:67:SER:C	2.52	0.52
11:H:31:THR:O	11:H:31:THR:HG22	2.10	0.52
12:I:13:MET:O	12:I:14:LEU:HD23	2.10	0.52
4:A:337:ARG:NH2	4:A:839:ARG:HH12	2.08	0.52
4:A:545:GLN:O	4:A:546:VAL:C	2.52	0.52
5:B:954:VAL:O	15:L:55:ILE:O	2.27	0.52
6:C:27:LEU:O	6:C:28:ALA:C	2.52	0.52
6:C:76:ASP:O	6:C:77:ILE:C	2.52	0.52
6:C:206:ASN:OD1	6:C:229:TYR:CD2	2.63	0.52
8:E:198:ILE:HD11	8:E:212:ARG:CG	2.33	0.52
12:I:55:THR:HG21	12:I:109:ILE:HD13	1.92	0.52
4:A:166:GLY:O	4:A:167:CYS:SG	2.68	0.52
4:A:277:GLU:C	4:A:279:LEU:H	2.18	0.52
4:A:535:THR:HG23	4:A:575:LYS:HE2	1.91	0.52
4:A:1066:VAL:O	4:A:1069:ALA:HB3	2.09	0.52
4:A:1193:LEU:HD12	4:A:1194:ARG:N	2.24	0.52
4:A:1213:GLY:O	4:A:1214:GLU:C	2.52	0.52
5:B:400:HIS:ND1	5:B:517:THR:HG21	2.25	0.52
6:C:6:PRO:HB3	6:C:25:VAL:HG12	1.92	0.52
6:C:60:ASP:OD2	15:L:60:ARG:NH2	2.42	0.52
7:D:64:VAL:C	7:D:66:ARG:N	2.68	0.52
12:I:55:THR:HG22	12:I:55:THR:O	2.10	0.52
13:J:56:LEU:O	13:J:57:ILE:C	2.53	0.52
15:L:61:THR:HG22	15:L:63:ARG:HG2	1.91	0.52
4:A:41:MET:O	4:A:50:ILE:HG13	2.11	0.51
4:A:427:GLN:HG3	4:A:430:TRP:CE2	2.44	0.51
4:A:567:LYS:CB	4:A:568:PRO:CD	2.87	0.51
4:A:788:SER:O	4:A:789:LYS:O	2.29	0.51
4:A:1156:PRO:O	4:A:1158:PRO:HD3	2.10	0.51
5:B:324:ILE:HD13	5:B:330:ALA:HA	1.92	0.51
5:B:549:THR:HG22	5:B:550:ASP:N	2.17	0.51
14:K:53:ASP:OD1	14:K:55:LYS:HB2	2.10	0.51
4:A:244:PRO:O	4:A:247:ARG:N	2.38	0.51
4:A:444:PHE:CB	4:A:458:HIS:HD2	2.24	0.51
4:A:1063:MET:SD	4:A:1436:ILE:HG12	2.50	0.51
5:B:503:GLY:H	5:B:507:LYS:HD2	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:890:TYR:OH	5:B:936:ASP:OD2	2.27	0.51
6:C:236:GLY:C	6:C:238:ILE:N	2.68	0.51
8:E:55:ARG:C	8:E:57:MET:N	2.67	0.51
8:E:153:HIS:HB3	8:E:196:VAL:CG1	2.38	0.51
10:G:99:PHE:CD1	10:G:99:PHE:C	2.88	0.51
11:H:138:GLU:O	11:H:139:ASN:C	2.52	0.51
14:K:21:ILE:HG23	14:K:31:VAL:HG11	1.92	0.51
4:A:93:VAL:CG2	4:A:301:ALA:HA	2.40	0.51
4:A:356:ASP:HB2	4:A:469:ARG:HH12	1.73	0.51
4:A:896:ARG:NH2	4:A:1030:ARG:NH2	2.58	0.51
4:A:920:LEU:HD23	4:A:920:LEU:C	2.35	0.51
4:A:1323:ASP:C	4:A:1325:THR:H	2.17	0.51
5:B:45:SER:O	5:B:46:GLN:C	2.53	0.51
5:B:552:MET:C	5:B:554:ILE:H	2.17	0.51
5:B:603:LEU:HD13	5:B:608:ASP:CB	2.38	0.51
5:B:1072:MET:HE1	5:B:1085:ILE:HB	1.88	0.51
7:D:50:LEU:HD11	10:G:4:ILE:HD11	1.93	0.51
7:D:51:ASN:C	7:D:52:LEU:O	2.52	0.51
7:D:56:ARG:HA	7:D:148:LEU:HD13	1.93	0.51
13:J:7:CYS:CB	13:J:46:CYS:HB3	2.41	0.51
4:A:60:SER:C	4:A:61:ILE:HG13	2.35	0.51
4:A:167:CYS:SG	4:A:167:CYS:O	2.69	0.51
4:A:1451:VAL:C	4:A:1453:TYR:H	2.18	0.51
5:B:20:ASP:O	5:B:22:SER:N	2.42	0.51
6:C:254:LYS:O	6:C:258:ILE:HD13	2.11	0.51
7:D:47:LEU:CD1	7:D:48:ILE:N	2.71	0.51
7:D:206:GLU:C	7:D:208:GLU:N	2.66	0.51
8:E:13:TRP:O	8:E:16:PHE:HB3	2.09	0.51
9:F:111:LEU:HD12	9:F:111:LEU:H	1.75	0.51
11:H:102:TYR:N	11:H:102:TYR:CD2	2.78	0.51
13:J:13:VAL:C	13:J:14:VAL:HG23	2.35	0.51
3:P:5:C:H2'	3:P:6:C:C6	2.45	0.51
4:A:1279:ILE:HG23	4:A:1308:THR:OG1	2.11	0.51
5:B:469:GLN:O	5:B:470:LYS:HB2	2.10	0.51
5:B:603:LEU:HB3	5:B:609:ILE:CD1	2.41	0.51
5:B:1172:ILE:HG22	5:B:1172:ILE:O	2.11	0.51
6:C:35:ARG:NH1	14:K:41:THR:H	2.08	0.51
6:C:116:LYS:HD3	6:C:140:ASN:HB3	1.93	0.51
7:D:141:LEU:O	7:D:142:LYS:C	2.54	0.51
10:G:79:PHE:HZ	10:G:106:MET:HE2	1.76	0.51
10:G:80:LYS:O	10:G:82:PHE:CE1	2.64	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:270:LEU:O	4:A:271:LYS:C	2.53	0.51
4:A:567:LYS:HD2	4:A:568:PRO:HD2	1.90	0.51
4:A:574:GLY:O	4:A:575:LYS:C	2.53	0.51
4:A:1144:LYS:HB2	4:A:1268:LEU:O	2.10	0.51
5:B:193:LYS:NZ	15:L:32:ALA:HB1	2.25	0.51
5:B:230:ALA:N	5:B:231:PRO:CD	2.73	0.51
11:H:98:TYR:C	11:H:118:PHE:HD2	2.18	0.51
15:L:27:LEU:HD13	15:L:37:LYS:HE2	1.92	0.51
4:A:37:PHE:N	4:A:37:PHE:CD1	2.79	0.51
4:A:357:PRO:HD2	5:B:833:TYR:CE1	2.46	0.51
4:A:416:ARG:C	4:A:417:TYR:CD2	2.89	0.51
4:A:1327:ILE:HG22	8:E:147:HIS:CE1	2.45	0.51
4:A:1438:THR:HB	5:B:1144:ALA:CB	2.40	0.51
5:B:115:GLN:HG2	5:B:193:LYS:CB	2.40	0.51
5:B:757:PRO:HD3	5:B:983:ARG:NH2	2.26	0.51
5:B:1084:GLN:NE2	5:B:1084:GLN:H	2.07	0.51
6:C:243:VAL:O	6:C:243:VAL:HG12	2.10	0.51
12:I:99:LEU:C	12:I:100:PHE:CD1	2.89	0.51
4:A:47:ARG:O	4:A:48:ALA:HB2	2.10	0.51
4:A:89:PRO:HB2	4:A:204:THR:HG22	1.92	0.51
4:A:102:VAL:O	4:A:105:CYS:HB2	2.11	0.51
4:A:353:ILE:HG21	4:A:487:MET:CE	2.41	0.51
4:A:1116:LEU:HG	4:A:1308:THR:HB	1.92	0.51
5:B:1034:VAL:C	5:B:1036:ALA:N	2.69	0.51
9:F:99:LEU:HD21	10:G:64:THR:O	2.10	0.51
10:G:49:LEU:N	10:G:49:LEU:HD23	2.26	0.51
12:I:25:LEU:HB3	12:I:38:ALA:HB2	1.93	0.51
12:I:50:THR:HG22	12:I:51:ASN:N	2.26	0.51
13:J:2:ILE:HG12	13:J:57:ILE:HD12	1.93	0.51
13:J:64:ASN:CB	13:J:65:PRO:CD	2.85	0.51
4:A:82:GLY:O	4:A:241:VAL:N	2.38	0.51
4:A:130:ASP:O	4:A:131:SER:C	2.54	0.51
4:A:278:THR:O	4:A:282:ASN:HB2	2.11	0.51
4:A:1063:MET:HG3	4:A:1436:ILE:HG23	1.92	0.51
5:B:298:LEU:N	5:B:298:LEU:CD2	2.74	0.51
5:B:778:MET:HE2	5:B:1094:ARG:CG	2.41	0.51
5:B:1177:HIS:C	5:B:1179:GLN:H	2.19	0.51
6:C:76:ASP:O	6:C:79:GLN:HG2	2.11	0.51
10:G:74:TYR:CD2	10:G:74:TYR:N	2.79	0.51
10:G:119:LEU:HD13	10:G:132:SER:HB2	1.93	0.51
13:J:7:CYS:HA	13:J:49:MET:HE3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:2:DA:H2''	2:N:3:DG:OP2	2.10	0.51
4:A:29:ALA:HB1	5:B:1184:GLY:HA2	1.91	0.51
4:A:1094:VAL:HG12	4:A:1095:THR:N	2.26	0.51
4:A:1101:LEU:O	4:A:1101:LEU:HD12	2.10	0.51
5:B:361:LEU:N	5:B:362:PRO:CD	2.73	0.51
5:B:410:GLY:O	5:B:412:LEU:N	2.44	0.51
5:B:455:SER:O	5:B:456:GLY:C	2.53	0.51
7:D:52:LEU:CD2	7:D:147:TYR:HE2	2.23	0.51
14:K:24:ASP:OD2	14:K:74:ARG:NH1	2.43	0.51
4:A:41:MET:O	4:A:42:ASP:C	2.54	0.50
4:A:84:ILE:HD11	4:A:270:LEU:CD1	2.29	0.50
4:A:626:ASN:C	4:A:628:GLY:H	2.19	0.50
4:A:666:ILE:H	5:B:1026:LEU:HD22	1.76	0.50
4:A:1333:ILE:HG22	4:A:1334:ASP:N	2.26	0.50
5:B:221:ASN:N	5:B:241:ARG:O	2.33	0.50
5:B:769:TYR:C	5:B:771:SER:N	2.69	0.50
6:C:33:LEU:HG	6:C:37:MET:HE2	1.93	0.50
7:D:153:ARG:C	7:D:154:PHE:CD1	2.89	0.50
8:E:61:GLN:HG2	8:E:62:ALA:N	2.26	0.50
14:K:56:VAL:HA	14:K:77:THR:HG22	1.93	0.50
1:T:18:DC:OP1	1:T:18:DC:H3'	2.11	0.50
4:A:44:THR:O	4:A:45:GLN:HB2	2.12	0.50
4:A:809:THR:H	4:A:812:GLU:HB2	1.76	0.50
4:A:817:ALA:HA	5:B:764:SER:OG	2.11	0.50
4:A:1451:VAL:O	4:A:1454:MET:HG2	2.11	0.50
5:B:48:LEU:O	5:B:51:PHE:N	2.42	0.50
5:B:580:VAL:HG22	5:B:624:LEU:HB3	1.93	0.50
5:B:841:MET:SD	5:B:846:ILE:HD11	2.51	0.50
5:B:882:THR:CG2	5:B:884:ARG:HB2	2.40	0.50
6:C:9:LYS:O	6:C:10:ILE:C	2.54	0.50
9:F:81:THR:HG21	9:F:136:ARG:CD	2.41	0.50
4:A:262:LEU:C	4:A:264:PHE:N	2.65	0.50
4:A:512:VAL:HA	4:A:519:PRO:HA	1.94	0.50
4:A:873:MET:HG2	4:A:957:PRO:HB3	1.92	0.50
5:B:48:LEU:O	5:B:49:ASP:C	2.52	0.50
5:B:1056:SER:HB3	5:B:1066:SER:HB2	1.94	0.50
9:F:143:PHE:C	9:F:143:PHE:CD1	2.90	0.50
10:G:99:PHE:HZ	10:G:163:ILE:HD13	1.76	0.50
13:J:44:TYR:CD2	13:J:44:TYR:N	2.79	0.50
4:A:79:GLY:HA3	4:A:243:PRO:HG3	1.93	0.50
4:A:1451:VAL:C	4:A:1453:TYR:N	2.68	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:770:GLN:OE1	5:B:983:ARG:CA	2.56	0.50
5:B:1177:HIS:O	5:B:1179:GLN:N	2.45	0.50
6:C:168:ALA:C	6:C:170:TRP:N	2.69	0.50
7:D:52:LEU:C	7:D:54:GLU:N	2.69	0.50
8:E:177:ARG:C	8:E:212:ARG:HD3	2.36	0.50
12:I:34:TYR:CE2	12:I:36:GLU:HB3	2.45	0.50
12:I:85:PHE:HD1	12:I:99:LEU:HD13	1.77	0.50
14:K:58:PHE:HB3	14:K:76:GLN:HE21	1.76	0.50
4:A:326:ARG:HH22	4:A:1407:GLU:HG3	1.76	0.50
4:A:418:SER:C	4:A:420:ARG:H	2.18	0.50
4:A:446:ARG:HB2	4:A:487:MET:HG2	1.94	0.50
4:A:784:LEU:HB3	4:A:785:PRO:HD2	1.94	0.50
5:B:377:PHE:C	5:B:379:GLY:N	2.67	0.50
5:B:658:ILE:HG22	5:B:659:ALA:N	2.27	0.50
5:B:825:VAL:HG12	5:B:826:ALA:N	2.26	0.50
6:C:55:THR:O	6:C:55:THR:HG22	2.11	0.50
7:D:64:VAL:C	7:D:66:ARG:H	2.19	0.50
7:D:137:ASN:C	7:D:137:ASN:HD22	2.19	0.50
11:H:123:MET:HG2	11:H:124:ARG:N	2.26	0.50
12:I:5:ARG:HD3	12:I:36:GLU:OE2	2.12	0.50
12:I:33:SER:O	12:I:35:VAL:HG23	2.11	0.50
12:I:111:THR:CG2	12:I:112:SER:N	2.74	0.50
4:A:324:SER:O	4:A:325:ILE:C	2.53	0.50
4:A:326:ARG:NH2	4:A:1407:GLU:HG3	2.26	0.50
4:A:412:ARG:NH2	5:B:1108:ARG:NH1	2.60	0.50
4:A:817:ALA:O	4:A:819:GLY:N	2.45	0.50
4:A:1072:ILE:C	4:A:1075:PRO:HD2	2.36	0.50
4:A:1430:LEU:O	5:B:1197:PRO:HD2	2.11	0.50
5:B:205:ILE:N	5:B:205:ILE:CD1	2.74	0.50
5:B:745:PRO:O	5:B:747:MET:N	2.44	0.50
5:B:778:MET:HE2	5:B:1094:ARG:CD	2.41	0.50
5:B:805:THR:HA	5:B:809:MET:HE1	1.93	0.50
5:B:1095:LEU:HD12	5:B:1095:LEU:N	2.22	0.50
7:D:33:PHE:CZ	10:G:80:LYS:CE	2.95	0.50
8:E:124:VAL:CG1	8:E:132:ILE:HB	2.39	0.50
11:H:84:ALA:C	11:H:86:ASP:N	2.69	0.50
12:I:85:PHE:HD2	12:I:85:PHE:N	1.89	0.50
4:A:341:MET:CE	5:B:1135:ARG:NH1	2.73	0.50
4:A:573:SER:OG	4:A:576:GLN:HB2	2.11	0.50
4:A:608:ILE:HD12	4:A:613:ILE:CD1	2.42	0.50
4:A:768:GLN:HG2	4:A:816:HIS:CA	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:836:TYR:O	4:A:837:ILE:C	2.55	0.50
4:A:886:ILE:HG13	4:A:943:LEU:CD1	2.42	0.50
4:A:963:ILE:HD11	4:A:1048:ASN:CB	2.28	0.50
4:A:1041:ALA:O	4:A:1044:TRP:HB3	2.12	0.50
5:B:235:SER:C	5:B:236:HIS:HD2	2.19	0.50
5:B:765:PRO:O	5:B:766:ARG:C	2.53	0.50
5:B:1182:CYS:C	5:B:1183:LYS:HE3	2.35	0.50
6:C:70:ILE:HD11	6:C:144:ILE:HG12	1.94	0.50
7:D:220:LEU:O	7:D:221:TYR:HD1	1.94	0.50
8:E:161:LYS:C	8:E:163:GLU:H	2.19	0.50
9:F:138:LEU:HB3	9:F:139:PRO:HD2	1.94	0.50
10:G:9:LEU:HG	10:G:10:ASN:N	2.27	0.50
11:H:27:GLU:HG2	11:H:39:THR:HG23	1.93	0.50
4:A:464:PRO:HG2	4:A:465:TYR:HD1	1.77	0.50
4:A:596:THR:C	4:A:598:LEU:N	2.67	0.50
4:A:1334:ASP:O	4:A:1336:MET:N	2.45	0.50
4:A:1410:PHE:HD2	5:B:1212:ILE:HD12	1.77	0.50
5:B:26:THR:O	5:B:29:ASP:HB2	2.11	0.50
5:B:681:TRP:O	5:B:683:SER:N	2.45	0.50
5:B:882:THR:O	5:B:883:LEU:HB2	2.11	0.50
6:C:88:CYS:SG	6:C:91:HIS:C	2.95	0.50
6:C:101:LEU:HD13	6:C:118:LEU:HD23	1.94	0.50
6:C:105:GLY:HA3	6:C:149:LYS:O	2.11	0.50
7:D:33:PHE:CE2	10:G:80:LYS:NZ	2.61	0.50
8:E:22:MET:CE	8:E:26:ARG:HH21	2.25	0.50
8:E:134:THR:C	8:E:135:PHE:CD1	2.89	0.50
11:H:89:LEU:C	11:H:91:ASP:N	2.70	0.50
12:I:69:PRO:HG2	12:I:85:PHE:CD2	2.47	0.50
4:A:65:LEU:O	4:A:66:LYS:O	2.30	0.50
4:A:289:ILE:C	4:A:291:GLU:N	2.70	0.50
4:A:547:LEU:HB3	14:K:58:PHE:CE1	2.44	0.50
4:A:552:TRP:O	4:A:554:PRO:HD3	2.12	0.50
4:A:658:LEU:HD23	4:A:659:HIS:HE1	1.76	0.50
4:A:1280:GLU:O	4:A:1281:ARG:C	2.54	0.50
5:B:734:HIS:O	5:B:735:ALA:HB2	2.12	0.50
5:B:865:LYS:NZ	5:B:869:SER:HA	2.27	0.50
6:C:35:ARG:NH1	14:K:41:THR:N	2.59	0.50
6:C:69:LEU:N	6:C:69:LEU:CD1	2.74	0.50
6:C:208:GLU:O	6:C:210:GLU:N	2.45	0.50
6:C:238:ILE:HG22	6:C:243:VAL:HG23	1.94	0.50
7:D:146:GLN:O	7:D:147:TYR:C	2.54	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:18:GLN:H	5:B:1215:ARG:HB2	1.76	0.49
4:A:30:ILE:HG23	5:B:1170:THR:HG23	1.94	0.49
4:A:442:VAL:CB	4:A:489:LEU:HD11	2.37	0.49
4:A:1120:LEU:HD12	4:A:1120:LEU:N	2.26	0.49
4:A:1142:THR:O	4:A:1143:LEU:C	2.54	0.49
5:B:115:GLN:HG2	5:B:193:LYS:HB2	1.93	0.49
5:B:171:PRO:HD2	5:B:457:LEU:CD1	2.39	0.49
5:B:175:ARG:HG2	5:B:175:ARG:HH11	1.77	0.49
5:B:525:ALA:O	5:B:768:THR:HA	2.11	0.49
5:B:763:GLN:O	5:B:764:SER:C	2.55	0.49
6:C:8:VAL:HG12	6:C:9:LYS:N	2.26	0.49
6:C:249:ASP:O	6:C:252:GLN:HB3	2.12	0.49
10:G:3:PHE:CD1	10:G:80:LYS:NZ	2.77	0.49
15:L:40:LEU:HD22	15:L:44:ASP:CB	2.42	0.49
1:T:19:DG:OP2	4:A:332:LYS:NZ	2.42	0.49
4:A:2:VAL:HG21	5:B:1158:PHE:N	2.27	0.49
4:A:808:LEU:HD23	4:A:813:PHE:CA	2.37	0.49
4:A:842:VAL:HG11	5:B:1136:ASP:OD2	2.12	0.49
4:A:947:PHE:CD2	4:A:954:TRP:CZ2	3.00	0.49
4:A:1124:HIS:HB3	4:A:1130:GLN:HG2	1.93	0.49
4:A:1209:MET:HE1	4:A:1236:LEU:HB3	1.94	0.49
4:A:1394:THR:O	4:A:1395:GLY:O	2.30	0.49
5:B:309:GLN:OE1	12:I:52:ILE:HD11	2.12	0.49
5:B:766:ARG:NH2	5:B:1020:ARG:HH11	2.10	0.49
6:C:34:ARG:O	6:C:38:ILE:HG13	2.11	0.49
6:C:66:ARG:CZ	13:J:2:ILE:HG21	2.42	0.49
7:D:33:PHE:CZ	10:G:80:LYS:NZ	2.79	0.49
8:E:35:VAL:O	8:E:37:LEU:N	2.44	0.49
9:F:148:VAL:O	9:F:149:GLU:C	2.54	0.49
14:K:88:LYS:O	14:K:89:ASN:C	2.55	0.49
15:L:46:VAL:O	15:L:46:VAL:HG12	2.11	0.49
4:A:283:GLY:O	4:A:285:PRO:HD3	2.12	0.49
4:A:317:LYS:O	4:A:318:SER:CB	2.60	0.49
4:A:418:SER:C	4:A:420:ARG:N	2.68	0.49
4:A:489:LEU:HD12	4:A:490:HIS:N	2.26	0.49
4:A:901:LEU:HA	4:A:907:THR:OG1	2.13	0.49
4:A:1059:HIS:O	4:A:1061:GLY:N	2.45	0.49
5:B:32:ALA:O	5:B:35:SER:HB2	2.11	0.49
5:B:189:LEU:O	5:B:190:TYR:C	2.55	0.49
5:B:487:THR:O	5:B:490:SER:HB3	2.12	0.49
5:B:642:ASP:HB3	5:B:649:LYS:HD2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:737:THR:O	5:B:738:PHE:C	2.55	0.49
5:B:1106:ARG:NH1	5:B:1110:PRO:CD	2.76	0.49
6:C:167:HIS:HD2	6:C:168:ALA:H	1.60	0.49
7:D:29:LEU:HD22	10:G:82:PHE:CD2	2.47	0.49
9:F:90:ARG:HD3	9:F:155:LEU:HD11	1.94	0.49
10:G:13:LEU:O	10:G:67:SER:HA	2.12	0.49
10:G:94:CYS:SG	10:G:99:PHE:HB3	2.51	0.49
10:G:143:ILE:HG22	10:G:144:ARG:H	1.76	0.49
11:H:41:ASP:O	11:H:42:ILE:HG13	2.13	0.49
13:J:45:CYS:SG	13:J:46:CYS:N	2.85	0.49
4:A:218:ASP:O	4:A:219:PHE:C	2.56	0.49
4:A:567:LYS:HB2	4:A:568:PRO:CD	2.43	0.49
4:A:839:ARG:O	4:A:840:ARG:C	2.54	0.49
4:A:863:VAL:HG11	4:A:866:PHE:CE2	2.48	0.49
5:B:25:ILE:HD11	5:B:653:VAL:C	2.37	0.49
5:B:708:GLU:O	5:B:709:ASP:C	2.56	0.49
6:C:91:HIS:HD2	6:C:91:HIS:O	1.94	0.49
4:A:65:LEU:O	4:A:66:LYS:C	2.55	0.49
4:A:113:LEU:O	4:A:114:LEU:HD23	2.13	0.49
4:A:166:GLY:O	4:A:167:CYS:CB	2.61	0.49
4:A:219:PHE:CE2	4:A:231:PRO:HD2	2.47	0.49
4:A:381:THR:HG21	4:A:383:TYR:CD1	2.48	0.49
4:A:457:ALA:HB3	4:A:506:ALA:HA	1.94	0.49
4:A:577:ILE:O	4:A:578:LEU:C	2.51	0.49
4:A:898:ARG:HB2	4:A:933:TYR:CE1	2.46	0.49
4:A:984:LYS:O	4:A:988:LEU:HB2	2.11	0.49
4:A:1149:ALA:CB	12:I:47:GLU:HA	2.43	0.49
4:A:1329:THR:HG23	4:A:1331:SER:H	1.75	0.49
5:B:96:TYR:HB2	5:B:129:PHE:HB2	1.94	0.49
5:B:235:SER:O	5:B:236:HIS:HD2	1.94	0.49
5:B:327:ARG:O	5:B:331:LEU:HD13	2.12	0.49
5:B:744:HIS:HD2	5:B:746:SER:OG	1.94	0.49
5:B:745:PRO:C	5:B:747:MET:N	2.70	0.49
5:B:765:PRO:O	5:B:768:THR:N	2.45	0.49
5:B:810:GLU:CB	5:B:815:ARG:HH22	2.26	0.49
5:B:860:MET:HG2	5:B:861:ASP:H	1.77	0.49
6:C:31:ASN:ND2	6:C:35:ARG:HD2	2.28	0.49
7:D:144:THR:HG21	10:G:46:LEU:HD13	1.95	0.49
8:E:48:ASP:CG	8:E:49:SER:N	2.68	0.49
11:H:33:GLN:C	11:H:35:GLN:H	2.21	0.49
11:H:84:ALA:C	11:H:86:ASP:H	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:53:ASP:HB3	14:K:56:VAL:HG23	1.93	0.49
4:A:4:GLN:O	4:A:5:GLN:O	2.31	0.49
4:A:298:PHE:HD2	4:A:299:HIS:CD2	2.31	0.49
4:A:595:THR:O	4:A:596:THR:HG23	2.12	0.49
4:A:870:GLU:HG2	8:E:208:TYR:CG	2.47	0.49
4:A:1130:GLN:O	4:A:1134:ILE:HG13	2.12	0.49
4:A:1265:ASN:C	4:A:1267:MET:N	2.68	0.49
5:B:281:PRO:O	5:B:283:VAL:N	2.45	0.49
5:B:579:ARG:N	5:B:589:VAL:HG13	2.28	0.49
5:B:728:ARG:NH1	5:B:1047:PHE:HB3	2.25	0.49
5:B:1039:GLY:HA2	13:J:51:LEU:CD2	2.42	0.49
5:B:1115:THR:HG21	5:B:1117:GLN:CD	2.38	0.49
10:G:145:VAL:CG1	10:G:146:LYS:N	2.76	0.49
14:K:107:THR:O	14:K:111:LEU:HG	2.12	0.49
4:A:381:THR:HG23	4:A:382:PRO:HD2	1.95	0.49
4:A:913:LEU:CD2	4:A:919:ILE:HD12	2.41	0.49
4:A:960:ILE:O	4:A:961:ARG:C	2.55	0.49
4:A:1070:GLN:O	4:A:1071:SER:C	2.55	0.49
4:A:1431:GLY:HA3	5:B:1152:MET:SD	2.53	0.49
5:B:465:ASN:N	5:B:465:ASN:ND2	2.61	0.49
5:B:498:THR:HB	5:B:537:LYS:O	2.12	0.49
5:B:622:LYS:CE	12:I:59:VAL:HG22	2.43	0.49
5:B:640:VAL:O	5:B:640:VAL:HG12	2.11	0.49
5:B:1065:GLN:NE2	5:B:1067:ARG:N	2.45	0.49
5:B:1106:ARG:HH12	5:B:1110:PRO:HG2	1.78	0.49
8:E:43:LYS:O	8:E:45:LYS:N	2.44	0.49
13:J:3:VAL:HG21	13:J:18:TRP:CB	2.38	0.49
15:L:49:LYS:O	15:L:50:ASP:CB	2.60	0.49
4:A:215:SER:HB3	4:A:218:ASP:OD2	2.12	0.49
4:A:295:LEU:O	4:A:298:PHE:HB3	2.12	0.49
4:A:606:LEU:HB3	4:A:614:PHE:CD2	2.47	0.49
4:A:723:ASN:C	4:A:725:ALA:N	2.68	0.49
5:B:205:ILE:HG22	5:B:206:ASN:N	2.28	0.49
5:B:591:ARG:O	5:B:592:ASN:C	2.55	0.49
5:B:879:ARG:O	5:B:880:THR:HB	2.12	0.49
10:G:115:MET:HB3	10:G:116:PRO:HD2	1.94	0.49
14:K:31:VAL:CG1	14:K:32:VAL:H	2.26	0.49
4:A:106:VAL:HG13	4:A:112:LYS:C	2.37	0.49
4:A:372:LYS:HA	4:A:435:HIS:ND1	2.28	0.49
4:A:652:VAL:O	4:A:653:VAL:C	2.56	0.49
4:A:871:ASP:OD1	4:A:871:ASP:C	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:921:GLY:O	4:A:922:ASP:C	2.54	0.49
4:A:1036:ARG:HG2	4:A:1036:ARG:HH11	1.77	0.49
4:A:1280:GLU:O	4:A:1281:ARG:O	2.30	0.49
5:B:307:ASP:O	5:B:309:GLN:N	2.46	0.49
5:B:460:ALA:HB1	5:B:466:TRP:CZ3	2.48	0.49
5:B:575:PRO:HG2	5:B:576:ASP:H	1.78	0.49
5:B:763:GLN:O	5:B:765:PRO:N	2.46	0.49
5:B:1032:SER:O	5:B:1036:ALA:HB2	2.12	0.49
6:C:10:ILE:HA	6:C:20:PHE:HB2	1.93	0.49
7:D:134:THR:CG2	7:D:135:GLY:H	2.26	0.49
10:G:74:TYR:HD2	10:G:74:TYR:N	2.07	0.49
4:A:535:THR:CG2	4:A:575:LYS:HE2	2.42	0.49
4:A:590:ARG:HH21	4:A:620:LYS:CB	2.24	0.49
5:B:102:VAL:CG2	5:B:112:LEU:HD22	2.43	0.49
5:B:1033:LYS:NZ	5:B:1070:GLU:OE1	2.45	0.49
5:B:1162:ILE:C	5:B:1171:VAL:HG21	2.38	0.49
8:E:175:LEU:HD23	8:E:176:PRO:CD	2.39	0.49
13:J:48:ARG:HE	13:J:49:MET:CE	2.26	0.49
13:J:57:ILE:O	13:J:60:PHE:HB2	2.13	0.49
14:K:12:LEU:H	14:K:12:LEU:CD1	2.24	0.49
4:A:18:GLN:HB3	5:B:1215:ARG:HG3	1.94	0.48
4:A:253:ASN:HB3	5:B:935:ARG:CZ	2.42	0.48
5:B:203:PHE:N	5:B:203:PHE:CD1	2.81	0.48
5:B:318:VAL:C	5:B:320:ASP:N	2.71	0.48
5:B:318:VAL:O	5:B:320:ASP:N	2.46	0.48
5:B:893:LEU:HD22	5:B:897:GLY:C	2.38	0.48
6:C:154:LYS:O	6:C:155:LEU:HD23	2.12	0.48
7:D:167:LEU:HB3	7:D:177:VAL:HG13	1.95	0.48
8:E:22:MET:HE3	8:E:26:ARG:HH21	1.78	0.48
8:E:46:TYR:CD2	8:E:58:MET:HG2	2.48	0.48
10:G:44:TYR:O	10:G:78:VAL:HA	2.13	0.48
4:A:18:GLN:CB	5:B:1215:ARG:HB2	2.42	0.48
4:A:164:ARG:CG	4:A:165:GLY:H	2.20	0.48
4:A:608:ILE:HB	4:A:613:ILE:HD11	1.94	0.48
5:B:844:SER:HB3	5:B:848:ARG:HH12	1.78	0.48
5:B:996:ARG:HH12	6:C:38:ILE:HG23	1.77	0.48
5:B:1187:ASN:O	5:B:1188:LYS:CB	2.61	0.48
5:B:1196:ILE:O	5:B:1196:ILE:HG13	2.11	0.48
7:D:189:ASP:O	7:D:193:THR:HB	2.13	0.48
9:F:75:PRO:O	9:F:77:ASP:O	2.31	0.48
12:I:85:PHE:N	12:I:85:PHE:CD2	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:53:HIS:CD2	13:J:54:VAL:N	2.81	0.48
14:K:65:HIS:CD2	14:K:67:PHE:HB2	2.48	0.48
14:K:82:ASP:OD1	14:K:84:LYS:N	2.45	0.48
4:A:382:PRO:HB3	4:A:428:TYR:CE2	2.41	0.48
4:A:1191:TRP:HB3	4:A:1260:LEU:HD23	1.96	0.48
4:A:1195:LEU:HD11	4:A:1267:MET:CE	2.44	0.48
4:A:1213:GLY:O	4:A:1216:ILE:N	2.46	0.48
5:B:240:ILE:HG23	5:B:240:ILE:O	2.13	0.48
5:B:1202:LEU:O	5:B:1203:LEU:C	2.56	0.48
6:C:258:ILE:N	6:C:258:ILE:CD1	2.75	0.48
7:D:68:ARG:C	7:D:70:PHE:H	2.20	0.48
11:H:99:GLY:N	11:H:118:PHE:CD2	2.80	0.48
14:K:87:LEU:O	14:K:88:LYS:C	2.56	0.48
4:A:532:ARG:O	4:A:535:THR:HB	2.13	0.48
4:A:668:ASP:HB3	4:A:743:VAL:HG23	1.94	0.48
4:A:809:THR:HG23	4:A:812:GLU:HG3	1.95	0.48
4:A:845:LEU:O	4:A:846:GLU:C	2.54	0.48
4:A:1102:LYS:HG2	4:A:1106:ASN:HD21	1.77	0.48
4:A:1162:VAL:O	4:A:1162:VAL:HG12	2.13	0.48
4:A:1373:ASP:HA	4:A:1376:THR:CG2	2.43	0.48
5:B:34:ILE:O	5:B:35:SER:C	2.57	0.48
5:B:910:VAL:HG12	5:B:911:ILE:N	2.28	0.48
10:G:88:ASP:HA	10:G:144:ARG:HA	1.96	0.48
4:A:7:SER:C	4:A:9:ALA:H	2.20	0.48
4:A:14:VAL:HG21	5:B:1216:LEU:HD13	1.95	0.48
4:A:115:LEU:HB3	4:A:122:MET:HE2	1.94	0.48
4:A:466:SER:HB3	5:B:1103:ILE:HG12	1.94	0.48
4:A:971:PHE:HE2	4:A:1040:GLN:HG2	1.79	0.48
4:A:1168:GLU:O	4:A:1172:LEU:HG	2.13	0.48
4:A:1279:ILE:HD11	4:A:1316:VAL:CG2	2.42	0.48
4:A:1291:VAL:HG13	4:A:1292:PRO:N	2.29	0.48
4:A:1344:GLY:O	4:A:1345:ARG:C	2.56	0.48
5:B:370:PHE:HE2	5:B:373:ARG:NH1	2.06	0.48
5:B:810:GLU:HB2	5:B:815:ARG:HH22	1.79	0.48
5:B:897:GLY:O	5:B:898:LEU:HD23	2.14	0.48
6:C:69:LEU:CD1	6:C:69:LEU:H	2.27	0.48
6:C:259:LEU:HD13	14:K:91:CYS:HB2	1.95	0.48
8:E:124:VAL:HG13	8:E:132:ILE:CB	2.40	0.48
10:G:20:PRO:HG2	10:G:21:ARG:N	2.28	0.48
11:H:23:VAL:HG13	11:H:42:ILE:O	2.14	0.48
14:K:5:ASP:O	14:K:6:ARG:C	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:313:GLN:O	4:A:314:ALA:HB3	2.13	0.48
4:A:381:THR:HG23	4:A:383:TYR:H	1.79	0.48
4:A:407:ARG:HB3	4:A:430:TRP:CE2	2.49	0.48
4:A:683:ILE:HD13	4:A:801:GLU:HG3	1.96	0.48
5:B:20:ASP:C	5:B:22:SER:H	2.22	0.48
5:B:120:ARG:HG2	5:B:955:THR:HG21	1.96	0.48
5:B:558:LEU:O	5:B:560:GLU:N	2.46	0.48
5:B:789:MET:HE3	5:B:965:LYS:HB3	1.94	0.48
5:B:806:THR:N	5:B:809:MET:HE3	2.29	0.48
5:B:815:ARG:HD3	5:B:1041:GLU:OE2	2.14	0.48
5:B:1084:GLN:HG2	6:C:201:TRP:CZ2	2.48	0.48
6:C:255:VAL:HG12	14:K:91:CYS:HB3	1.94	0.48
8:E:117:THR:O	8:E:120:ALA:N	2.45	0.48
4:A:335:ARG:CA	4:A:339:ASN:HB2	2.41	0.48
4:A:770:VAL:HA	4:A:822:GLU:OE1	2.14	0.48
4:A:775:ILE:HB	4:A:797:LYS:O	2.14	0.48
4:A:958:VAL:O	4:A:958:VAL:HG12	2.12	0.48
4:A:1116:LEU:CD1	4:A:1118:VAL:HG13	2.43	0.48
5:B:333:PHE:O	5:B:334:ILE:HG13	2.14	0.48
5:B:345:LYS:O	5:B:347:LYS:HG2	2.13	0.48
5:B:834:ASN:HB3	5:B:840:ILE:HG13	1.95	0.48
5:B:1039:GLY:HA2	13:J:51:LEU:HD21	1.95	0.48
7:D:53:SER:HB3	7:D:153:ARG:H	1.79	0.48
12:I:34:TYR:O	12:I:35:VAL:HG23	2.13	0.48
1:T:15:DT:H1'	4:A:1386:ARG:HH12	1.77	0.48
3:P:5:C:H2'	3:P:6:C:H6	1.78	0.48
4:A:243:PRO:O	4:A:244:PRO:C	2.57	0.48
4:A:760:GLN:OE1	5:B:1021:MET:HE1	2.14	0.48
4:A:1430:LEU:C	5:B:1197:PRO:HD2	2.39	0.48
5:B:29:ASP:HB3	5:B:658:ILE:CD1	2.44	0.48
5:B:129:PHE:HA	5:B:165:VAL:O	2.14	0.48
5:B:180:TYR:HD1	5:B:180:TYR:H	1.61	0.48
5:B:957:ASN:O	5:B:958:GLN:C	2.57	0.48
6:C:215:GLU:O	6:C:217:ASP:N	2.46	0.48
7:D:19:GLU:O	7:D:21:GLU:N	2.47	0.48
8:E:96:PHE:CZ	8:E:100:ILE:HD11	2.49	0.48
10:G:10:ASN:OD1	10:G:71:ASN:HA	2.13	0.48
10:G:20:PRO:CG	10:G:21:ARG:H	2.26	0.48
10:G:143:ILE:CG2	10:G:144:ARG:N	2.77	0.48
13:J:28:ASP:O	13:J:29:GLU:C	2.57	0.48
4:A:95:PHE:O	4:A:98:LYS:N	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:388:LEU:HD22	4:A:432:VAL:HG21	1.96	0.48
4:A:407:ARG:HG2	4:A:430:TRP:CZ3	2.49	0.48
4:A:408:ASP:C	4:A:410:GLY:N	2.72	0.48
4:A:565:ILE:O	4:A:570:PRO:HA	2.14	0.48
4:A:626:ASN:O	4:A:631:HIS:CD2	2.67	0.48
4:A:1396:ALA:O	4:A:1398:MET:N	2.47	0.48
4:A:1441:PHE:CE2	9:F:89:GLU:HG2	2.49	0.48
4:A:1450:LEU:HD21	10:G:19:GLY:O	2.13	0.48
5:B:992:ILE:HD11	14:K:66:PRO:HB2	1.95	0.48
5:B:1077:THR:HG22	14:K:44:ASN:HD21	1.78	0.48
5:B:1187:ASN:O	5:B:1188:LYS:HB2	2.13	0.48
8:E:129:PRO:O	8:E:130:ALA:C	2.56	0.48
8:E:154:ILE:H	8:E:196:VAL:HG12	1.79	0.48
11:H:100:THR:HG22	11:H:101:ALA:H	1.79	0.48
14:K:83:PRO:O	14:K:84:LYS:C	2.56	0.48
4:A:545:GLN:O	4:A:548:ASN:N	2.47	0.48
4:A:1211:GLN:O	4:A:1212:VAL:C	2.57	0.48
4:A:1341:ILE:O	4:A:1344:GLY:N	2.47	0.48
5:B:642:ASP:CB	5:B:649:LYS:HG3	2.43	0.48
5:B:758:PHE:HB2	5:B:1024:ALA:HB1	1.96	0.48
5:B:1001:PHE:CD1	5:B:1001:PHE:C	2.92	0.48
5:B:1064:TYR:O	5:B:1065:GLN:C	2.57	0.48
6:C:3:GLU:HG2	6:C:4:GLU:N	2.29	0.48
4:A:381:THR:O	4:A:384:ASN:N	2.43	0.47
4:A:577:ILE:O	4:A:580:VAL:HG23	2.14	0.47
4:A:608:ILE:HG13	4:A:613:ILE:HD12	1.95	0.47
4:A:784:LEU:C	4:A:786:HIS:H	2.21	0.47
5:B:63:ILE:HA	5:B:421:PHE:CE2	2.49	0.47
5:B:95:ILE:CG1	5:B:130:VAL:HG22	2.41	0.47
5:B:205:ILE:CG2	5:B:206:ASN:N	2.76	0.47
5:B:542:MET:HE3	5:B:636:PRO:CG	2.44	0.47
5:B:1065:GLN:HG3	5:B:1067:ARG:H	1.78	0.47
9:F:99:LEU:C	9:F:99:LEU:HD12	2.38	0.47
10:G:125:SER:OG	10:G:128:PRO:HA	2.14	0.47
4:A:53:LEU:CD2	4:A:54:ASN:N	2.60	0.47
4:A:172:PRO:HG3	4:A:185:TRP:CZ2	2.49	0.47
4:A:265:LYS:CE	4:A:322:VAL:HG13	2.44	0.47
4:A:853:ASP:O	4:A:854:ASN:CB	2.60	0.47
4:A:856:THR:HG22	4:A:864:ILE:HB	1.95	0.47
4:A:966:ASN:O	4:A:967:ALA:C	2.57	0.47
4:A:1013:ASP:O	4:A:1015:VAL:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:97:VAL:HG12	5:B:178:ASN:HD21	1.77	0.47
5:B:371:GLU:CD	5:B:371:GLU:N	2.70	0.47
5:B:401:PHE:HD2	5:B:521:LEU:HD12	1.79	0.47
6:C:74:SER:HB2	6:C:77:ILE:HG12	1.94	0.47
11:H:40:LEU:HD22	11:H:123:MET:HE3	1.96	0.47
11:H:106:GLU:O	11:H:108:SER:N	2.46	0.47
13:J:56:LEU:O	13:J:59:LYS:N	2.47	0.47
15:L:40:LEU:HD13	15:L:44:ASP:CB	2.43	0.47
3:P:7:A:H2'	3:P:8:G:O4'	2.14	0.47
4:A:172:PRO:HB3	4:A:185:TRP:CE2	2.49	0.47
4:A:356:ASP:C	4:A:358:ASN:H	2.22	0.47
4:A:369:SER:HB3	14:K:2:ASN:HD21	1.78	0.47
4:A:666:ILE:CD1	4:A:667:GLY:N	2.77	0.47
4:A:1025:ARG:O	4:A:1026:LEU:HD23	2.14	0.47
5:B:446:LEU:N	5:B:446:LEU:HD23	2.29	0.47
5:B:522:VAL:HG12	5:B:523:CYS:N	2.27	0.47
5:B:710:LEU:C	5:B:711:GLU:HG2	2.39	0.47
7:D:184:ALA:O	7:D:185:CYS:SG	2.69	0.47
9:F:75:PRO:HG3	9:F:78:GLN:OE1	2.14	0.47
11:H:91:ASP:O	11:H:93:TYR:N	2.47	0.47
11:H:116:TYR:HE2	11:H:140:ALA:CB	2.27	0.47
11:H:128:ASN:CG	11:H:128:ASN:O	2.57	0.47
4:A:872:GLY:O	4:A:1058:VAL:HG23	2.14	0.47
4:A:1053:PHE:C	4:A:1055:ARG:H	2.21	0.47
5:B:102:VAL:CG2	5:B:112:LEU:HB2	2.41	0.47
5:B:258:LEU:O	5:B:259:TYR:O	2.33	0.47
5:B:386:LEU:O	5:B:388:CYS:N	2.48	0.47
5:B:435:THR:CG2	5:B:437:GLU:HB2	2.44	0.47
5:B:593:PRO:O	5:B:594:ALA:C	2.57	0.47
5:B:615:MET:CB	5:B:626:ILE:HG12	2.43	0.47
5:B:1040:ASN:O	5:B:1042:GLY:N	2.47	0.47
5:B:1081:LEU:O	5:B:1083:ALA:O	2.33	0.47
6:C:36:VAL:HG21	6:C:251:LEU:HB2	1.94	0.47
10:G:26:LEU:O	10:G:29:LYS:N	2.47	0.47
10:G:117:GLN:C	10:G:119:LEU:H	2.22	0.47
4:A:67:CYS:O	4:A:68:GLN:HB2	2.14	0.47
4:A:90:VAL:HG13	4:A:297:GLN:CD	2.39	0.47
4:A:746:MET:HE3	5:B:1018:PRO:CG	2.36	0.47
4:A:1105:LEU:HD22	4:A:1384:VAL:HG21	1.97	0.47
4:A:1445:ILE:HG12	10:G:18:PHE:HE2	1.77	0.47
5:B:173:MET:HE2	5:B:203:PHE:HE1	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:756:ILE:O	5:B:759:PRO:HD3	2.14	0.47
5:B:903:VAL:HG12	5:B:904:ARG:N	2.28	0.47
5:B:1084:GLN:H	5:B:1084:GLN:HE21	1.62	0.47
5:B:1214:PRO:O	5:B:1214:PRO:HG2	2.14	0.47
8:E:177:ARG:CZ	8:E:215:MET:HE2	2.45	0.47
11:H:11:GLN:HA	11:H:53:ASP:O	2.15	0.47
4:A:58:LEU:O	4:A:59:GLY:O	2.32	0.47
4:A:277:GLU:O	4:A:279:LEU:N	2.47	0.47
4:A:1059:HIS:ND1	9:F:86:THR:HA	2.30	0.47
4:A:1115:SER:OG	4:A:1116:LEU:N	2.47	0.47
4:A:1406:VAL:O	4:A:1407:GLU:C	2.58	0.47
5:B:33:VAL:O	5:B:34:ILE:C	2.58	0.47
5:B:54:PHE:HA	5:B:58:THR:HB	1.95	0.47
5:B:293:PRO:C	5:B:294:ASP:O	2.52	0.47
5:B:558:LEU:C	5:B:560:GLU:N	2.72	0.47
5:B:820:GLY:N	5:B:1091:TYR:OH	2.48	0.47
5:B:969:ARG:NH1	6:C:61:GLU:OE1	2.48	0.47
5:B:1216:LEU:O	5:B:1217:TYR:HD1	1.96	0.47
6:C:183:TRP:CE2	6:C:207:CYS:HB3	2.50	0.47
10:G:27:LYS:O	10:G:30:LEU:HB3	2.14	0.47
15:L:58:LYS:O	15:L:59:ALA:O	2.31	0.47
4:A:43:GLU:O	4:A:44:THR:CB	2.63	0.47
4:A:471:ASN:O	4:A:474:VAL:HG12	2.15	0.47
4:A:525:GLN:O	4:A:526:ASP:C	2.58	0.47
4:A:533:LYS:HE3	4:A:745:GLN:HE22	1.79	0.47
4:A:567:LYS:HD2	4:A:568:PRO:CD	2.45	0.47
4:A:726:ARG:HD2	4:A:765:VAL:O	2.15	0.47
4:A:755:PHE:O	4:A:756:ILE:C	2.58	0.47
4:A:852:TYR:HA	4:A:1060:PRO:HB3	1.96	0.47
4:A:889:SER:C	4:A:891:ALA:N	2.69	0.47
4:A:1066:VAL:O	4:A:1067:LEU:C	2.58	0.47
4:A:1265:ASN:O	4:A:1268:LEU:N	2.41	0.47
4:A:1365:TYR:O	4:A:1366:ARG:C	2.57	0.47
4:A:1437:GLY:HA3	9:F:88:TYR:CD2	2.50	0.47
5:B:711:GLU:H	5:B:712:PRO:HD2	1.79	0.47
5:B:787:VAL:O	5:B:787:VAL:HG12	2.15	0.47
5:B:916:THR:O	5:B:935:ARG:HG3	2.14	0.47
5:B:1070:GLU:OE1	13:J:44:TYR:OH	2.33	0.47
5:B:1085:ILE:N	5:B:1085:ILE:CD1	2.75	0.47
5:B:1183:LYS:HA	5:B:1186:ASP:HA	1.96	0.47
6:C:29:MET:HE2	14:K:98:LEU:CD2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:90:ASP:CG	6:C:90:ASP:O	2.58	0.47
6:C:92:CYS:C	6:C:94:LYS:N	2.71	0.47
7:D:24:ALA:HA	10:G:83:LYS:O	2.15	0.47
7:D:191:ALA:C	7:D:193:THR:H	2.23	0.47
7:D:195:ILE:O	7:D:197:SER:N	2.47	0.47
8:E:78:LEU:HD21	8:E:80:VAL:HG23	1.97	0.47
8:E:168:TYR:HB2	8:E:170:LEU:HG	1.97	0.47
10:G:14:HIS:HD2	10:G:16:SER:CB	2.27	0.47
10:G:149:GLY:O	10:G:159:ALA:HB1	2.15	0.47
13:J:36:LEU:O	13:J:39:LEU:N	2.48	0.47
1:T:23:DG:H2'	1:T:24:DG:H8	1.78	0.47
4:A:117:GLU:H	4:A:117:GLU:CD	2.22	0.47
4:A:343:LYS:HE2	5:B:1156:ASP:OD2	2.15	0.47
4:A:492:PRO:HB2	4:A:497:THR:HG22	1.96	0.47
4:A:836:TYR:CZ	4:A:840:ARG:HD2	2.50	0.47
5:B:593:PRO:HG2	5:B:617:ARG:NH2	2.29	0.47
5:B:1174:LYS:O	5:B:1176:ASN:HB2	2.14	0.47
6:C:46:ILE:HG13	6:C:72:LEU:HD11	1.97	0.47
6:C:89:GLU:O	6:C:90:ASP:HB3	2.15	0.47
10:G:25:TYR:O	10:G:26:LEU:C	2.58	0.47
12:I:51:ASN:O	12:I:54:GLU:HG3	2.15	0.47
12:I:77:LYS:C	12:I:79:HIS:H	2.23	0.47
4:A:300:VAL:O	4:A:300:VAL:HG12	2.13	0.47
4:A:350:ARG:HH11	4:A:350:ARG:HG3	1.80	0.47
4:A:933:TYR:C	4:A:935:GLN:H	2.21	0.47
4:A:1305:VAL:CG1	4:A:1306:LEU:N	2.77	0.47
4:A:1342:GLU:CG	8:E:198:ILE:HD13	2.45	0.47
4:A:1453:TYR:O	4:A:1454:MET:HB3	2.15	0.47
5:B:235:SER:C	5:B:236:HIS:CD2	2.93	0.47
5:B:798:TYR:HE2	6:C:62:PHE:HE2	1.52	0.47
5:B:838:SER:HA	5:B:989:THR:O	2.15	0.47
5:B:948:ILE:O	5:B:968:VAL:HG13	2.15	0.47
6:C:46:ILE:HG23	6:C:157:CYS:HB3	1.97	0.47
8:E:161:LYS:C	8:E:163:GLU:N	2.71	0.47
11:H:91:ASP:C	11:H:93:TYR:N	2.73	0.47
11:H:143:LEU:C	11:H:144:ILE:HG13	2.40	0.47
12:I:25:LEU:O	12:I:38:ALA:HB2	2.15	0.47
15:L:40:LEU:CD1	15:L:44:ASP:HB3	2.45	0.47
4:A:89:PRO:HB2	4:A:204:THR:CG2	2.45	0.47
4:A:352:VAL:O	4:A:467:THR:HB	2.15	0.47
4:A:406:ILE:HG13	4:A:431:LYS:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:630:ILE:HD13	4:A:646:PHE:HZ	1.79	0.47
4:A:996:ASN:O	4:A:998:LEU:HD12	2.15	0.47
4:A:1018:PHE:O	4:A:1021:LEU:HB3	2.15	0.47
5:B:39:ARG:HH21	5:B:665:GLU:CG	2.25	0.47
5:B:311:LEU:O	5:B:312:GLU:C	2.58	0.47
5:B:366:GLN:O	5:B:367:LEU:O	2.33	0.47
5:B:487:THR:CG2	5:B:488:TYR:N	2.78	0.47
5:B:582:VAL:HA	5:B:626:ILE:O	2.15	0.47
5:B:899:ILE:HD12	5:B:911:ILE:HG23	1.96	0.47
5:B:984:HIS:CG	5:B:1025:HIS:HB2	2.50	0.47
5:B:1001:PHE:HE2	6:C:34:ARG:CZ	2.27	0.47
5:B:1069:PHE:CD1	5:B:1069:PHE:N	2.80	0.47
5:B:1174:LYS:O	5:B:1176:ASN:N	2.47	0.47
7:D:135:GLY:C	7:D:137:ASN:H	2.22	0.47
8:E:128:PRO:HA	8:E:129:PRO:C	2.40	0.47
11:H:127:GLY:HA3	11:H:130:ARG:NH2	2.29	0.47
4:A:231:PRO:O	4:A:233:TRP:N	2.48	0.46
4:A:241:VAL:O	4:A:242:PRO:C	2.58	0.46
4:A:308:ILE:HG22	4:A:309:ALA:N	2.29	0.46
4:A:939:ASP:OD1	4:A:1023:ARG:NH1	2.48	0.46
4:A:971:PHE:O	4:A:972:HIS:C	2.58	0.46
4:A:1157:ASP:C	4:A:1159:ARG:H	2.23	0.46
5:B:94:LYS:HG2	5:B:95:ILE:N	2.30	0.46
5:B:225:VAL:CG1	5:B:385:LEU:HA	2.44	0.46
5:B:570:VAL:HA	5:B:571:PRO:HD2	1.73	0.46
5:B:834:ASN:ND2	5:B:1013:ASN:HA	2.30	0.46
5:B:1034:VAL:O	5:B:1036:ALA:N	2.48	0.46
5:B:1178:ASN:O	5:B:1179:GLN:C	2.58	0.46
6:C:140:ASN:O	6:C:141:GLY:O	2.32	0.46
6:C:229:TYR:N	6:C:229:TYR:CD1	2.83	0.46
8:E:192:ARG:HG3	8:E:192:ARG:NH1	2.28	0.46
9:F:132:LEU:O	9:F:148:VAL:HG22	2.15	0.46
11:H:58:THR:HG22	11:H:59:ILE:N	2.30	0.46
14:K:49:GLU:HG3	14:K:94:ILE:HG13	1.97	0.46
1:T:20:DC:H2''	1:T:21:DC:O5'	2.15	0.46
4:A:57:ARG:HB3	4:A:68:GLN:HG2	1.97	0.46
4:A:337:ARG:CZ	4:A:839:ARG:HH12	2.28	0.46
4:A:427:GLN:HB2	4:A:430:TRP:NE1	2.30	0.46
4:A:549:MET:SD	4:A:577:ILE:HD11	2.55	0.46
4:A:844:ALA:HB2	4:A:1389:PHE:CE2	2.49	0.46
4:A:1315:GLU:C	4:A:1317:MET:N	2.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:681:TRP:C	5:B:683:SER:N	2.73	0.46
5:B:838:SER:CA	5:B:989:THR:O	2.62	0.46
5:B:970:THR:HG22	5:B:971:THR:N	2.30	0.46
7:D:51:ASN:OD1	7:D:52:LEU:O	2.33	0.46
8:E:94:LYS:HG3	8:E:98:ILE:CD1	2.45	0.46
12:I:77:LYS:O	12:I:79:HIS:N	2.48	0.46
13:J:32:GLU:O	13:J:34:THR:N	2.48	0.46
14:K:59:ALA:HA	14:K:74:ARG:O	2.15	0.46
14:K:68:PHE:N	14:K:68:PHE:CD2	2.80	0.46
15:L:46:VAL:CG1	15:L:56:LEU:HD12	2.45	0.46
4:A:693:VAL:HA	4:A:696:GLU:HB3	1.97	0.46
4:A:883:LEU:CD2	4:A:1021:LEU:HB2	2.45	0.46
4:A:996:ASN:HB3	4:A:1050:GLU:OE2	2.16	0.46
4:A:1048:ASN:O	4:A:1049:ILE:C	2.58	0.46
4:A:1102:LYS:O	4:A:1106:ASN:ND2	2.48	0.46
4:A:1332:PHE:O	4:A:1333:ILE:C	2.57	0.46
4:A:1348:LEU:HG	4:A:1372:VAL:HG22	1.94	0.46
4:A:1405:THR:HB	4:A:1406:VAL:H	1.47	0.46
4:A:1447:GLU:OE2	10:G:23:LYS:HB2	2.15	0.46
5:B:108:VAL:CG1	5:B:109:THR:H	2.19	0.46
5:B:589:VAL:CG1	5:B:590:HIS:H	2.00	0.46
6:C:107:SER:C	6:C:109:SER:N	2.74	0.46
6:C:226:ASP:O	6:C:227:THR:CB	2.63	0.46
10:G:99:PHE:CE2	10:G:115:MET:HE2	2.50	0.46
11:H:116:TYR:HE2	11:H:140:ALA:HB1	1.81	0.46
14:K:47:ARG:HD3	14:K:59:ALA:O	2.15	0.46
14:K:93:SER:O	14:K:97:LYS:HG3	2.16	0.46
4:A:356:ASP:OD2	14:K:65:HIS:HE1	1.99	0.46
4:A:500:GLU:OE2	4:A:1438:THR:HG21	2.15	0.46
4:A:562:THR:HA	4:A:563:PRO:HD3	1.83	0.46
4:A:722:LEU:HD22	4:A:799:PHE:CD1	2.51	0.46
4:A:846:GLU:OE1	4:A:1425:SER:OG	2.33	0.46
5:B:189:LEU:HD23	5:B:192:LEU:HD12	1.97	0.46
5:B:364:ILE:HG22	5:B:365:THR:N	2.31	0.46
5:B:424:LEU:O	5:B:428:ILE:HG13	2.16	0.46
6:C:15:LYS:O	6:C:240:VAL:HG22	2.16	0.46
12:I:83:ASN:HA	12:I:102:VAL:O	2.16	0.46
12:I:111:THR:CG2	12:I:112:SER:H	2.29	0.46
13:J:1:MET:N	13:J:56:LEU:H	2.13	0.46
2:N:3:DG:OP2	2:N:3:DG:H2'	2.16	0.46
4:A:42:ASP:HB3	4:A:45:GLN:CA	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:116:ASP:O	4:A:118:HIS:N	2.48	0.46
4:A:259:GLU:HA	4:A:259:GLU:OE1	2.14	0.46
4:A:500:GLU:OE2	5:B:1145:SER:CB	2.64	0.46
4:A:785:PRO:HG2	4:A:786:HIS:CD2	2.47	0.46
5:B:38:PHE:CD1	5:B:811:TYR:CD2	3.04	0.46
5:B:638:PHE:HD2	5:B:690:VAL:HG22	1.80	0.46
5:B:695:ALA:O	5:B:698:GLU:HB3	2.16	0.46
8:E:18:THR:O	8:E:19:VAL:C	2.57	0.46
9:F:109:VAL:HG12	9:F:110:ASP:N	2.30	0.46
10:G:22:MET:O	10:G:23:LYS:C	2.58	0.46
10:G:115:MET:CB	10:G:116:PRO:CD	2.94	0.46
4:A:277:GLU:C	4:A:279:LEU:N	2.74	0.46
4:A:490:HIS:HB3	5:B:1150:ARG:NH1	2.31	0.46
4:A:1289:ARG:HD2	4:A:1303:GLU:OE2	2.16	0.46
4:A:1446:ASP:HB3	4:A:1449:SER:OG	2.16	0.46
5:B:329:THR:O	5:B:332:ASP:HB3	2.16	0.46
5:B:405:ARG:HA	5:B:631:GLY:O	2.16	0.46
5:B:758:PHE:HZ	5:B:1031:LEU:HD22	1.81	0.46
5:B:1143:ALA:O	5:B:1144:ALA:C	2.58	0.46
7:D:35:LEU:HD21	7:D:173:HIS:HB3	1.97	0.46
8:E:54:GLN:O	8:E:57:MET:HB3	2.16	0.46
11:H:82:PRO:C	11:H:84:ALA:N	2.74	0.46
4:A:684:ALA:O	4:A:687:LYS:HB2	2.15	0.46
4:A:853:ASP:OD1	4:A:853:ASP:C	2.59	0.46
4:A:1028:THR:O	4:A:1032:LEU:HD12	2.16	0.46
5:B:310:MET:HG3	5:B:386:LEU:CD1	2.46	0.46
5:B:552:MET:C	5:B:554:ILE:N	2.71	0.46
5:B:780:VAL:HG12	5:B:782:LEU:O	2.16	0.46
5:B:1072:MET:CE	5:B:1087:PHE:HD1	2.28	0.46
6:C:154:LYS:C	6:C:155:LEU:HD23	2.40	0.46
6:C:248:ILE:HD13	14:K:101:LEU:HD22	1.98	0.46
8:E:46:TYR:CE2	8:E:58:MET:HA	2.51	0.46
10:G:53:ASN:HD22	10:G:53:ASN:N	2.13	0.46
12:I:98:VAL:HG12	12:I:99:LEU:H	1.80	0.46
14:K:31:VAL:HG12	14:K:32:VAL:H	1.80	0.46
4:A:11:LEU:HB2	5:B:1193:GLN:OE1	2.16	0.46
4:A:551:TYR:CE2	14:K:62:LYS:HE2	2.50	0.46
4:A:715:GLU:OE2	4:A:774:ARG:NH1	2.49	0.46
4:A:1153:TYR:CD2	4:A:1163:ILE:HD11	2.51	0.46
4:A:1327:ILE:HG22	8:E:147:HIS:HE1	1.81	0.46
5:B:562:GLY:HA3	5:B:590:HIS:ND1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:999:MET:HG2	5:B:1007:VAL:HG22	1.98	0.46
5:B:1183:LYS:HE3	5:B:1183:LYS:O	2.15	0.46
6:C:70:ILE:O	6:C:70:ILE:HG22	2.16	0.46
6:C:99:LEU:HD23	6:C:99:LEU:N	2.31	0.46
6:C:163:ILE:O	6:C:165:LYS:N	2.48	0.46
7:D:35:LEU:CD2	7:D:174:PRO:HD2	2.45	0.46
9:F:109:VAL:HG13	9:F:127:GLU:OE1	2.16	0.46
9:F:123:LYS:O	9:F:124:GLU:C	2.57	0.46
9:F:147:SER:O	9:F:148:VAL:C	2.59	0.46
11:H:22:LYS:O	11:H:23:VAL:HG23	2.15	0.46
12:I:82:GLU:O	12:I:104:LEU:HG	2.16	0.46
1:T:15:DT:H2''	1:T:16:DT:H5'	1.97	0.46
4:A:206:GLU:O	4:A:207:ILE:C	2.59	0.46
4:A:404:TYR:CE2	4:A:414:ASP:HA	2.50	0.46
4:A:446:ARG:NH1	4:A:479:ASN:O	2.49	0.46
4:A:470:LEU:HD22	4:A:487:MET:CE	2.46	0.46
4:A:482:PHE:C	4:A:484:GLY:H	2.24	0.46
4:A:626:ASN:O	4:A:628:GLY:N	2.46	0.46
4:A:723:ASN:O	4:A:724:GLU:C	2.59	0.46
4:A:913:LEU:HD23	4:A:919:ILE:HD12	1.97	0.46
4:A:1115:SER:C	4:A:1308:THR:CG2	2.88	0.46
4:A:1237:ILE:HG22	4:A:1238:ILE:N	2.31	0.46
5:B:210:LYS:HG3	5:B:461:LEU:O	2.15	0.46
5:B:303:TYR:CD2	5:B:303:TYR:N	2.82	0.46
5:B:314:LEU:O	5:B:315:LYS:C	2.59	0.46
5:B:333:PHE:C	5:B:334:ILE:HG13	2.41	0.46
5:B:566:LEU:O	5:B:567:GLU:C	2.58	0.46
5:B:814:PHE:O	5:B:816:GLU:N	2.49	0.46
5:B:1096:ARG:O	5:B:1097:HIS:CB	2.54	0.46
6:C:75:MET:O	6:C:246:ARG:NH2	2.48	0.46
6:C:239:PRO:O	6:C:240:VAL:C	2.58	0.46
7:D:138:ASN:C	7:D:140:ASP:N	2.72	0.46
9:F:81:THR:HB	9:F:136:ARG:HH11	1.80	0.46
12:I:8:ARG:O	12:I:10:CYS:N	2.49	0.46
12:I:61:ASP:C	12:I:63:GLY:N	2.73	0.46
14:K:45:LEU:C	14:K:47:ARG:H	2.23	0.46
14:K:53:ASP:C	14:K:55:LYS:H	2.24	0.46
4:A:340:LEU:CD2	5:B:1199:ALA:HB3	2.45	0.46
4:A:596:THR:O	4:A:598:LEU:N	2.49	0.46
4:A:630:ILE:HG23	4:A:642:CYS:SG	2.56	0.46
4:A:874:ASP:N	4:A:1058:VAL:CG2	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:933:TYR:C	4:A:935:GLN:N	2.74	0.46
4:A:1001:ARG:HG2	4:A:1001:ARG:HH11	1.81	0.46
4:A:1222:ASN:O	4:A:1223:ASP:HB3	2.15	0.46
4:A:1425:SER:O	4:A:1426:GLU:C	2.59	0.46
5:B:29:ASP:HB3	5:B:658:ILE:HD13	1.96	0.46
5:B:283:VAL:O	5:B:286:PHE:N	2.49	0.46
5:B:1060:ARG:HD2	5:B:1060:ARG:HA	1.48	0.46
5:B:1182:CYS:O	5:B:1183:LYS:O	2.34	0.46
6:C:70:ILE:HD11	6:C:144:ILE:CG1	2.46	0.46
8:E:17:ARG:O	8:E:20:LYS:HB2	2.16	0.46
9:F:111:LEU:HD12	9:F:111:LEU:N	2.29	0.46
10:G:121:PHE:HB2	10:G:130:TYR:CE2	2.51	0.46
11:H:93:TYR:N	11:H:93:TYR:CD1	2.83	0.46
14:K:42:LEU:HD21	14:K:46:ILE:HD11	1.98	0.46
4:A:73:GLY:O	4:A:74:MET:C	2.59	0.45
4:A:103:CYS:O	4:A:106:VAL:O	2.34	0.45
4:A:231:PRO:C	4:A:233:TRP:N	2.74	0.45
4:A:325:ILE:CG2	5:B:1210:MET:HE2	2.45	0.45
4:A:563:PRO:HG3	4:A:572:TRP:CE2	2.50	0.45
4:A:774:ARG:O	4:A:775:ILE:O	2.34	0.45
4:A:854:ASN:HB3	4:A:1000:LEU:HD21	1.98	0.45
4:A:856:THR:HG22	4:A:856:THR:O	2.15	0.45
4:A:903:ASN:ND2	4:A:903:ASN:C	2.58	0.45
4:A:993:LEU:O	4:A:994:GLN:C	2.59	0.45
5:B:842:ASN:ND2	5:B:845:SER:CB	2.78	0.45
5:B:865:LYS:C	5:B:866:TYR:CD1	2.95	0.45
5:B:882:THR:HB	5:B:934:LYS:O	2.15	0.45
5:B:1065:GLN:NE2	5:B:1067:ARG:HG2	2.31	0.45
6:C:181:ASP:OD2	6:C:184:ASN:HA	2.14	0.45
10:G:49:LEU:O	10:G:50:ASP:C	2.59	0.45
11:H:58:THR:HB	11:H:143:LEU:HD13	1.98	0.45
14:K:43:GLY:HA3	14:K:61:TYR:CE1	2.50	0.45
4:A:337:ARG:CZ	4:A:839:ARG:NH1	2.79	0.45
4:A:1011:GLN:NE2	4:A:1015:VAL:HG21	2.32	0.45
4:A:1045:VAL:O	4:A:1049:ILE:HG13	2.16	0.45
4:A:1409:LEU:CD1	5:B:1207:LEU:HD21	2.36	0.45
4:A:1435:PRO:HA	4:A:1439:GLY:O	2.16	0.45
5:B:38:PHE:HD1	5:B:811:TYR:CD2	2.34	0.45
5:B:114:PRO:O	5:B:116:GLU:N	2.49	0.45
5:B:581:PHE:N	5:B:624:LEU:O	2.39	0.45
6:C:179:GLU:CG	6:C:180:TYR:N	2.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:241:ASP:OD1	6:C:242:GLN:N	2.48	0.45
12:I:13:MET:HG3	12:I:14:LEU:H	1.80	0.45
4:A:58:LEU:HD22	4:A:80:HIS:O	2.16	0.45
4:A:325:ILE:HG22	5:B:1210:MET:HE2	1.99	0.45
4:A:415:LEU:HA	4:A:415:LEU:HD23	1.69	0.45
4:A:791:ASP:C	4:A:791:ASP:OD1	2.59	0.45
4:A:907:THR:HG23	4:A:908:LEU:H	1.81	0.45
4:A:909:ASP:C	4:A:911:SER:N	2.73	0.45
4:A:1147:THR:HA	4:A:1197:LEU:HD23	1.98	0.45
4:A:1289:ARG:NH1	4:A:1326:ARG:NH1	2.63	0.45
4:A:1342:GLU:OE2	8:E:212:ARG:NH1	2.49	0.45
5:B:769:TYR:O	5:B:772:ALA:N	2.49	0.45
5:B:1007:VAL:HG22	5:B:1008:PRO:CD	2.35	0.45
5:B:1115:THR:CG2	5:B:1117:GLN:HG3	2.46	0.45
5:B:1186:ASP:C	5:B:1186:ASP:OD1	2.59	0.45
6:C:10:ILE:HA	6:C:20:PHE:CB	2.46	0.45
6:C:168:ALA:C	6:C:170:TRP:H	2.24	0.45
8:E:114:ASN:O	8:E:115:ASN:CB	2.64	0.45
10:G:13:LEU:CD2	10:G:17:PHE:HB2	2.39	0.45
4:A:590:ARG:HD2	4:A:605:MET:CB	2.46	0.45
4:A:590:ARG:O	4:A:591:PHE:HB2	2.15	0.45
4:A:690:VAL:O	4:A:691:LEU:C	2.59	0.45
4:A:808:LEU:CD2	4:A:813:PHE:HA	2.38	0.45
4:A:1118:VAL:O	4:A:1118:VAL:HG23	2.15	0.45
5:B:69:LEU:HD22	5:B:429:PHE:CE1	2.51	0.45
5:B:199:MET:SD	5:B:199:MET:N	2.83	0.45
5:B:864:LYS:N	5:B:872:GLU:OE1	2.48	0.45
5:B:918:ILE:HG21	5:B:935:ARG:HH11	1.81	0.45
4:A:185:TRP:HZ3	4:A:200:ARG:HG2	1.82	0.45
4:A:438:ASP:OD1	4:A:462:VAL:HG23	2.16	0.45
4:A:477:PRO:CG	4:A:521:MET:HG2	2.47	0.45
4:A:511:ILE:O	4:A:519:PRO:HA	2.16	0.45
4:A:526:ASP:OD1	5:B:1013:ASN:ND2	2.49	0.45
4:A:596:THR:C	4:A:598:LEU:H	2.24	0.45
4:A:622:VAL:O	4:A:622:VAL:HG22	2.17	0.45
4:A:794:PRO:C	4:A:796:SER:N	2.75	0.45
4:A:816:HIS:HE2	5:B:764:SER:H	1.64	0.45
4:A:1437:GLY:C	4:A:1439:GLY:N	2.74	0.45
5:B:113:TYR:CD2	5:B:192:LEU:HD22	2.51	0.45
5:B:570:VAL:HG23	5:B:573:GLN:HB3	1.97	0.45
8:E:157:SER:O	8:E:159:ASP:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:90:ARG:HD3	9:F:155:LEU:HD12	1.97	0.45
10:G:23:LYS:HG2	10:G:27:LYS:HE3	1.98	0.45
13:J:27:GLU:O	13:J:29:GLU:N	2.49	0.45
13:J:50:ILE:O	13:J:52:THR:N	2.49	0.45
15:L:32:ALA:HB3	15:L:55:ILE:CD1	2.47	0.45
1:T:16:DT:C5'	4:A:1386:ARG:NH1	2.80	0.45
4:A:344:ARG:HD2	5:B:1118:PRO:O	2.17	0.45
4:A:432:VAL:O	4:A:433:GLU:C	2.59	0.45
4:A:575:LYS:NZ	4:A:615:GLY:H	2.15	0.45
4:A:645:LEU:O	4:A:646:PHE:C	2.58	0.45
4:A:709:THR:HB	4:A:712:GLU:HG3	1.99	0.45
4:A:784:LEU:HD11	4:A:815:PHE:CE2	2.51	0.45
4:A:833:GLU:O	4:A:834:THR:C	2.59	0.45
4:A:841:LEU:O	4:A:845:LEU:HG	2.17	0.45
4:A:1040:GLN:O	4:A:1041:ALA:C	2.59	0.45
4:A:1070:GLN:C	4:A:1072:ILE:N	2.74	0.45
4:A:1102:LYS:HG2	4:A:1106:ASN:ND2	2.30	0.45
4:A:1370:LEU:O	4:A:1373:ASP:N	2.48	0.45
4:A:1444:MET:HE1	9:F:135:ARG:NE	2.31	0.45
5:B:195:CYS:SG	5:B:196:PRO:HD2	2.56	0.45
5:B:221:ASN:OD1	5:B:242:SER:HA	2.15	0.45
5:B:321:GLY:C	5:B:323:VAL:N	2.74	0.45
5:B:563:MET:CE	5:B:580:VAL:HB	2.45	0.45
5:B:918:ILE:HD12	5:B:935:ARG:CD	2.47	0.45
5:B:979:LYS:O	5:B:980:PHE:CD2	2.70	0.45
5:B:1103:ILE:O	5:B:1122:ARG:NH1	2.49	0.45
7:D:35:LEU:HD12	7:D:35:LEU:N	2.32	0.45
12:I:4:PHE:CD1	12:I:4:PHE:C	2.95	0.45
12:I:61:ASP:O	12:I:63:GLY:N	2.49	0.45
12:I:69:PRO:HG2	12:I:85:PHE:CE2	2.52	0.45
4:A:282:ASN:O	4:A:284:ALA:N	2.50	0.45
4:A:479:ASN:O	4:A:479:ASN:OD1	2.34	0.45
4:A:492:PRO:O	4:A:493:GLN:NE2	2.50	0.45
4:A:650:GLN:C	4:A:654:ASN:ND2	2.75	0.45
4:A:774:ARG:H	4:A:774:ARG:HG2	1.62	0.45
4:A:815:PHE:O	4:A:816:HIS:C	2.60	0.45
4:A:1013:ASP:C	4:A:1015:VAL:N	2.75	0.45
4:A:1074:GLU:HB3	4:A:1075:PRO:CD	2.46	0.45
5:B:386:LEU:C	5:B:388:CYS:N	2.74	0.45
5:B:637:LEU:HD23	5:B:742:GLU:HA	1.97	0.45
5:B:732:SER:HB2	5:B:734:HIS:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:766:ARG:NH2	5:B:1020:ARG:HD3	2.31	0.45
5:B:797:TYR:HE1	5:B:854:LEU:HD21	1.81	0.45
5:B:814:PHE:C	5:B:816:GLU:N	2.75	0.45
5:B:865:LYS:HZ2	5:B:869:SER:HA	1.82	0.45
8:E:136:ASN:OD1	8:E:138:ALA:N	2.50	0.45
10:G:20:PRO:CG	10:G:21:ARG:N	2.80	0.45
10:G:111:THR:HG22	10:G:113:HIS:H	1.82	0.45
12:I:26:LEU:CD2	12:I:37:GLU:HA	2.41	0.45
4:A:1053:PHE:C	4:A:1055:ARG:N	2.73	0.45
4:A:1265:ASN:O	4:A:1267:MET:N	2.50	0.45
4:A:1348:LEU:O	4:A:1352:VAL:HG23	2.17	0.45
5:B:596:LEU:O	5:B:600:LEU:HG	2.16	0.45
5:B:863:GLU:O	5:B:961:LEU:HD22	2.16	0.45
5:B:1027:ILE:O	5:B:1028:GLU:C	2.60	0.45
6:C:58:LEU:CD2	6:C:58:LEU:N	2.80	0.45
6:C:133:ILE:HD12	6:C:237:SER:HA	1.99	0.45
8:E:98:ILE:C	8:E:100:ILE:N	2.74	0.45
8:E:129:PRO:O	8:E:130:ALA:O	2.34	0.45
10:G:14:HIS:HD2	10:G:16:SER:HB2	1.82	0.45
4:A:7:SER:OG	5:B:1193:GLN:NE2	2.50	0.45
4:A:446:ARG:CD	4:A:480:ALA:HB2	2.47	0.45
4:A:477:PRO:HG2	4:A:521:MET:HG2	1.98	0.45
4:A:566:ILE:O	4:A:567:LYS:O	2.34	0.45
4:A:590:ARG:NH2	4:A:620:LYS:CB	2.75	0.45
4:A:1004:ASN:OD1	4:A:1005:GLU:N	2.50	0.45
4:A:1006:ILE:HD12	8:E:163:GLU:CG	2.46	0.45
4:A:1074:GLU:C	4:A:1076:ALA:H	2.25	0.45
4:A:1100:ARG:NH2	4:A:1351:GLU:HG2	2.32	0.45
4:A:1148:ILE:HB	4:A:1196:GLU:O	2.17	0.45
4:A:1206:ASP:HB3	4:A:1274:ARG:NH1	2.31	0.45
4:A:1265:ASN:C	4:A:1267:MET:H	2.25	0.45
5:B:594:ALA:HA	5:B:617:ARG:HH12	1.79	0.45
5:B:789:MET:HE2	5:B:953:LEU:HD22	1.97	0.45
5:B:980:PHE:HE2	5:B:1094:ARG:CB	2.30	0.45
5:B:1001:PHE:HD2	6:C:34:ARG:NH2	2.15	0.45
4:A:28:ARG:O	4:A:29:ALA:C	2.60	0.45
4:A:57:ARG:O	4:A:68:GLN:NE2	2.49	0.45
4:A:682:THR:HG23	4:A:728:LYS:HE3	1.99	0.45
4:A:846:GLU:HB2	4:A:847:ASP:H	1.64	0.45
4:A:1111:MET:H	4:A:1111:MET:HG2	1.52	0.45
4:A:1118:VAL:HG12	4:A:1327:ILE:HG13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1377:THR:O	4:A:1378:GLN:C	2.60	0.45
5:B:948:ILE:C	5:B:949:VAL:O	2.58	0.45
5:B:1208:MET:HA	5:B:1212:ILE:O	2.17	0.45
7:D:202:ILE:CG2	7:D:207:LEU:HB2	2.44	0.45
8:E:98:ILE:O	8:E:99:HIS:C	2.60	0.45
8:E:202:SER:HB3	8:E:205:SER:O	2.15	0.45
13:J:2:ILE:HG22	13:J:3:VAL:O	2.17	0.45
13:J:13:VAL:O	13:J:14:VAL:CG2	2.65	0.45
4:A:42:ASP:HB3	4:A:45:GLN:N	2.30	0.44
4:A:871:ASP:HB3	8:E:204:THR:HG23	2.00	0.44
4:A:1106:ASN:O	4:A:1107:VAL:HB	2.17	0.44
4:A:1164:PRO:O	4:A:1166:ASP:N	2.50	0.44
5:B:247:GLY:C	5:B:249:ARG:H	2.24	0.44
5:B:351:TYR:CD1	5:B:355:ILE:HD11	2.52	0.44
5:B:386:LEU:O	5:B:387:LEU:C	2.60	0.44
5:B:410:GLY:O	5:B:411:PRO:C	2.60	0.44
5:B:785:TYR:CD1	5:B:786:ASN:N	2.85	0.44
5:B:785:TYR:C	5:B:787:VAL:N	2.74	0.44
5:B:843:GLN:HB2	5:B:993:THR:HB	1.98	0.44
5:B:1081:LEU:O	5:B:1082:MET:C	2.59	0.44
5:B:1200:ALA:O	5:B:1203:LEU:HB3	2.17	0.44
6:C:112:ASN:CB	6:C:114:TYR:CE1	2.99	0.44
8:E:124:VAL:HA	8:E:132:ILE:HD12	1.99	0.44
9:F:119:ARG:NH1	9:F:119:ARG:CG	2.80	0.44
13:J:31:ASP:O	13:J:32:GLU:C	2.60	0.44
13:J:48:ARG:HE	13:J:49:MET:HE2	1.81	0.44
14:K:67:PHE:C	14:K:68:PHE:CD2	2.96	0.44
15:L:28:LYS:HB2	15:L:39:SER:HA	1.98	0.44
2:N:5:DA:H1'	2:N:6:DC:O5'	2.18	0.44
4:A:3:GLY:O	4:A:4:GLN:CB	2.64	0.44
4:A:7:SER:HB2	5:B:1175:LEU:HD22	1.99	0.44
4:A:144:THR:O	4:A:146:MET:HG3	2.18	0.44
4:A:168:GLY:O	4:A:169:ASN:C	2.60	0.44
4:A:268:ASP:HB3	4:A:299:HIS:CE1	2.52	0.44
4:A:353:ILE:HB	4:A:470:LEU:CD2	2.48	0.44
4:A:605:MET:HE3	4:A:606:LEU:H	1.82	0.44
4:A:1191:TRP:HD1	4:A:1256:GLU:HB2	1.81	0.44
4:A:1349:TYR:CA	4:A:1372:VAL:HG21	2.46	0.44
5:B:181:LEU:HD22	5:B:189:LEU:HD22	1.99	0.44
5:B:436:VAL:O	5:B:436:VAL:HG12	2.17	0.44
5:B:653:VAL:HG23	5:B:689:LEU:HB3	1.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:687:GLU:O	5:B:689:LEU:HG	2.18	0.44
5:B:833:TYR:N	5:B:833:TYR:CD1	2.84	0.44
5:B:1106:ARG:NH2	5:B:1109:GLY:H	2.14	0.44
5:B:1138:MET:HA	5:B:1138:MET:HE3	1.99	0.44
5:B:1216:LEU:C	5:B:1217:TYR:HD1	2.26	0.44
6:C:170:TRP:O	6:C:171:GLY:C	2.58	0.44
8:E:98:ILE:O	8:E:100:ILE:N	2.50	0.44
11:H:42:ILE:HG23	11:H:95:TYR:CE1	2.41	0.44
4:A:225:ASN:ND2	4:A:227:VAL:H	2.14	0.44
4:A:289:ILE:O	4:A:291:GLU:N	2.50	0.44
4:A:298:PHE:O	4:A:301:ALA:HB3	2.16	0.44
4:A:532:ARG:O	4:A:533:LYS:C	2.61	0.44
4:A:573:SER:O	4:A:574:GLY:C	2.61	0.44
4:A:807:GLY:HA2	5:B:760:ASP:O	2.17	0.44
4:A:823:GLY:O	4:A:825:ILE:N	2.50	0.44
4:A:901:LEU:HD22	4:A:919:ILE:HG22	2.00	0.44
4:A:1098:VAL:N	4:A:1099:PRO:HD2	2.33	0.44
4:A:1404:GLU:O	4:A:1405:THR:C	2.60	0.44
5:B:378:LEU:HD12	5:B:378:LEU:C	2.43	0.44
5:B:575:PRO:C	5:B:577:ALA:H	2.25	0.44
5:B:1201:LYS:HE2	5:B:1205:GLN:CD	2.43	0.44
6:C:35:ARG:HH11	14:K:41:THR:CA	2.30	0.44
7:D:126:ILE:HD13	7:D:145:MET:HE3	2.00	0.44
12:I:68:LEU:HB3	12:I:84:VAL:HG23	1.98	0.44
14:K:82:ASP:O	14:K:85:ASP:HB2	2.17	0.44
15:L:27:LEU:HD23	15:L:27:LEU:N	2.31	0.44
4:A:84:ILE:O	4:A:84:ILE:CG2	2.64	0.44
4:A:441:PRO:HD2	4:A:498:ARG:NH2	2.33	0.44
4:A:504:LEU:HD12	4:A:504:LEU:N	2.31	0.44
4:A:507:VAL:HG13	4:A:521:MET:HE1	1.99	0.44
4:A:650:GLN:O	4:A:651:LYS:C	2.60	0.44
4:A:666:ILE:HD12	4:A:667:GLY:N	2.31	0.44
4:A:673:GLY:N	4:A:674:PRO:HD2	2.32	0.44
4:A:901:LEU:HD22	4:A:919:ILE:HG21	2.00	0.44
4:A:1215:ARG:HA	4:A:1215:ARG:HD2	1.73	0.44
4:A:1236:LEU:C	4:A:1237:ILE:HG13	2.42	0.44
4:A:1239:ARG:NH1	4:A:1239:ARG:HB3	2.32	0.44
4:A:1349:TYR:O	4:A:1350:LYS:C	2.59	0.44
4:A:1437:GLY:C	4:A:1439:GLY:H	2.26	0.44
4:A:1450:LEU:O	4:A:1450:LEU:CG	2.64	0.44
5:B:217:ARG:HG3	5:B:405:ARG:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:603:LEU:HB3	5:B:609:ILE:HD11	1.99	0.44
5:B:882:THR:HG21	5:B:935:ARG:HA	1.98	0.44
5:B:1106:ARG:HD2	5:B:1125:ASP:O	2.18	0.44
6:C:74:SER:HB2	6:C:77:ILE:CG1	2.47	0.44
6:C:123:ASN:ND2	6:C:125:MET:SD	2.90	0.44
6:C:187:LYS:C	6:C:189:THR:H	2.24	0.44
8:E:116:ILE:HG22	8:E:117:THR:N	2.32	0.44
10:G:49:LEU:HG	10:G:76:ALA:HA	2.00	0.44
10:G:127:PRO:HG2	10:G:138:THR:HG21	1.99	0.44
12:I:6:PHE:HA	12:I:14:LEU:HG	1.98	0.44
12:I:87:GLN:O	12:I:88:SER:C	2.60	0.44
4:A:61:ILE:HG22	4:A:62:ASP:N	2.32	0.44
4:A:427:GLN:O	4:A:428:TYR:C	2.59	0.44
4:A:543:LEU:O	4:A:544:ASP:C	2.60	0.44
4:A:608:ILE:O	4:A:610:GLY:N	2.50	0.44
4:A:618:GLU:O	4:A:619:LYS:C	2.60	0.44
5:B:376:PHE:O	5:B:586:TRP:HZ3	2.00	0.44
5:B:507:LYS:N	5:B:512:ARG:HH21	2.11	0.44
5:B:680:THR:O	5:B:684:LEU:HD12	2.18	0.44
5:B:753:ALA:O	5:B:756:ILE:HG13	2.17	0.44
5:B:769:TYR:C	5:B:771:SER:H	2.24	0.44
5:B:812:LEU:O	5:B:813:LYS:C	2.60	0.44
5:B:842:ASN:ND2	5:B:845:SER:OG	2.50	0.44
5:B:1031:LEU:HA	5:B:1055:ILE:HD13	2.00	0.44
6:C:31:ASN:OD1	6:C:34:ARG:NH1	2.51	0.44
6:C:256:ALA:C	6:C:258:ILE:H	2.26	0.44
8:E:147:HIS:O	8:E:148:GLU:C	2.60	0.44
9:F:98:ALA:O	9:F:99:LEU:C	2.60	0.44
10:G:38:CYS:SG	10:G:44:TYR:CE1	3.11	0.44
12:I:34:TYR:O	12:I:35:VAL:CG2	2.66	0.44
14:K:12:LEU:HD12	14:K:12:LEU:N	2.26	0.44
14:K:52:ASN:O	14:K:53:ASP:C	2.60	0.44
14:K:55:LYS:HB3	14:K:81:TYR:CD1	2.53	0.44
4:A:93:VAL:HG21	4:A:301:ALA:O	2.17	0.44
4:A:547:LEU:HD22	14:K:58:PHE:CE1	2.52	0.44
4:A:650:GLN:O	4:A:654:ASN:ND2	2.51	0.44
4:A:853:ASP:OD1	4:A:855:THR:CG2	2.63	0.44
4:A:1205:LYS:O	4:A:1206:ASP:C	2.60	0.44
4:A:1356:ILE:HD12	4:A:1368:MET:SD	2.58	0.44
4:A:1430:LEU:O	5:B:1196:ILE:HG22	2.18	0.44
5:B:435:THR:C	5:B:437:GLU:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:983:ARG:HD2	5:B:1091:TYR:HD2	1.83	0.44
5:B:1065:GLN:NE2	5:B:1066:SER:H	2.14	0.44
6:C:256:ALA:C	6:C:258:ILE:N	2.75	0.44
7:D:206:GLU:C	7:D:208:GLU:H	2.24	0.44
10:G:17:PHE:C	10:G:19:GLY:H	2.26	0.44
11:H:110:ASP:O	11:H:128:ASN:ND2	2.49	0.44
12:I:85:PHE:CD1	12:I:99:LEU:HD13	2.53	0.44
4:A:23:SER:O	4:A:24:PRO:C	2.59	0.44
4:A:103:CYS:C	4:A:105:CYS:N	2.74	0.44
4:A:224:PHE:CZ	4:A:231:PRO:HG3	2.52	0.44
4:A:255:SER:OG	5:B:918:ILE:HG23	2.17	0.44
4:A:668:ASP:HA	4:A:741:ASN:OD1	2.18	0.44
4:A:699:ALA:O	4:A:700:ASN:HB3	2.18	0.44
4:A:784:LEU:C	4:A:786:HIS:N	2.75	0.44
4:A:853:ASP:OD1	4:A:855:THR:CB	2.66	0.44
4:A:877:HIS:C	4:A:878:ILE:HG13	2.43	0.44
4:A:919:ILE:O	4:A:920:LEU:C	2.60	0.44
4:A:1334:ASP:C	4:A:1336:MET:N	2.74	0.44
4:A:1396:ALA:O	4:A:1397:LEU:C	2.61	0.44
5:B:603:LEU:HB3	5:B:609:ILE:HG13	1.98	0.44
5:B:616:ILE:HG13	5:B:697:GLU:HA	2.00	0.44
5:B:1174:LYS:O	5:B:1175:LEU:C	2.61	0.44
14:K:45:LEU:C	14:K:47:ARG:N	2.76	0.44
14:K:52:ASN:O	14:K:54:ARG:N	2.51	0.44
4:A:23:SER:O	4:A:26:GLU:N	2.50	0.44
4:A:340:LEU:HD21	5:B:1199:ALA:HB3	2.00	0.44
4:A:376:TYR:OH	4:A:498:ARG:HD2	2.18	0.44
4:A:630:ILE:O	4:A:631:HIS:C	2.60	0.44
4:A:711:ARG:NH1	12:I:95:THR:HB	2.33	0.44
4:A:896:ARG:NH2	4:A:1030:ARG:HH21	2.16	0.44
4:A:1028:THR:O	4:A:1029:ARG:C	2.61	0.44
4:A:1138:ILE:O	4:A:1139:GLU:C	2.61	0.44
4:A:1141:THR:OG1	4:A:1205:LYS:HD3	2.17	0.44
4:A:1170:ILE:H	4:A:1170:ILE:HG13	1.61	0.44
4:A:1227:ILE:CG2	4:A:1228:TRP:N	2.81	0.44
4:A:1420:ASP:O	4:A:1421:CYS:HB2	2.18	0.44
5:B:29:ASP:OD1	5:B:658:ILE:HD13	2.18	0.44
5:B:318:VAL:C	5:B:320:ASP:H	2.26	0.44
5:B:368:GLU:O	5:B:370:PHE:N	2.49	0.44
5:B:882:THR:O	5:B:883:LEU:CB	2.64	0.44
5:B:1204:PHE:O	5:B:1207:LEU:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1223:ASP:HB3	5:B:1224:PHE:H	1.68	0.44
7:D:35:LEU:HD23	7:D:174:PRO:CD	2.47	0.44
7:D:130:LEU:HD22	7:D:134:THR:OG1	2.18	0.44
8:E:82:PHE:CD1	8:E:82:PHE:N	2.86	0.44
9:F:101:ILE:HD13	9:F:120:ILE:CG2	2.47	0.44
10:G:14:HIS:CD2	10:G:16:SER:HB2	2.53	0.44
11:H:10:PHE:N	11:H:10:PHE:CD1	2.85	0.44
12:I:86:PHE:CE1	12:I:100:PHE:HB2	2.52	0.44
13:J:7:CYS:CA	13:J:49:MET:HE3	2.48	0.44
1:T:15:DT:H1'	1:T:16:DT:H5'	2.00	0.44
2:N:1:DA:C1'	2:N:2:DA:O5'	2.66	0.44
4:A:381:THR:O	4:A:382:PRO:C	2.60	0.44
4:A:442:VAL:HB	4:A:489:LEU:CD1	2.42	0.44
4:A:567:LYS:HZ2	11:H:47:PHE:CB	2.31	0.44
4:A:774:ARG:CZ	4:A:797:LYS:CB	2.96	0.44
4:A:858:ASN:HD21	4:A:860:LEU:H	1.60	0.44
4:A:1015:VAL:O	4:A:1016:THR:C	2.60	0.44
5:B:639:ILE:HD11	5:B:691:GLU:HB2	2.00	0.44
5:B:726:ALA:HB1	5:B:1051:THR:HG21	1.99	0.44
5:B:763:GLN:HG2	5:B:765:PRO:CD	2.47	0.44
6:C:184:ASN:CG	6:C:187:LYS:HA	2.42	0.44
8:E:35:VAL:C	8:E:37:LEU:N	2.71	0.44
8:E:124:VAL:N	8:E:125:PRO:HD2	2.33	0.44
8:E:207:ARG:CB	8:E:207:ARG:NH1	2.80	0.44
10:G:4:ILE:O	10:G:4:ILE:HG22	2.18	0.44
15:L:27:LEU:O	15:L:28:LYS:HG2	2.18	0.44
4:A:15:LYS:O	4:A:1421:CYS:HB2	2.18	0.43
4:A:242:PRO:HD3	5:B:1209:ALA:CB	2.48	0.43
4:A:311:GLN:HB3	4:A:312:PRO:HD3	2.00	0.43
4:A:399:HIS:CG	4:A:400:PRO:N	2.82	0.43
4:A:508:PRO:O	4:A:511:ILE:HG13	2.18	0.43
4:A:567:LYS:HG3	4:A:568:PRO:CD	2.38	0.43
4:A:1005:GLU:O	4:A:1006:ILE:C	2.61	0.43
4:A:1058:VAL:O	4:A:1060:PRO:HD3	2.18	0.43
5:B:29:ASP:O	5:B:30:SER:C	2.60	0.43
5:B:879:ARG:HH11	5:B:883:LEU:CD2	2.27	0.43
5:B:1163:CYS:SG	5:B:1166:CYS:N	2.83	0.43
6:C:91:HIS:CD2	6:C:91:HIS:O	2.70	0.43
7:D:211:LEU:HD23	7:D:214:LEU:HD12	1.99	0.43
8:E:168:TYR:CB	8:E:170:LEU:HG	2.47	0.43
8:E:205:SER:O	8:E:206:GLY:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:1:MET:SD	10:G:79:PHE:CE1	3.10	0.43
10:G:117:GLN:O	10:G:119:LEU:N	2.51	0.43
1:T:19:DG:H2''	1:T:20:DC:O5'	2.18	0.43
4:A:42:ASP:OD1	4:A:45:GLN:O	2.36	0.43
4:A:230:ARG:N	4:A:233:TRP:CZ3	2.80	0.43
4:A:254:GLU:HG3	5:B:935:ARG:HH22	1.82	0.43
4:A:260:ASP:O	4:A:261:ASP:C	2.60	0.43
4:A:871:ASP:OD2	4:A:873:MET:HB2	2.18	0.43
4:A:872:GLY:C	4:A:1058:VAL:HG23	2.42	0.43
5:B:112:LEU:HD12	5:B:113:TYR:N	2.29	0.43
5:B:484:ASN:ND2	5:B:486:TYR:CE1	2.86	0.43
5:B:527:THR:OG1	5:B:528:PRO:HD2	2.18	0.43
5:B:579:ARG:HG2	5:B:579:ARG:NH1	2.32	0.43
5:B:1050:ILE:CG2	5:B:1051:THR:N	2.81	0.43
6:C:6:PRO:HB3	6:C:25:VAL:CG1	2.49	0.43
6:C:186:LEU:N	6:C:186:LEU:HD12	2.33	0.43
6:C:232:VAL:HG21	6:C:244:VAL:CG2	2.41	0.43
6:C:250:THR:O	6:C:251:LEU:C	2.61	0.43
8:E:101:GLN:NE2	8:E:127:ILE:HG21	2.33	0.43
9:F:85:MET:HE2	9:F:93:ILE:HD12	2.00	0.43
11:H:5:LEU:O	11:H:6:PHE:HB2	2.16	0.43
11:H:15:VAL:HG22	11:H:26:ILE:CG1	2.48	0.43
11:H:59:ILE:CG2	11:H:60:ALA:N	2.68	0.43
1:T:14:DC:C6	1:T:15:DT:H73	2.53	0.43
4:A:34:LYS:HD3	4:A:34:LYS:N	2.33	0.43
4:A:70:CYS:O	4:A:71:GLN:C	2.61	0.43
4:A:114:LEU:O	4:A:115:LEU:HG	2.18	0.43
4:A:493:GLN:H	4:A:497:THR:HG21	1.82	0.43
4:A:738:LYS:HZ1	6:C:194:GLU:C	2.25	0.43
4:A:779:PHE:CE1	4:A:785:PRO:CD	2.90	0.43
5:B:204:ILE:C	5:B:205:ILE:HD12	2.43	0.43
5:B:307:ASP:O	5:B:308:TRP:C	2.60	0.43
5:B:421:PHE:O	5:B:424:LEU:HB3	2.18	0.43
5:B:1135:ARG:O	5:B:1138:MET:N	2.51	0.43
6:C:56:THR:HG22	6:C:58:LEU:HD23	2.00	0.43
6:C:116:LYS:HD3	6:C:140:ASN:HA	2.01	0.43
7:D:24:ALA:C	7:D:26:THR:H	2.25	0.43
8:E:157:SER:HG	8:E:160:GLU:HG3	1.82	0.43
12:I:59:VAL:C	12:I:61:ASP:H	2.26	0.43
4:A:34:LYS:HB3	4:A:36:ARG:HE	1.83	0.43
4:A:113:LEU:C	4:A:114:LEU:HD23	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:184:SER:HB3	4:A:199:LEU:CD2	2.49	0.43
4:A:336:ILE:HG22	4:A:337:ARG:N	2.32	0.43
4:A:660:ASN:O	4:A:661:GLY:O	2.36	0.43
4:A:738:LYS:C	4:A:740:LEU:H	2.26	0.43
4:A:809:THR:O	4:A:810:PRO:C	2.60	0.43
4:A:852:TYR:CD2	4:A:1060:PRO:CB	3.02	0.43
4:A:1044:TRP:O	4:A:1045:VAL:C	2.62	0.43
4:A:1385:THR:O	4:A:1387:HIS:N	2.51	0.43
5:B:91:SER:OG	5:B:133:LYS:HB2	2.19	0.43
5:B:283:VAL:O	5:B:284:ILE:C	2.61	0.43
5:B:464:GLY:HA2	5:B:479:VAL:O	2.19	0.43
5:B:642:ASP:CA	5:B:649:LYS:HG3	2.47	0.43
5:B:792:MET:HA	5:B:856:PHE:O	2.17	0.43
8:E:133:GLU:HB3	8:E:135:PHE:HE1	1.84	0.43
10:G:9:LEU:CG	10:G:10:ASN:N	2.82	0.43
10:G:117:GLN:C	10:G:119:LEU:N	2.75	0.43
11:H:83:GLN:C	11:H:85:GLY:N	2.77	0.43
12:I:34:TYR:C	12:I:35:VAL:HG23	2.43	0.43
4:A:77:CYS:O	4:A:77:CYS:SG	2.76	0.43
4:A:113:LEU:HG	4:A:218:ASP:OD1	2.18	0.43
4:A:116:ASP:C	4:A:118:HIS:N	2.74	0.43
4:A:174:ILE:HG23	4:A:182:VAL:O	2.18	0.43
4:A:535:THR:O	4:A:575:LYS:HG3	2.19	0.43
4:A:786:HIS:CD2	4:A:786:HIS:N	2.86	0.43
4:A:1239:ARG:CB	4:A:1239:ARG:HH11	2.32	0.43
4:A:1334:ASP:C	4:A:1336:MET:H	2.26	0.43
5:B:839:MET:HE3	5:B:1010:LEU:HD21	1.99	0.43
5:B:859:TYR:CE1	5:B:941:LEU:HD12	2.53	0.43
6:C:33:LEU:O	6:C:34:ARG:C	2.61	0.43
6:C:181:ASP:CG	6:C:186:LEU:HD13	2.44	0.43
10:G:88:ASP:CB	10:G:144:ARG:HA	2.47	0.43
12:I:15:TYR:N	12:I:15:TYR:CD1	2.86	0.43
14:K:10:PHE:N	14:K:10:PHE:HD2	2.16	0.43
14:K:40:HIS:O	14:K:41:THR:C	2.62	0.43
14:K:85:ASP:O	14:K:88:LYS:HB2	2.19	0.43
4:A:7:SER:CB	5:B:1175:LEU:HD22	2.49	0.43
4:A:41:MET:HB3	4:A:48:ALA:O	2.18	0.43
4:A:42:ASP:HA	4:A:46:THR:O	2.19	0.43
4:A:264:PHE:O	4:A:267:ALA:N	2.51	0.43
4:A:325:ILE:O	4:A:326:ARG:C	2.61	0.43
4:A:335:ARG:HB3	4:A:336:ILE:H	1.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:650:GLN:HB3	4:A:654:ASN:HD21	1.83	0.43
4:A:857:ARG:CZ	9:F:139:PRO:HG3	2.48	0.43
5:B:104:GLU:OE1	15:L:54:ARG:NH2	2.52	0.43
5:B:299:GLU:OE1	5:B:571:PRO:HG2	2.19	0.43
5:B:399:ASP:OD2	5:B:510:LYS:HB2	2.17	0.43
5:B:432:MET:C	5:B:434:ARG:H	2.27	0.43
5:B:459:TYR:C	5:B:459:TYR:CD2	2.96	0.43
5:B:521:LEU:HD13	5:B:633:VAL:CG1	2.48	0.43
6:C:131:HIS:O	6:C:132:PRO:C	2.60	0.43
7:D:66:ARG:O	7:D:67:ARG:C	2.62	0.43
10:G:35:GLU:OE2	10:G:48:VAL:HG23	2.19	0.43
11:H:82:PRO:O	11:H:84:ALA:N	2.35	0.43
13:J:44:TYR:HA	13:J:47:ARG:HB3	1.98	0.43
4:A:106:VAL:HA	4:A:114:LEU:HD21	2.00	0.43
4:A:474:VAL:O	4:A:474:VAL:HG13	2.18	0.43
4:A:562:THR:HB	11:H:98:TYR:CD2	2.54	0.43
4:A:605:MET:HE1	4:A:612:ILE:HG23	1.99	0.43
4:A:667:GLY:HA3	6:C:192:TRP:HH2	1.83	0.43
4:A:907:THR:CG2	4:A:908:LEU:H	2.29	0.43
4:A:1156:PRO:HA	4:A:1190:PRO:HB3	2.00	0.43
5:B:23:ALA:O	5:B:654:ARG:HD2	2.18	0.43
5:B:294:ASP:OD2	5:B:294:ASP:N	2.48	0.43
5:B:520:GLY:H	5:B:748:ILE:HG22	1.82	0.43
5:B:644:GLU:C	5:B:646:LEU:N	2.76	0.43
5:B:653:VAL:O	5:B:654:ARG:HD3	2.19	0.43
5:B:1142:GLY:HA3	9:F:88:TYR:HE2	1.84	0.43
6:C:69:LEU:HB3	13:J:6:ARG:HD3	2.01	0.43
7:D:29:LEU:O	7:D:30:GLY:C	2.61	0.43
7:D:210:ILE:O	7:D:214:LEU:HG	2.18	0.43
8:E:93:MET:SD	8:E:97:VAL:CG2	3.06	0.43
8:E:124:VAL:HG13	8:E:132:ILE:CG1	2.48	0.43
9:F:95:GLY:O	9:F:96:THR:C	2.61	0.43
9:F:132:LEU:HD23	9:F:132:LEU:N	2.34	0.43
12:I:56:ALA:O	12:I:57:GLY:C	2.62	0.43
12:I:84:VAL:HG13	12:I:84:VAL:O	2.19	0.43
13:J:43:ARG:H	13:J:43:ARG:HG2	1.70	0.43
14:K:7:PHE:CD1	14:K:7:PHE:C	2.96	0.43
4:A:16:GLU:HB3	4:A:1418:LEU:HD11	1.99	0.43
4:A:21:LEU:HD11	4:A:1414:ALA:HA	2.00	0.43
4:A:23:SER:O	4:A:25:GLU:N	2.51	0.43
4:A:120:GLU:C	4:A:122:MET:N	2.74	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:535:THR:HG21	4:A:616:VAL:CA	2.35	0.43
4:A:871:ASP:HB3	8:E:204:THR:CG2	2.48	0.43
4:A:988:LEU:HD23	4:A:988:LEU:HA	1.91	0.43
4:A:1074:GLU:HB3	4:A:1075:PRO:HD3	2.00	0.43
4:A:1199:ARG:O	4:A:1200:ALA:C	2.62	0.43
5:B:31:TRP:CE3	5:B:34:ILE:HD12	2.54	0.43
5:B:34:ILE:O	5:B:37:PHE:HB3	2.19	0.43
5:B:97:VAL:HG12	5:B:178:ASN:ND2	2.34	0.43
5:B:509:ALA:C	5:B:511:PRO:CD	2.92	0.43
5:B:616:ILE:CG1	5:B:697:GLU:HA	2.49	0.43
5:B:797:TYR:O	5:B:799:PRO:HD3	2.19	0.43
5:B:820:GLY:C	5:B:1091:TYR:CE1	2.97	0.43
5:B:911:ILE:O	5:B:911:ILE:HG22	2.19	0.43
5:B:936:ASP:OD1	5:B:938:SER:N	2.45	0.43
5:B:1001:PHE:CE2	6:C:34:ARG:NE	2.86	0.43
12:I:50:THR:HG22	12:I:52:ILE:N	2.30	0.43
14:K:17:SER:O	14:K:18:LYS:C	2.61	0.43
4:A:56:PRO:C	4:A:57:ARG:HG3	2.36	0.43
4:A:62:ASP:O	4:A:63:ARG:C	2.62	0.43
4:A:79:GLY:CA	4:A:243:PRO:CG	2.96	0.43
4:A:562:THR:HB	11:H:98:TYR:CE2	2.54	0.43
4:A:817:ALA:C	4:A:819:GLY:N	2.77	0.43
4:A:1139:GLU:O	4:A:1275:GLY:HA3	2.18	0.43
4:A:1199:ARG:O	4:A:1202:MET:N	2.48	0.43
4:A:1261:LYS:HA	4:A:1264:GLU:HB3	2.00	0.43
4:A:1437:GLY:O	4:A:1438:THR:C	2.62	0.43
5:B:310:MET:HG3	5:B:386:LEU:HD13	2.01	0.43
5:B:563:MET:HA	5:B:589:VAL:O	2.19	0.43
5:B:959:ASP:HB2	5:B:961:LEU:HG	2.01	0.43
5:B:986:GLN:O	5:B:987:LYS:C	2.61	0.43
6:C:63:ILE:O	6:C:64:ALA:C	2.62	0.43
7:D:51:ASN:ND2	7:D:54:GLU:OE2	2.51	0.43
8:E:131:THR:HG21	8:E:191:LYS:NZ	2.33	0.43
14:K:19:LEU:HD22	14:K:33:ILE:CG2	2.49	0.43
4:A:350:ARG:HG3	4:A:350:ARG:NH1	2.34	0.43
4:A:445:ASN:CG	4:A:446:ARG:N	2.77	0.43
4:A:503:GLN:NE2	9:F:90:ARG:NH2	2.62	0.43
4:A:767:GLN:NE2	4:A:774:ARG:CB	2.82	0.43
4:A:853:ASP:CG	4:A:855:THR:HG22	2.44	0.43
5:B:33:VAL:HG21	5:B:638:PHE:HZ	1.84	0.43
5:B:179:CYS:SG	5:B:181:LEU:CB	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:294:ASP:C	5:B:296:GLU:H	2.25	0.43
5:B:321:GLY:C	5:B:323:VAL:H	2.27	0.43
5:B:949:VAL:HG12	5:B:950:ASP:N	2.34	0.43
5:B:1182:CYS:O	5:B:1183:LYS:C	2.62	0.43
5:B:1201:LYS:O	5:B:1204:PHE:HB2	2.19	0.43
9:F:85:MET:HE2	9:F:93:ILE:CD1	2.48	0.43
9:F:143:PHE:C	9:F:143:PHE:HD1	2.25	0.43
10:G:77:VAL:O	10:G:77:VAL:HG12	2.19	0.43
13:J:5:VAL:HG12	13:J:6:ARG:CG	2.33	0.43
14:K:83:PRO:O	14:K:86:ALA:N	2.52	0.43
15:L:30:ILE:HD11	15:L:59:ALA:HB2	2.00	0.43
4:A:55:ASP:N	4:A:56:PRO:CD	2.82	0.42
4:A:62:ASP:HB3	4:A:64:ASN:ND2	2.34	0.42
4:A:231:PRO:HA	4:A:234:MET:HE2	2.01	0.42
4:A:365:GLY:HA3	4:A:463:ILE:HD13	2.01	0.42
4:A:392:VAL:CG1	4:A:415:LEU:HD11	2.39	0.42
4:A:556:TRP:CZ2	4:A:558:GLY:HA2	2.54	0.42
4:A:939:ASP:OD2	4:A:1020:CYS:HA	2.19	0.42
4:A:1376:THR:O	4:A:1377:THR:C	2.62	0.42
4:A:1431:GLY:HA3	5:B:1197:PRO:HD3	2.01	0.42
5:B:259:TYR:HD1	5:B:259:TYR:H	1.67	0.42
5:B:429:PHE:HA	5:B:432:MET:CE	2.49	0.42
5:B:1068:GLY:O	5:B:1069:PHE:C	2.62	0.42
5:B:1115:THR:CG2	5:B:1117:GLN:NE2	2.82	0.42
6:C:39:ALA:O	6:C:164:ALA:HB3	2.19	0.42
6:C:173:ALA:O	6:C:174:ALA:HB3	2.19	0.42
6:C:179:GLU:CG	6:C:180:TYR:H	2.31	0.42
8:E:14:ARG:HH21	8:E:141:VAL:HG11	1.81	0.42
8:E:22:MET:CE	8:E:26:ARG:NH2	2.82	0.42
14:K:53:ASP:C	14:K:55:LYS:N	2.76	0.42
15:L:55:ILE:HG12	15:L:55:ILE:H	1.46	0.42
4:A:53:LEU:O	4:A:54:ASN:C	2.61	0.42
4:A:306:ASN:ND2	4:A:322:VAL:HB	2.34	0.42
4:A:325:ILE:HG21	5:B:1210:MET:CG	2.46	0.42
4:A:767:GLN:HE21	4:A:774:ARG:HB3	1.84	0.42
4:A:825:ILE:CG2	5:B:508:LEU:CD1	2.95	0.42
4:A:1313:LEU:C	4:A:1315:GLU:N	2.77	0.42
4:A:1362:TYR:HD1	4:A:1363:VAL:N	2.16	0.42
5:B:759:PRO:C	5:B:761:HIS:H	2.27	0.42
6:C:82:TYR:O	6:C:83:SER:C	2.62	0.42
6:C:88:CYS:SG	6:C:91:HIS:CA	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:77:ASP:O	9:F:79:ARG:N	2.53	0.42
10:G:126:ASN:HD22	10:G:126:ASN:HA	1.59	0.42
2:N:2:DA:H1'	2:N:3:DG:O5'	2.19	0.42
4:A:276:LEU:O	4:A:277:GLU:C	2.63	0.42
4:A:332:LYS:O	4:A:334:GLY:N	2.52	0.42
4:A:355:GLY:N	4:A:482:PHE:CE1	2.87	0.42
4:A:603:ASN:O	4:A:604:GLY:C	2.60	0.42
4:A:795:GLU:CD	4:A:795:GLU:H	2.26	0.42
4:A:1434:ALA:HA	4:A:1435:PRO:HD3	1.88	0.42
5:B:654:ARG:C	5:B:656:GLY:H	2.27	0.42
5:B:1180:PHE:HB3	5:B:1191:ILE:CD1	2.48	0.42
6:C:90:ASP:O	6:C:91:HIS:CB	2.67	0.42
6:C:248:ILE:HG13	6:C:248:ILE:H	1.55	0.42
7:D:51:ASN:O	7:D:52:LEU:C	2.59	0.42
9:F:118:LEU:HD12	9:F:118:LEU:O	2.19	0.42
10:G:1:MET:HE2	10:G:3:PHE:HE1	1.83	0.42
12:I:54:GLU:HB3	12:I:100:PHE:CE2	2.54	0.42
12:I:88:SER:C	12:I:90:GLN:H	2.26	0.42
12:I:103:CYS:HB3	12:I:106:CYS:SG	2.59	0.42
13:J:1:MET:HE2	13:J:56:LEU:HD12	2.01	0.42
3:P:4:A:O2'	3:P:5:C:H5'	2.18	0.42
4:A:334:GLY:O	4:A:335:ARG:C	2.62	0.42
4:A:600:PRO:HG2	4:A:601:LYS:H	1.84	0.42
4:A:774:ARG:CZ	4:A:797:LYS:HG3	2.49	0.42
4:A:857:ARG:HG2	4:A:863:VAL:HA	2.02	0.42
4:A:870:GLU:HB2	8:E:204:THR:HG21	2.01	0.42
4:A:1343:ALA:O	4:A:1346:ALA:HB3	2.19	0.42
4:A:1362:TYR:CD1	4:A:1362:TYR:C	2.95	0.42
4:A:1409:LEU:HD13	5:B:1207:LEU:CD2	2.37	0.42
5:B:102:VAL:HG22	5:B:112:LEU:HD22	2.01	0.42
5:B:273:LEU:HD12	5:B:280:ILE:HD12	2.01	0.42
5:B:305:VAL:O	5:B:305:VAL:HG12	2.19	0.42
5:B:455:SER:O	5:B:458:LYS:N	2.52	0.42
5:B:470:LYS:HB3	5:B:471:LYS:H	1.65	0.42
5:B:862:GLN:HG2	5:B:963:PHE:CD1	2.51	0.42
6:C:70:ILE:HA	6:C:71:PRO:HD2	1.83	0.42
6:C:143:LEU:HD21	6:C:146:LYS:CE	2.48	0.42
7:D:38:ILE:HG22	7:D:39:ASN:O	2.19	0.42
9:F:111:LEU:C	9:F:113:GLY:N	2.70	0.42
10:G:44:TYR:O	10:G:78:VAL:HG12	2.20	0.42
13:J:1:MET:HA	13:J:57:ILE:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:58:GLU:HA	13:J:61:LEU:HD12	2.02	0.42
1:T:19:DG:H4'	5:B:1133:MET:SD	2.58	0.42
4:A:93:VAL:CG1	4:A:301:ALA:HB1	2.42	0.42
4:A:223:GLY:O	4:A:224:PHE:CD1	2.73	0.42
4:A:261:ASP:O	4:A:264:PHE:HB2	2.20	0.42
4:A:528:LEU:O	4:A:529:CYS:C	2.62	0.42
4:A:596:THR:O	4:A:597:LEU:C	2.63	0.42
4:A:789:LYS:HE3	12:I:67:THR:OG1	2.19	0.42
4:A:1011:GLN:O	4:A:1012:ARG:C	2.61	0.42
4:A:1056:SER:C	4:A:1057:VAL:O	2.61	0.42
4:A:1364:ASN:C	4:A:1364:ASN:ND2	2.74	0.42
5:B:496:ARG:HH12	5:B:539:LEU:HB2	1.82	0.42
5:B:581:PHE:HA	5:B:585:VAL:O	2.19	0.42
5:B:984:HIS:CD2	5:B:1025:HIS:HB2	2.54	0.42
6:C:30:ALA:O	6:C:33:LEU:HB3	2.19	0.42
7:D:68:ARG:C	7:D:70:PHE:N	2.78	0.42
8:E:20:LYS:O	8:E:21:GLU:C	2.62	0.42
10:G:9:LEU:HD12	10:G:10:ASN:N	2.32	0.42
11:H:101:ALA:HB2	11:H:116:TYR:CE1	2.54	0.42
12:I:29:CYS:SG	12:I:32:CYS:SG	3.17	0.42
14:K:95:ILE:O	14:K:98:LEU:HB2	2.19	0.42
4:A:417:TYR:O	4:A:418:SER:C	2.63	0.42
4:A:1118:VAL:HG23	4:A:1306:LEU:HB2	2.00	0.42
4:A:1173:HIS:C	4:A:1174:PHE:CD1	2.98	0.42
5:B:259:TYR:HB2	5:B:268:THR:HG23	2.01	0.42
5:B:352:ALA:O	5:B:353:LYS:C	2.63	0.42
5:B:361:LEU:HD21	5:B:377:PHE:HD2	1.79	0.42
5:B:806:THR:CG2	5:B:808:ALA:HB3	2.49	0.42
5:B:975:GLN:HG2	5:B:976:ILE:N	2.32	0.42
5:B:1106:ARG:NH1	5:B:1110:PRO:HG2	2.33	0.42
6:C:80:LEU:HD12	6:C:95:CYS:HA	2.02	0.42
6:C:240:VAL:O	6:C:244:VAL:HG23	2.19	0.42
9:F:72:LYS:O	9:F:73:ALA:HB3	2.19	0.42
10:G:18:PHE:HZ	10:G:68:ALA:HB2	1.85	0.42
10:G:47:CYS:SG	10:G:48:VAL:N	2.92	0.42
10:G:88:ASP:HB3	10:G:144:ARG:CA	2.49	0.42
11:H:15:VAL:HG22	11:H:26:ILE:CD1	2.49	0.42
14:K:113:THR:O	14:K:114:LEU:CB	2.62	0.42
4:A:67:CYS:O	4:A:68:GLN:CB	2.68	0.42
4:A:78:PRO:HG3	5:B:1160:VAL:HG13	2.00	0.42
4:A:526:ASP:O	4:A:527:THR:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:737:LEU:HA	4:A:737:LEU:HD23	1.75	0.42
4:A:881:GLN:O	4:A:953:ASN:HA	2.19	0.42
4:A:889:SER:O	4:A:890:ASP:C	2.61	0.42
4:A:920:LEU:C	4:A:920:LEU:CD2	2.93	0.42
4:A:1329:THR:O	4:A:1335:ILE:HD12	2.20	0.42
4:A:1345:ARG:O	4:A:1346:ALA:C	2.62	0.42
4:A:1438:THR:O	4:A:1438:THR:HG22	2.18	0.42
5:B:383:ASN:O	5:B:384:ARG:C	2.63	0.42
5:B:763:GLN:HG2	5:B:765:PRO:CG	2.50	0.42
5:B:872:GLU:HG2	5:B:916:THR:OG1	2.20	0.42
5:B:1147:LEU:O	5:B:1148:LYS:C	2.62	0.42
5:B:1156:ASP:O	5:B:1157:ALA:O	2.37	0.42
5:B:1160:VAL:HG11	5:B:1169:MET:SD	2.59	0.42
6:C:155:LEU:O	6:C:156:THR:OG1	2.34	0.42
8:E:114:ASN:HD22	8:E:114:ASN:HA	1.63	0.42
9:F:99:LEU:HD12	9:F:99:LEU:O	2.19	0.42
12:I:110:PHE:CD2	12:I:110:PHE:N	2.88	0.42
13:J:13:VAL:C	13:J:14:VAL:CG2	2.93	0.42
15:L:43:THR:C	15:L:45:ALA:H	2.28	0.42
4:A:514:PRO:HB2	4:A:875:ALA:HB3	2.01	0.42
4:A:810:PRO:HA	5:B:1047:PHE:CE2	2.54	0.42
4:A:860:LEU:HD11	4:A:1393:ASN:HB2	2.02	0.42
4:A:867:ILE:O	4:A:868:TYR:C	2.62	0.42
4:A:896:ARG:HD3	4:A:897:TYR:HE1	1.84	0.42
4:A:1193:LEU:HD22	4:A:1260:LEU:HD11	2.02	0.42
4:A:1333:ILE:O	4:A:1337:GLU:HG3	2.19	0.42
4:A:1368:MET:O	4:A:1372:VAL:HB	2.19	0.42
4:A:1423:GLY:H	4:A:1426:GLU:HG3	1.85	0.42
4:A:1444:MET:HG2	10:G:60:ARG:CA	2.48	0.42
5:B:287:ARG:NH1	5:B:324:ILE:O	2.53	0.42
5:B:520:GLY:CA	5:B:748:ILE:HG22	2.50	0.42
5:B:758:PHE:CZ	5:B:1031:LEU:HD22	2.54	0.42
5:B:1163:CYS:SG	5:B:1165:ILE:CB	3.04	0.42
6:C:163:ILE:C	6:C:165:LYS:H	2.27	0.42
11:H:76:THR:O	11:H:76:THR:HG22	2.19	0.42
12:I:33:SER:O	12:I:34:TYR:C	2.63	0.42
1:T:16:DT:H5"	4:A:1386:ARG:NH1	2.35	0.42
4:A:33:ALA:O	4:A:83:HIS:CD2	2.67	0.42
4:A:445:ASN:HB2	4:A:455:MET:HA	2.01	0.42
4:A:464:PRO:C	4:A:465:TYR:O	2.62	0.42
4:A:767:GLN:HE21	4:A:774:ARG:CB	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:874:ASP:O	4:A:875:ALA:C	2.62	0.42
4:A:1426:GLU:H	4:A:1426:GLU:HG2	1.56	0.42
5:B:644:GLU:C	5:B:646:LEU:H	2.26	0.42
5:B:1031:LEU:HD23	5:B:1044:ALA:HB2	2.02	0.42
7:D:128:VAL:O	7:D:132:GLN:HG3	2.20	0.42
9:F:109:VAL:HG11	9:F:123:LYS:CG	2.50	0.42
4:A:219:PHE:O	4:A:222:LEU:O	2.36	0.42
4:A:332:LYS:HG3	4:A:333:GLU:N	2.35	0.42
4:A:584:ASN:O	4:A:637:LYS:HE3	2.20	0.42
4:A:1381:LEU:HD23	4:A:1381:LEU:HA	1.88	0.42
5:B:314:LEU:O	5:B:317:CYS:HB3	2.20	0.42
5:B:317:CYS:O	5:B:318:VAL:C	2.61	0.42
5:B:365:THR:HG23	5:B:367:LEU:N	2.31	0.42
5:B:510:LYS:N	5:B:511:PRO:HD3	2.35	0.42
6:C:56:THR:HG22	6:C:58:LEU:H	1.85	0.42
6:C:259:LEU:CD1	14:K:91:CYS:HB2	2.50	0.42
7:D:45:GLU:O	7:D:46:GLU:C	2.62	0.42
8:E:90:VAL:CA	8:E:120:ALA:HB2	2.47	0.42
10:G:18:PHE:HA	10:G:22:MET:HE2	2.02	0.42
10:G:142:ARG:O	10:G:171:ILE:HG13	2.20	0.42
4:A:218:ASP:O	4:A:219:PHE:O	2.38	0.41
4:A:220:THR:O	4:A:221:SER:C	2.63	0.41
4:A:782:ARG:HB3	4:A:789:LYS:HA	2.02	0.41
4:A:794:PRO:O	4:A:796:SER:N	2.53	0.41
4:A:964:ILE:O	4:A:967:ALA:HB3	2.19	0.41
4:A:1067:LEU:O	4:A:1068:ALA:C	2.63	0.41
4:A:1424:VAL:CG1	5:B:1139:ILE:HD13	2.45	0.41
5:B:324:ILE:CG2	5:B:325:GLN:N	2.82	0.41
5:B:414:ALA:O	5:B:415:GLN:C	2.63	0.41
5:B:683:SER:O	5:B:687:GLU:HB2	2.20	0.41
5:B:766:ARG:HD3	5:B:766:ARG:HA	1.77	0.41
5:B:910:VAL:CG1	5:B:911:ILE:N	2.82	0.41
5:B:1065:GLN:HG3	5:B:1068:GLY:H	1.84	0.41
6:C:77:ILE:C	6:C:79:GLN:H	2.28	0.41
6:C:213:PRO:HG2	6:C:214:ASN:H	1.85	0.41
7:D:167:LEU:O	7:D:170:THR:OG1	2.31	0.41
7:D:191:ALA:O	7:D:193:THR:N	2.53	0.41
9:F:97:ARG:HD2	9:F:97:ARG:HA	1.76	0.41
12:I:101:PHE:N	12:I:101:PHE:HD1	2.18	0.41
4:A:26:GLU:O	4:A:27:VAL:C	2.62	0.41
4:A:40:THR:CG2	4:A:41:MET:HG3	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:417:TYR:O	4:A:418:SER:O	2.37	0.41
4:A:814:PHE:O	4:A:817:ALA:HB3	2.20	0.41
4:A:898:ARG:NH1	4:A:930:ASP:OD1	2.50	0.41
4:A:1073:GLY:O	4:A:1076:ALA:HB3	2.20	0.41
5:B:519:TRP:CD1	5:B:519:TRP:C	2.98	0.41
5:B:604:ARG:C	5:B:606:LYS:H	2.28	0.41
5:B:859:TYR:OH	5:B:941:LEU:CD1	2.62	0.41
5:B:971:THR:OG1	6:C:61:GLU:HG3	2.20	0.41
5:B:998:ASP:HB3	5:B:1076:HIS:HE1	1.85	0.41
6:C:62:PHE:O	6:C:66:ARG:HG3	2.20	0.41
6:C:262:LEU:HA	6:C:262:LEU:HD23	1.80	0.41
9:F:103:MET:HE1	10:G:65:ASP:HB2	2.01	0.41
15:L:38:LEU:O	15:L:39:SER:CB	2.61	0.41
4:A:18:GLN:HG2	4:A:1418:LEU:HD13	2.01	0.41
4:A:29:ALA:HB1	5:B:1184:GLY:CA	2.50	0.41
4:A:381:THR:HG23	4:A:382:PRO:CD	2.50	0.41
4:A:452:LYS:HB3	4:A:452:LYS:HE2	1.85	0.41
4:A:868:TYR:CD2	4:A:1058:VAL:HG21	2.48	0.41
4:A:1013:ASP:C	4:A:1015:VAL:H	2.28	0.41
4:A:1111:MET:CE	4:A:1330:ASN:OD1	2.68	0.41
4:A:1242:VAL:O	4:A:1243:VAL:CB	2.66	0.41
5:B:125:SER:CA	5:B:171:PRO:HA	2.49	0.41
5:B:258:LEU:O	5:B:258:LEU:HG	2.19	0.41
5:B:526:GLU:OE2	5:B:752:ALA:HB2	2.20	0.41
5:B:651:LEU:HD11	5:B:707:PRO:CB	2.50	0.41
5:B:654:ARG:O	5:B:656:GLY:N	2.53	0.41
5:B:765:PRO:O	5:B:767:ASN:N	2.53	0.41
5:B:990:ILE:CG2	5:B:991:GLY:N	2.83	0.41
5:B:1164:GLY:HA3	5:B:1190:ASP:OD2	2.20	0.41
8:E:9:ILE:C	8:E:11:ARG:N	2.78	0.41
8:E:16:PHE:CE2	8:E:20:LYS:HE2	2.53	0.41
12:I:55:THR:HG23	12:I:58:VAL:HG21	2.01	0.41
13:J:23:ASN:O	13:J:25:LEU:N	2.52	0.41
4:A:254:GLU:HB2	5:B:935:ARG:NH1	2.29	0.41
4:A:278:THR:O	4:A:278:THR:HG22	2.19	0.41
4:A:279:LEU:O	4:A:284:ALA:HB2	2.20	0.41
4:A:629:LEU:O	4:A:633:VAL:HG23	2.21	0.41
4:A:676:MET:O	4:A:679:ILE:HB	2.21	0.41
4:A:1227:ILE:HG22	4:A:1228:TRP:H	1.80	0.41
4:A:1409:LEU:O	4:A:1412:ALA:HB3	2.21	0.41
5:B:27:ALA:C	5:B:29:ASP:N	2.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:34:ILE:O	5:B:37:PHE:N	2.53	0.41
5:B:121:ASN:OD1	5:B:963:PHE:HZ	2.04	0.41
5:B:170:LEU:HA	5:B:171:PRO:HD2	1.82	0.41
5:B:278:GLN:HG2	5:B:279:ASP:N	2.35	0.41
5:B:281:PRO:C	5:B:283:VAL:N	2.77	0.41
5:B:376:PHE:HB3	5:B:586:TRP:CZ3	2.55	0.41
5:B:468:GLU:HB3	5:B:469:GLN:H	1.49	0.41
5:B:834:ASN:CA	5:B:838:SER:O	2.69	0.41
7:D:179:GLN:O	7:D:183:LEU:HB2	2.20	0.41
9:F:103:MET:HE3	10:G:66:GLY:H	1.85	0.41
10:G:106:MET:HG2	10:G:107:LYS:N	2.36	0.41
10:G:138:THR:HG22	10:G:139:ILE:HG13	2.02	0.41
12:I:34:TYR:CD2	12:I:34:TYR:C	2.97	0.41
4:A:255:SER:C	4:A:256:GLN:HG3	2.45	0.41
4:A:402:ALA:CB	4:A:434:ARG:HA	2.51	0.41
4:A:404:TYR:CD2	4:A:414:ASP:HA	2.55	0.41
4:A:463:ILE:HB	4:A:464:PRO:CD	2.49	0.41
4:A:823:GLY:O	4:A:824:LEU:C	2.63	0.41
4:A:970:THR:O	4:A:970:THR:HG22	2.20	0.41
5:B:365:THR:CG2	5:B:366:GLN:N	2.81	0.41
5:B:412:LEU:O	5:B:413:LEU:C	2.64	0.41
5:B:758:PHE:N	5:B:759:PRO:HD2	2.35	0.41
5:B:797:TYR:C	5:B:798:TYR:HD2	2.29	0.41
5:B:842:ASN:HB3	5:B:1009:ASP:HA	2.03	0.41
5:B:980:PHE:CA	5:B:1095:LEU:HD11	2.50	0.41
5:B:1068:GLY:O	5:B:1069:PHE:O	2.39	0.41
5:B:1187:ASN:OD1	5:B:1188:LYS:N	2.45	0.41
7:D:63:LEU:HD22	7:D:63:LEU:HA	1.91	0.41
11:H:95:TYR:CE2	11:H:97:MET:CG	3.04	0.41
12:I:4:PHE:HE1	12:I:6:PHE:HE2	1.69	0.41
4:A:207:ILE:CG2	4:A:211:PHE:CE1	3.03	0.41
4:A:680:THR:HG23	5:B:729:ILE:CD1	2.51	0.41
4:A:947:PHE:CD2	4:A:954:TRP:CE2	3.08	0.41
4:A:1388:GLY:O	4:A:1390:ASN:N	2.53	0.41
5:B:413:LEU:O	5:B:414:ALA:C	2.63	0.41
5:B:578:THR:HG22	5:B:578:THR:O	2.21	0.41
5:B:744:HIS:CD2	5:B:745:PRO:HD2	2.55	0.41
5:B:861:ASP:OD1	5:B:914:LYS:HD2	2.21	0.41
6:C:66:ARG:NH1	13:J:2:ILE:CG2	2.82	0.41
6:C:191:TYR:CD2	6:C:201:TRP:CD1	3.03	0.41
12:I:4:PHE:HE1	12:I:6:PHE:CE2	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:17:SER:C	14:K:19:LEU:N	2.76	0.41
4:A:262:LEU:HD12	4:A:328:ARG:NH2	2.35	0.41
4:A:332:LYS:C	4:A:334:GLY:N	2.77	0.41
4:A:344:ARG:C	4:A:345:VAL:CG1	2.94	0.41
4:A:527:THR:O	4:A:531:ILE:HB	2.21	0.41
4:A:768:GLN:HG3	4:A:816:HIS:HA	2.01	0.41
4:A:1074:GLU:C	4:A:1076:ALA:N	2.78	0.41
4:A:1193:LEU:HD12	4:A:1193:LEU:C	2.43	0.41
4:A:1315:GLU:C	4:A:1317:MET:H	2.28	0.41
4:A:1419:ASP:CG	4:A:1426:GLU:OE1	2.64	0.41
5:B:435:THR:C	5:B:437:GLU:N	2.79	0.41
5:B:878:GLN:O	5:B:879:ARG:C	2.63	0.41
5:B:1065:GLN:HE21	5:B:1066:SER:CA	2.33	0.41
6:C:11:ARG:HD3	6:C:209:TYR:CE2	2.56	0.41
6:C:31:ASN:O	6:C:34:ARG:HB3	2.20	0.41
6:C:147:LEU:HD23	6:C:147:LEU:N	2.36	0.41
6:C:260:LEU:O	6:C:263:THR:HB	2.20	0.41
9:F:97:ARG:NH1	9:F:100:GLN:OE1	2.53	0.41
12:I:101:PHE:HD1	12:I:101:PHE:H	1.67	0.41
14:K:38:GLU:HA	14:K:38:GLU:OE1	2.20	0.41
4:A:146:MET:CA	4:A:171:GLN:HB2	2.50	0.41
4:A:211:PHE:O	4:A:212:LYS:C	2.63	0.41
4:A:304:MET:HG2	5:B:1210:MET:HG2	2.03	0.41
4:A:306:ASN:HD22	4:A:322:VAL:HG12	1.86	0.41
4:A:343:LYS:NZ	5:B:1151:LEU:O	2.43	0.41
4:A:403:LYS:O	4:A:404:TYR:CD2	2.74	0.41
4:A:574:GLY:O	4:A:577:ILE:N	2.51	0.41
4:A:608:ILE:CG1	4:A:613:ILE:HD12	2.51	0.41
4:A:871:ASP:CG	4:A:1366:ARG:HH22	2.28	0.41
4:A:964:ILE:O	4:A:967:ALA:N	2.54	0.41
4:A:1373:ASP:CA	4:A:1376:THR:HG22	2.50	0.41
5:B:388:CYS:O	5:B:391:ASP:N	2.50	0.41
5:B:604:ARG:O	5:B:607:GLY:N	2.54	0.41
5:B:730:ARG:O	5:B:731:VAL:O	2.39	0.41
5:B:1200:ALA:O	5:B:1201:LYS:C	2.63	0.41
6:C:54:ASN:HB2	6:C:153:LEU:HD12	2.03	0.41
7:D:180:LEU:HA	7:D:180:LEU:HD23	1.87	0.41
9:F:89:GLU:O	9:F:90:ARG:C	2.63	0.41
10:G:21:ARG:HD3	10:G:21:ARG:HA	1.85	0.41
12:I:98:VAL:HG12	12:I:99:LEU:N	2.36	0.41
13:J:44:TYR:HD2	13:J:44:TYR:N	2.13	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:31:VAL:O	14:K:74:ARG:HA	2.21	0.41
15:L:38:LEU:CD1	15:L:49:LYS:HE2	2.50	0.41
4:A:61:ILE:CG2	4:A:62:ASP:H	2.29	0.41
4:A:93:VAL:HA	4:A:96:ILE:CD1	2.51	0.41
4:A:203:SER:O	4:A:204:THR:C	2.64	0.41
4:A:296:LEU:O	4:A:297:GLN:C	2.63	0.41
4:A:556:TRP:NE1	4:A:559:VAL:H	2.18	0.41
4:A:590:ARG:HD3	4:A:604:GLY:O	2.20	0.41
4:A:722:LEU:HD21	4:A:794:PRO:HB3	2.03	0.41
4:A:954:TRP:HB3	4:A:955:PRO:HD2	2.02	0.41
4:A:973:ILE:HD13	4:A:1037:LEU:HA	2.03	0.41
4:A:1041:ALA:O	4:A:1045:VAL:HG23	2.20	0.41
4:A:1127:ASP:O	4:A:1130:GLN:HB3	2.20	0.41
4:A:1435:PRO:C	4:A:1436:ILE:HG13	2.44	0.41
4:A:1445:ILE:H	4:A:1445:ILE:CD1	2.19	0.41
5:B:60:GLN:O	5:B:63:ILE:HG22	2.21	0.41
5:B:62:ILE:HG23	5:B:418:LYS:HG2	2.03	0.41
5:B:129:PHE:CD2	5:B:166:PHE:HA	2.56	0.41
5:B:251:ILE:O	5:B:251:ILE:HG22	2.19	0.41
5:B:261:ARG:NH1	5:B:261:ARG:HB3	2.35	0.41
5:B:281:PRO:O	5:B:282:ILE:C	2.63	0.41
5:B:285:ILE:O	5:B:288:ALA:HB3	2.21	0.41
5:B:298:LEU:N	5:B:298:LEU:HD22	2.35	0.41
5:B:464:GLY:CA	5:B:479:VAL:O	2.68	0.41
5:B:492:LEU:HB2	5:B:751:VAL:HG11	2.03	0.41
5:B:516:ASN:ND2	5:B:516:ASN:H	2.16	0.41
5:B:704:ALA:HB3	5:B:741:CYS:SG	2.61	0.41
5:B:840:ILE:CG2	5:B:994:TYR:HD1	2.34	0.41
5:B:873:THR:O	5:B:914:LYS:HA	2.20	0.41
5:B:899:ILE:CG2	5:B:903:VAL:HG21	2.50	0.41
5:B:953:LEU:HD23	5:B:965:LYS:H	1.86	0.41
5:B:992:ILE:HG12	5:B:993:THR:N	2.36	0.41
5:B:1110:PRO:HG3	5:B:1124:ARG:O	2.21	0.41
6:C:18:VAL:O	6:C:20:PHE:CD2	2.71	0.41
6:C:67:LEU:HD11	6:C:155:LEU:HD12	2.01	0.41
6:C:100:THR:CG2	6:C:101:LEU:N	2.84	0.41
6:C:181:ASP:OD1	6:C:186:LEU:HD13	2.21	0.41
7:D:118:THR:O	7:D:118:THR:HG22	2.20	0.41
8:E:14:ARG:NH2	8:E:141:VAL:HG12	2.34	0.41
8:E:78:LEU:HA	8:E:107:THR:HB	2.02	0.41
8:E:163:GLU:O	8:E:164:LEU:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:191:LYS:O	8:E:193:GLY:N	2.54	0.41
10:G:88:ASP:HB3	10:G:144:ARG:CB	2.51	0.41
11:H:25:ARG:HA	11:H:41:ASP:HA	2.03	0.41
11:H:62:SER:OG	11:H:63:LEU:N	2.53	0.41
12:I:54:GLU:OE2	12:I:118:ARG:NH1	2.53	0.41
13:J:3:VAL:HA	13:J:4:PRO:HD3	1.84	0.41
13:J:32:GLU:O	13:J:35:ALA:N	2.54	0.41
13:J:48:ARG:HD2	13:J:48:ARG:C	2.46	0.41
4:A:274:ILE:O	4:A:275:SER:C	2.62	0.41
4:A:414:ASP:OD1	4:A:416:ARG:CG	2.69	0.41
4:A:604:GLY:O	4:A:605:MET:HB2	2.21	0.41
4:A:817:ALA:O	4:A:820:GLY:N	2.54	0.41
4:A:1062:GLU:OE2	9:F:88:TYR:OH	2.36	0.41
5:B:807:ARG:HG2	5:B:1045:SER:OG	2.21	0.41
5:B:949:VAL:HG12	5:B:950:ASP:H	1.86	0.41
5:B:1074:ASN:HB2	5:B:1081:LEU:HD21	2.03	0.41
5:B:1187:ASN:OD1	5:B:1189:ILE:N	2.53	0.41
6:C:18:VAL:O	6:C:19:ASP:C	2.61	0.41
7:D:63:LEU:HD12	7:D:129:LEU:HG	2.03	0.41
8:E:94:LYS:HG3	8:E:98:ILE:HD11	2.01	0.41
8:E:96:PHE:O	8:E:97:VAL:C	2.64	0.41
4:A:79:GLY:CA	4:A:243:PRO:HG3	2.51	0.40
4:A:332:LYS:C	4:A:334:GLY:H	2.29	0.40
4:A:690:VAL:O	4:A:693:VAL:N	2.54	0.40
4:A:1129:GLU:O	4:A:1130:GLN:C	2.64	0.40
4:A:1364:ASN:O	4:A:1366:ARG:HG3	2.21	0.40
5:B:33:VAL:O	5:B:36:ALA:N	2.55	0.40
5:B:753:ALA:HA	5:B:756:ILE:CD1	2.51	0.40
5:B:1106:ARG:HG3	5:B:1107:ALA:N	2.35	0.40
6:C:90:ASP:O	6:C:91:HIS:HB3	2.20	0.40
7:D:198:LEU:O	7:D:199:ASN:C	2.64	0.40
10:G:52:ASP:C	10:G:54:ILE:H	2.29	0.40
12:I:59:VAL:C	12:I:61:ASP:N	2.79	0.40
13:J:51:LEU:O	13:J:51:LEU:HD12	2.21	0.40
14:K:7:PHE:HA	14:K:10:PHE:HE2	1.78	0.40
4:A:6:TYR:CD1	4:A:7:SER:N	2.89	0.40
4:A:239:LEU:CD1	4:A:240:PRO:HD2	2.46	0.40
4:A:241:VAL:HA	4:A:242:PRO:HD2	1.93	0.40
4:A:265:LYS:HZ3	4:A:322:VAL:HG13	1.87	0.40
4:A:341:MET:HE3	4:A:341:MET:HB3	1.98	0.40
4:A:349:ALA:CA	5:B:1128:LEU:HD11	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:516:SER:O	4:A:517:ASN:C	2.63	0.40
4:A:577:ILE:O	4:A:579:SER:N	2.55	0.40
4:A:715:GLU:O	4:A:716:ASP:C	2.65	0.40
4:A:767:GLN:NE2	4:A:774:ARG:HB2	2.36	0.40
4:A:857:ARG:NH1	9:F:139:PRO:HB2	2.36	0.40
4:A:886:ILE:HD11	4:A:943:LEU:CB	2.45	0.40
4:A:1131:ALA:O	4:A:1132:LYS:C	2.64	0.40
4:A:1219:THR:HG21	4:A:1271:ILE:HG13	2.02	0.40
4:A:1339:LEU:O	8:E:150:VAL:HG21	2.21	0.40
4:A:1409:LEU:HA	4:A:1409:LEU:HD23	1.85	0.40
5:B:257:LYS:O	5:B:258:LEU:HB2	2.21	0.40
5:B:263:GLY:O	5:B:264:SER:C	2.64	0.40
5:B:446:LEU:O	5:B:447:ALA:CB	2.67	0.40
5:B:546:SER:OG	5:B:631:GLY:N	2.42	0.40
5:B:901:PRO:HD2	15:L:59:ALA:O	2.21	0.40
5:B:977:GLY:HA3	5:B:1099:VAL:CG2	2.52	0.40
6:C:246:ARG:HA	6:C:249:ASP:HB3	2.02	0.40
11:H:40:LEU:CD1	11:H:123:MET:HB2	2.45	0.40
11:H:59:ILE:CG2	11:H:60:ALA:H	2.27	0.40
12:I:88:SER:HB3	12:I:95:THR:HG21	2.02	0.40
14:K:78:THR:O	14:K:79:GLU:C	2.64	0.40
4:A:49:LYS:NZ	4:A:61:ILE:CG1	2.79	0.40
4:A:59:GLY:HA2	4:A:67:CYS:SG	2.62	0.40
4:A:524:VAL:HG12	4:A:525:GLN:HE21	1.85	0.40
4:A:755:PHE:O	4:A:758:ILE:N	2.55	0.40
4:A:962:ARG:O	4:A:963:ILE:C	2.64	0.40
4:A:1072:ILE:O	4:A:1075:PRO:CD	2.69	0.40
4:A:1161:THR:C	4:A:1163:ILE:H	2.29	0.40
4:A:1339:LEU:HD13	8:E:147:HIS:CD2	2.56	0.40
5:B:635:ARG:HB2	5:B:636:PRO:HD2	2.03	0.40
5:B:654:ARG:C	5:B:656:GLY:N	2.79	0.40
5:B:662:MET:HA	5:B:665:GLU:HB2	2.02	0.40
5:B:729:ILE:O	5:B:729:ILE:HG22	2.21	0.40
5:B:899:ILE:HD13	5:B:905:VAL:HG11	2.03	0.40
5:B:1047:PHE:CD1	5:B:1047:PHE:N	2.81	0.40
6:C:174:ALA:O	6:C:175:ALA:CB	2.69	0.40
6:C:177:GLU:CB	6:C:231:ASN:HB3	2.48	0.40
7:D:56:ARG:HH22	7:D:57:LEU:HD21	1.83	0.40
7:D:64:VAL:O	7:D:66:ARG:N	2.55	0.40
7:D:177:VAL:HG23	7:D:177:VAL:H	1.67	0.40
8:E:31:THR:OG1	8:E:34:GLU:N	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:79:TRP:CD1	8:E:96:PHE:HE1	2.38	0.40
9:F:103:MET:O	9:F:104:ASN:CB	2.61	0.40
10:G:45:ILE:HD13	10:G:45:ILE:HA	1.94	0.40
11:H:59:ILE:O	11:H:60:ALA:HB3	2.20	0.40
12:I:8:ARG:HG3	12:I:8:ARG:H	1.72	0.40
13:J:47:ARG:HH11	13:J:47:ARG:CG	2.34	0.40
4:A:54:ASN:HA	4:A:58:LEU:HD12	2.04	0.40
4:A:79:GLY:C	4:A:243:PRO:HG3	2.45	0.40
4:A:103:CYS:C	4:A:105:CYS:H	2.29	0.40
4:A:350:ARG:NH1	4:A:488:ASN:OD1	2.49	0.40
4:A:543:LEU:HD12	4:A:547:LEU:HG	2.03	0.40
4:A:679:ILE:O	4:A:680:THR:C	2.65	0.40
4:A:809:THR:CG2	4:A:812:GLU:HG3	2.52	0.40
4:A:1125:ALA:C	4:A:1127:ASP:H	2.30	0.40
4:A:1437:GLY:CA	9:F:88:TYR:CD2	3.04	0.40
5:B:27:ALA:O	5:B:30:SER:OG	2.36	0.40
5:B:168:GLY:HA2	5:B:454:THR:OG1	2.21	0.40
5:B:458:LYS:O	5:B:459:TYR:C	2.65	0.40
5:B:461:LEU:N	5:B:461:LEU:HD12	2.35	0.40
5:B:470:LYS:C	5:B:472:ALA:N	2.79	0.40
5:B:550:ASP:OD1	5:B:551:PRO:HD2	2.22	0.40
5:B:582:VAL:HG12	5:B:587:HIS:NE2	2.37	0.40
5:B:641:GLU:C	5:B:643:ASP:H	2.29	0.40
5:B:765:PRO:C	5:B:767:ASN:N	2.79	0.40
5:B:979:LYS:HG2	5:B:1095:LEU:CD1	2.51	0.40
5:B:1167:GLY:O	5:B:1215:ARG:HA	2.22	0.40
5:B:1207:LEU:O	5:B:1210:MET:HB2	2.21	0.40
6:C:59:ALA:O	6:C:60:ASP:C	2.64	0.40
7:D:40:HIS:C	7:D:42:GLY:N	2.77	0.40
7:D:191:ALA:C	7:D:193:THR:N	2.79	0.40
8:E:30:ILE:HG22	8:E:31:THR:N	2.35	0.40
4:A:353:ILE:HD13	4:A:487:MET:HG3	2.04	0.40
4:A:599:SER:HA	4:A:600:PRO:HD2	1.95	0.40
4:A:709:THR:HG22	4:A:710:LEU:N	2.37	0.40
4:A:886:ILE:HG13	4:A:943:LEU:HD13	2.03	0.40
4:A:1115:SER:O	4:A:1311:VAL:CG2	2.70	0.40
4:A:1206:ASP:O	4:A:1274:ARG:NH1	2.52	0.40
4:A:1215:ARG:O	4:A:1216:ILE:C	2.65	0.40
4:A:1335:ILE:O	4:A:1335:ILE:CG2	2.69	0.40
4:A:1385:THR:C	4:A:1387:HIS:N	2.79	0.40
5:B:35:SER:HA	5:B:811:TYR:CE2	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:180:TYR:CD1	5:B:180:TYR:N	2.90	0.40
5:B:294:ASP:C	5:B:296:GLU:N	2.79	0.40
5:B:294:ASP:OD1	12:I:12:ASN:HB3	2.21	0.40
5:B:371:GLU:N	5:B:371:GLU:OE1	2.55	0.40
5:B:376:PHE:CE2	5:B:569:TYR:CD2	3.02	0.40
5:B:564:GLU:HA	5:B:565:PRO:HD2	1.91	0.40
5:B:637:LEU:CD2	5:B:742:GLU:HA	2.51	0.40
5:B:1008:PRO:HB2	5:B:1010:LEU:O	2.21	0.40
6:C:22:LEU:CD2	6:C:25:VAL:HG21	2.50	0.40
6:C:58:LEU:N	6:C:58:LEU:HD22	2.37	0.40
6:C:169:LYS:NZ	15:L:69:ALA:HB3	2.37	0.40
7:D:55:ALA:O	7:D:56:ARG:C	2.63	0.40
8:E:17:ARG:O	8:E:21:GLU:HG3	2.22	0.40
8:E:177:ARG:O	8:E:212:ARG:CD	2.70	0.40
9:F:82:THR:HA	9:F:83:PRO:HD3	1.81	0.40
9:F:94:LEU:HD21	9:F:122:MET:HA	2.03	0.40
11:H:41:ASP:HB2	11:H:121:LEU:HB3	2.02	0.40
11:H:58:THR:HG22	11:H:59:ILE:H	1.86	0.40
13:J:1:MET:HE2	13:J:1:MET:HB2	1.61	0.40
14:K:24:ASP:OD1	14:K:26:LYS:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
4	A	1406/1733 (81%)	936 (67%)	311 (22%)	159 (11%)	0	5
5	B	1096/1224 (90%)	740 (68%)	215 (20%)	141 (13%)	0	4
6	C	264/318 (83%)	166 (63%)	64 (24%)	34 (13%)	0	4
7	D	173/221 (78%)	118 (68%)	38 (22%)	17 (10%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	E	212/215 (99%)	154 (73%)	44 (21%)	14 (7%)	1	15
9	F	82/155 (53%)	63 (77%)	16 (20%)	3 (4%)	2	22
10	G	169/171 (99%)	133 (79%)	24 (14%)	12 (7%)	1	14
11	H	129/146 (88%)	85 (66%)	28 (22%)	16 (12%)	0	4
12	I	117/122 (96%)	79 (68%)	27 (23%)	11 (9%)	0	10
13	J	63/70 (90%)	34 (54%)	15 (24%)	14 (22%)	0	1
14	K	112/120 (93%)	87 (78%)	17 (15%)	8 (7%)	1	14
15	L	44/70 (63%)	17 (39%)	18 (41%)	9 (20%)	0	1
All	All	3867/4565 (85%)	2612 (68%)	817 (21%)	438 (11%)	0	5

All (438) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	5	GLN
4	A	48	ALA
4	A	54	ASN
4	A	55	ASP
4	A	57	ARG
4	A	62	ASP
4	A	65	LEU
4	A	66	LYS
4	A	70	CYS
4	A	74	MET
4	A	76	GLU
4	A	93	VAL
4	A	154	SER
4	A	167	CYS
4	A	244	PRO
4	A	255	SER
4	A	286	HIS
4	A	311	GLN
4	A	318	SER
4	A	322	VAL
4	A	335	ARG
4	A	385	ILE
4	A	409	SER
4	A	418	SER
4	A	423	ASP
4	A	536	LEU

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Mol	Chain	Res	Type
4	A	567	LYS
4	A	619	LYS
4	A	626	ASN
4	A	666	ILE
4	A	765	VAL
4	A	775	ILE
4	A	780	VAL
4	A	789	LYS
4	A	847	ASP
4	A	968	GLN
4	A	1002	GLY
4	A	1016	THR
4	A	1036	ARG
4	A	1115	SER
4	A	1116	LEU
4	A	1122	PRO
4	A	1212	VAL
4	A	1223	ASP
4	A	1281	ARG
4	A	1314	SER
4	A	1341	ILE
4	A	1365	TYR
4	A	1366	ARG
4	A	1378	GLN
4	A	1403	GLU
4	A	1438	THR
5	B	28	GLU
5	B	45	SER
5	B	108	VAL
5	B	206	ASN
5	B	258	LEU
5	B	259	TYR
5	B	308	TRP
5	B	367	LEU
5	B	467	GLY
5	B	474	SER
5	B	504	ARG
5	B	509	ALA
5	B	511	PRO
5	B	629	ASP
5	B	643	ASP
5	B	709	ASP

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Mol	Chain	Res	Type
5	B	731	VAL
5	B	751	VAL
5	B	881	ASN
5	B	907	GLY
5	B	943	SER
5	B	958	GLN
5	B	1046	PRO
5	B	1100	ASP
5	B	1108	ARG
5	B	1157	ALA
5	B	1171	VAL
5	B	1175	LEU
5	B	1181	GLU
5	B	1182	CYS
5	B	1186	ASP
5	B	1188	LYS
6	C	91	HIS
6	C	110	THR
6	C	141	GLY
6	C	149	LYS
6	C	156	THR
6	C	161	LYS
6	C	184	ASN
6	C	213	PRO
6	C	214	ASN
6	C	215	GLU
6	C	231	ASN
7	D	6	SER
7	D	8	PHE
7	D	19	GLU
7	D	20	GLU
7	D	21	GLU
7	D	52	LEU
7	D	131	GLU
7	D	177	VAL
7	D	199	ASN
8	E	106	GLN
8	E	130	ALA
9	F	81	THR
10	G	63	PRO
10	G	139	ILE
11	H	81	PRO

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Mol	Chain	Res	Type
11	H	128	ASN
11	H	140	ALA
12	I	3	THR
12	I	9	ASP
12	I	57	GLY
12	I	79	HIS
13	J	2	ILE
13	J	6	ARG
13	J	32	GLU
13	J	64	ASN
15	L	50	ASP
15	L	53	HIS
15	L	59	ALA
4	A	42	ASP
4	A	44	THR
4	A	59	GLY
4	A	111	GLY
4	A	113	LEU
4	A	117	GLU
4	A	219	PHE
4	A	226	GLU
4	A	232	GLU
4	A	263	THR
4	A	278	THR
4	A	290	GLU
4	A	300	VAL
4	A	312	PRO
4	A	364	VAL
4	A	399	HIS
4	A	421	ALA
4	A	424	ILE
4	A	661	GLY
4	A	731	ARG
4	A	753	GLY
4	A	795	GLU
4	A	830	LYS
4	A	846	GLU
4	A	986	ILE
4	A	1014	ALA
4	A	1071	SER
4	A	1165	GLU
4	A	1221	LYS

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Mol	Chain	Res	Type
4	A	1386	ARG
4	A	1395	GLY
4	A	1397	LEU
4	A	1405	THR
5	B	21	GLU
5	B	27	ALA
5	B	46	GLN
5	B	114	PRO
5	B	115	GLN
5	B	186	GLU
5	B	229	ALA
5	B	257	LYS
5	B	260	GLY
5	B	282	ILE
5	B	322	PHE
5	B	334	ILE
5	B	369	GLY
5	B	468	GLU
5	B	470	LYS
5	B	513	GLN
5	B	540	SER
5	B	559	SER
5	B	682	SER
5	B	746	SER
5	B	770	GLN
5	B	848	ARG
5	B	869	SER
5	B	891	ASP
5	B	1006	ILE
5	B	1041	GLU
5	B	1069	PHE
5	B	1126	GLY
5	B	1156	ASP
5	B	1167	GLY
5	B	1178	ASN
5	B	1183	LYS
6	C	78	GLU
6	C	164	ALA
6	C	167	HIS
6	C	175	ALA
6	C	202	PRO
6	C	209	TYR

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Mol	Chain	Res	Type
6	C	216	GLY
6	C	240	VAL
6	C	264	GLN
7	D	12	ARG
7	D	53	SER
7	D	192	LYS
8	E	36	GLU
8	E	44	ALA
8	E	59	SER
8	E	73	PRO
8	E	74	ASP
8	E	192	ARG
8	E	206	GLY
10	G	35	GLU
10	G	53	ASN
10	G	154	VAL
11	H	21	ASN
11	H	32	THR
11	H	59	ILE
11	H	82	PRO
11	H	84	ALA
11	H	92	ASP
11	H	108	SER
12	I	78	CYS
12	I	106	CYS
13	J	8	PHE
13	J	14	VAL
13	J	18	TRP
13	J	28	ASP
13	J	29	GLU
13	J	33	GLY
13	J	51	LEU
14	K	7	PHE
14	K	15	GLY
14	K	29	ASN
14	K	53	ASP
14	K	88	LYS
4	A	4	GLN
4	A	61	ILE
4	A	67	CYS
4	A	69	THR
4	A	71	GLN

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Mol	Chain	Res	Type
4	A	223	GLY
4	A	245	PRO
4	A	253	ASN
4	A	317	LYS
4	A	357	PRO
4	A	419	LYS
4	A	439	ASN
4	A	517	ASN
4	A	525	GLN
4	A	534	LEU
4	A	817	ALA
4	A	818	MET
4	A	824	LEU
4	A	829	VAL
4	A	1008	GLN
4	A	1028	THR
4	A	1067	LEU
4	A	1114	PRO
4	A	1127	ASP
4	A	1133	LEU
4	A	1240	CYS
4	A	1242	VAL
4	A	1335	ILE
4	A	1389	PHE
5	B	48	LEU
5	B	58	THR
5	B	100	PRO
5	B	266	ALA
5	B	319	GLU
5	B	387	LEU
5	B	591	ARG
5	B	605	ARG
5	B	636	PRO
5	B	641	GLU
5	B	648	HIS
5	B	655	LYS
5	B	711	GLU
5	B	867	GLY
5	B	878	GLN
5	B	951	GLN
5	B	1003	ALA
5	B	1017	ILE

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Mol	Chain	Res	Type
5	B	1035	ALA
5	B	1097	HIS
5	B	1112	GLN
5	B	1144	ALA
5	B	1153	GLU
5	B	1155	SER
6	C	87	PHE
6	C	169	LYS
6	C	255	VAL
7	D	15	LEU
7	D	218	GLU
8	E	115	ASN
8	E	138	ALA
9	F	150	GLU
10	G	62	LEU
10	G	118	ASP
11	H	17	PRO
11	H	44	VAL
11	H	77	ARG
11	H	107	VAL
12	I	47	GLU
12	I	62	ILE
13	J	17	LYS
15	L	35	SER
15	L	40	LEU
15	L	43	THR
15	L	54	ARG
15	L	56	LEU
4	A	58	LEU
4	A	250	ILE
4	A	283	GLY
4	A	333	GLU
4	A	336	ILE
4	A	400	PRO
4	A	465	TYR
4	A	526	ASP
4	A	592	ASP
4	A	605	MET
4	A	648	ASN
4	A	652	VAL
4	A	910	PRO
4	A	958	VAL

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Mol	Chain	Res	Type
4	A	1231	ASP
4	A	1266	THR
4	A	1302	PRO
5	B	49	ASP
5	B	67	SER
5	B	364	ILE
5	B	418	LYS
5	B	466	TRP
5	B	590	HIS
5	B	727	LYS
5	B	735	ALA
5	B	738	PHE
5	B	752	ALA
5	B	754	SER
5	B	764	SER
5	B	792	MET
5	B	815	ARG
5	B	883	LEU
5	B	884	ARG
5	B	888	GLY
5	B	953	LEU
5	B	982	SER
5	B	1065	GLN
5	B	1103	ILE
5	B	1176	ASN
6	C	60	ASP
6	C	108	GLU
6	C	142	VAL
6	C	212	PRO
6	C	257	SER
7	D	30	GLY
8	E	45	LYS
8	E	99	HIS
10	G	115	MET
11	H	52	GLN
12	I	11	ASN
12	I	34	TYR
14	K	70	ARG
14	K	79	GLU
14	K	104	ASN
4	A	101	LYS
4	A	386	ASP

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Mol	Chain	Res	Type
4	A	599	SER
4	A	920	LEU
4	A	1120	LEU
4	A	1164	PRO
4	A	1370	LEU
5	B	30	SER
5	B	65	GLU
5	B	94	LYS
5	B	309	GLN
5	B	383	ASN
5	B	401	PHE
5	B	411	PRO
5	B	414	ALA
5	B	510	LYS
5	B	571	PRO
5	B	880	THR
5	B	942	ARG
5	B	1011	ILE
6	C	56	THR
6	C	84	ARG
7	D	196	PRO
9	F	149	GLU
10	G	17	PHE
10	G	20	PRO
11	H	135	LEU
13	J	24	LEU
13	J	27	GLU
4	A	276	LEU
4	A	492	PRO
4	A	598	LEU
4	A	649	ILE
4	A	756	ILE
4	A	1006	ILE
4	A	1057	VAL
4	A	1377	THR
5	B	261	ARG
5	B	844	SER
5	B	1082	MET
6	C	89	GLU
10	G	34	VAL
12	I	32	CYS
4	A	38	PRO

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Mol	Chain	Res	Type
4	A	96	ILE
5	B	23	ALA
5	B	295	GLY
5	B	410	GLY
5	B	478	GLY
5	B	520	GLY
5	B	551	PRO
5	B	1018	PRO
5	B	1099	VAL
6	C	77	ILE
4	A	84	ILE
4	A	196	GLU
4	A	1158	PRO
5	B	575	PRO
5	B	613	VAL
6	C	10	ILE
4	A	396	PRO
4	A	653	VAL
4	A	1384	VAL
4	A	1454	MET
5	B	283	VAL
5	B	712	PRO
5	B	824	ILE
6	C	172	PRO
10	G	19	GLY
15	L	46	VAL
4	A	1060	PRO
7	D	202	ILE
4	A	73	GLY
4	A	321	PRO
4	A	1406	VAL
5	B	611	PRO
5	B	758	PHE
8	E	129	PRO

5.3.2 Protein sidechains ⓘ

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	
4	A	1239/1520 (82%)	1121 (90%)	118 (10%)	8	28
5	B	964/1061 (91%)	874 (91%)	90 (9%)	8	29
6	C	234/274 (85%)	216 (92%)	18 (8%)	12	35
7	D	140/200 (70%)	118 (84%)	22 (16%)	2	15
8	E	196/197 (100%)	188 (96%)	8 (4%)	27	49
9	F	74/137 (54%)	65 (88%)	9 (12%)	5	21
10	G	152/152 (100%)	137 (90%)	15 (10%)	7	27
11	H	117/128 (91%)	110 (94%)	7 (6%)	17	42
12	I	113/116 (97%)	101 (89%)	12 (11%)	6	24
13	J	60/65 (92%)	56 (93%)	4 (7%)	15	39
14	K	99/102 (97%)	91 (92%)	8 (8%)	11	34
15	L	40/57 (70%)	38 (95%)	2 (5%)	22	45
All	All	3428/4009 (86%)	3115 (91%)	313 (9%)	9	30

All (313) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	2	VAL
4	A	11	LEU
4	A	22	PHE
4	A	34	LYS
4	A	38	PRO
4	A	62	ASP
4	A	67	CYS
4	A	93	VAL
4	A	105	CYS
4	A	108	MET
4	A	208	LEU
4	A	215	SER
4	A	221	SER
4	A	236	LEU
4	A	245	PRO
4	A	270	LEU
4	A	289	ILE
4	A	293	GLU
4	A	302	THR
4	A	312	PRO
4	A	320	ARG
4	A	321	PRO

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Mol	Chain	Res	Type
4	A	335	ARG
4	A	345	VAL
4	A	350	ARG
4	A	354	SER
4	A	381	THR
4	A	385	ILE
4	A	396	PRO
4	A	404	TYR
4	A	406	ILE
4	A	407	ARG
4	A	408	ASP
4	A	418	SER
4	A	425	GLN
4	A	443	LEU
4	A	445	ASN
4	A	449	SER
4	A	450	LEU
4	A	451	HIS
4	A	454	SER
4	A	460	VAL
4	A	461	LYS
4	A	462	VAL
4	A	469	ARG
4	A	493	GLN
4	A	497	THR
4	A	498	ARG
4	A	503	GLN
4	A	515	GLN
4	A	524	VAL
4	A	525	GLN
4	A	560	ILE
4	A	562	THR
4	A	576	GLN
4	A	598	LEU
4	A	616	VAL
4	A	629	LEU
4	A	659	HIS
4	A	666	ILE
4	A	670	ILE
4	A	711	ARG
4	A	768	GLN
4	A	774	ARG

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Mol	Chain	Res	Type
4	A	779	PHE
4	A	821	ARG
4	A	827	THR
4	A	831	THR
4	A	834	THR
4	A	845	LEU
4	A	854	ASN
4	A	858	ASN
4	A	871	ASP
4	A	886	ILE
4	A	890	ASP
4	A	903	ASN
4	A	907	THR
4	A	919	ILE
4	A	929	LEU
4	A	949	ASP
4	A	969	GLN
4	A	1006	ILE
4	A	1016	THR
4	A	1029	ARG
4	A	1030	ARG
4	A	1035	TYR
4	A	1067	LEU
4	A	1110	ASN
4	A	1111	MET
4	A	1116	LEU
4	A	1122	PRO
4	A	1127	ASP
4	A	1152	ILE
4	A	1155	ASP
4	A	1170	ILE
4	A	1173	HIS
4	A	1193	LEU
4	A	1264	GLU
4	A	1271	ILE
4	A	1276	VAL
4	A	1291	VAL
4	A	1295	THR
4	A	1299	VAL
4	A	1300	LYS
4	A	1309	ASP
4	A	1325	THR

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Mol	Chain	Res	Type
4	A	1329	THR
4	A	1332	PHE
4	A	1333	ILE
4	A	1359	ASP
4	A	1372	VAL
4	A	1386	ARG
4	A	1394	THR
4	A	1405	THR
4	A	1432	GLN
4	A	1443	VAL
4	A	1445	ILE
4	A	1447	GLU
5	B	30	SER
5	B	44	VAL
5	B	57	TYR
5	B	175	ARG
5	B	188	ASP
5	B	194	GLU
5	B	223	VAL
5	B	225	VAL
5	B	261	ARG
5	B	268	THR
5	B	294	ASP
5	B	298	LEU
5	B	323	VAL
5	B	365	THR
5	B	371	GLU
5	B	378	LEU
5	B	393	LYS
5	B	396	ASP
5	B	399	ASP
5	B	401	PHE
5	B	411	PRO
5	B	427	ASP
5	B	429	PHE
5	B	463	THR
5	B	465	ASN
5	B	466	TRP
5	B	476	ARG
5	B	487	THR
5	B	496	ARG
5	B	498	THR

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Mol	Chain	Res	Type
5	B	502	ILE
5	B	513	GLN
5	B	516	ASN
5	B	555	ILE
5	B	557	PHE
5	B	570	VAL
5	B	582	VAL
5	B	593	PRO
5	B	603	LEU
5	B	615	MET
5	B	628	THR
5	B	635	ARG
5	B	636	PRO
5	B	644	GLU
5	B	649	LYS
5	B	682	SER
5	B	701	ILE
5	B	724	ASP
5	B	737	THR
5	B	742	GLU
5	B	748	ILE
5	B	751	VAL
5	B	830	TYR
5	B	835	GLN
5	B	839	MET
5	B	858	SER
5	B	860	MET
5	B	878	GLN
5	B	901	PRO
5	B	909	ASP
5	B	953	LEU
5	B	999	MET
5	B	1002	THR
5	B	1006	ILE
5	B	1010	LEU
5	B	1018	PRO
5	B	1034	VAL
5	B	1047	PHE
5	B	1051	THR
5	B	1069	PHE
5	B	1071	VAL
5	B	1077	THR

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Mol	Chain	Res	Type
5	B	1084	GLN
5	B	1095	LEU
5	B	1099	VAL
5	B	1103	ILE
5	B	1119	VAL
5	B	1120	GLU
5	B	1122	ARG
5	B	1159	ARG
5	B	1160	VAL
5	B	1163	CYS
5	B	1169	MET
5	B	1170	THR
5	B	1176	ASN
5	B	1183	LYS
5	B	1191	ILE
5	B	1202	LEU
5	B	1212	ILE
5	B	1216	LEU
6	C	22	LEU
6	C	29	MET
6	C	54	ASN
6	C	57	VAL
6	C	58	LEU
6	C	77	ILE
6	C	89	GLU
6	C	106	GLU
6	C	108	GLU
6	C	140	ASN
6	C	147	LEU
6	C	166	GLU
6	C	195	GLN
6	C	202	PRO
6	C	233	GLU
6	C	240	VAL
6	C	259	LEU
6	C	266	ASP
7	D	32	GLU
7	D	47	LEU
7	D	61	GLU
7	D	63	LEU
7	D	70	PHE
7	D	120	GLU

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Mol	Chain	Res	Type
7	D	124	GLU
7	D	126	ILE
7	D	137	ASN
7	D	139	LYS
7	D	148	LEU
7	D	149	THR
7	D	152	SER
7	D	156	ASP
7	D	170	THR
7	D	177	VAL
7	D	182	SER
7	D	187	THR
7	D	192	LYS
7	D	193	THR
7	D	202	ILE
7	D	208	GLU
8	E	60	PHE
8	E	74	ASP
8	E	78	LEU
8	E	114	ASN
8	E	175	LEU
8	E	183	PRO
8	E	207	ARG
8	E	215	MET
9	F	79	ARG
9	F	81	THR
9	F	90	ARG
9	F	99	LEU
9	F	103	MET
9	F	119	ARG
9	F	132	LEU
9	F	148	VAL
9	F	153	VAL
10	G	1	MET
10	G	13	LEU
10	G	17	PHE
10	G	38	CYS
10	G	49	LEU
10	G	63	PRO
10	G	74	TYR
10	G	78	VAL
10	G	80	LYS

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Mol	Chain	Res	Type
10	G	88	ASP
10	G	93	SER
10	G	96	GLN
10	G	115	MET
10	G	126	ASN
10	G	171	ILE
11	H	26	ILE
11	H	62	SER
11	H	86	ASP
11	H	93	TYR
11	H	102	TYR
11	H	130	ARG
11	H	143	LEU
12	I	8	ARG
12	I	9	ASP
12	I	13	MET
12	I	15	TYR
12	I	31	THR
12	I	75	CYS
12	I	85	PHE
12	I	86	PHE
12	I	94	ASP
12	I	100	PHE
12	I	101	PHE
12	I	106	CYS
13	J	1	MET
13	J	9	SER
13	J	44	TYR
13	J	46	CYS
14	K	5	ASP
14	K	10	PHE
14	K	25	THR
14	K	47	ARG
14	K	50	LEU
14	K	61	TYR
14	K	78	THR
14	K	114	LEU
15	L	55	ILE
15	L	68	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	5	GLN
4	A	68	GLN
4	A	71	GLN
4	A	83	HIS
4	A	209	ASN
4	A	213	HIS
4	A	225	ASN
4	A	256	GLN
4	A	287	HIS
4	A	299	HIS
4	A	306	ASN
4	A	316	GLN
4	A	427	GLN
4	A	435	HIS
4	A	445	ASN
4	A	479	ASN
4	A	493	GLN
4	A	503	GLN
4	A	517	ASN
4	A	525	GLN
4	A	611	GLN
4	A	654	ASN
4	A	698	GLN
4	A	706	HIS
4	A	741	ASN
4	A	757	ASN
4	A	767	GLN
4	A	768	GLN
4	A	786	HIS
4	A	838	GLN
4	A	858	ASN
4	A	865	GLN
4	A	903	ASN
4	A	926	GLN
4	A	1009	ASN
4	A	1040	GLN
4	A	1070	GLN
4	A	1130	GLN
4	A	1140	HIS
4	A	1187	GLN
4	A	1222	ASN
4	A	1265	ASN
4	A	1364	ASN

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Mol	Chain	Res	Type
4	A	1378	GLN
4	A	1387	HIS
4	A	1432	GLN
5	B	178	ASN
5	B	236	HIS
5	B	350	GLN
5	B	363	HIS
5	B	366	GLN
5	B	383	ASN
5	B	465	ASN
5	B	484	ASN
5	B	515	HIS
5	B	516	ASN
5	B	518	HIS
5	B	538	ASN
5	B	734	HIS
5	B	744	HIS
5	B	776	GLN
5	B	821	GLN
5	B	842	ASN
5	B	951	GLN
5	B	975	GLN
5	B	1015	HIS
5	B	1065	GLN
5	B	1076	HIS
5	B	1084	GLN
5	B	1097	HIS
5	B	1117	GLN
5	B	1179	GLN
5	B	1193	GLN
6	C	65	HIS
6	C	73	GLN
6	C	91	HIS
6	C	112	ASN
6	C	123	ASN
6	C	140	ASN
6	C	231	ASN
6	C	252	GLN
7	D	40	HIS
7	D	132	GLN
7	D	137	ASN
7	D	157	GLN

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Mol	Chain	Res	Type
7	D	216	ASN
8	E	8	ASN
8	E	63	ASN
8	E	101	GLN
8	E	104	ASN
8	E	114	ASN
8	E	147	HIS
10	G	14	HIS
10	G	53	ASN
10	G	96	GLN
10	G	97	HIS
10	G	126	ASN
10	G	153	GLN
12	I	11	ASN
12	I	12	ASN
12	I	60	GLN
12	I	89	GLN
13	J	64	ASN
14	K	44	ASN
14	K	65	HIS
14	K	76	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	P	9/10 (90%)	1 (11%)	1 (11%)

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	P	3	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	P	2	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	T	18/19 (94%)	-0.43	0 100 100	69, 103, 131, 137	0
2	N	6/7 (85%)	-0.48	0 100 100	97, 99, 108, 108	0
3	P	10/10 (100%)	-0.90	0 100 100	80, 94, 125, 127	0
4	A	1416/1733 (81%)	-1.00	0 100 100	21, 75, 151, 195	0
5	B	1112/1224 (90%)	-0.97	0 100 100	20, 87, 156, 186	0
6	C	266/318 (83%)	-1.06	0 100 100	34, 71, 130, 150	0
7	D	177/221 (80%)	-1.00	0 100 100	43, 99, 137, 155	0
8	E	214/215 (99%)	-0.96	0 100 100	47, 132, 177, 181	0
9	F	84/155 (54%)	-1.11	0 100 100	21, 49, 93, 113	0
10	G	171/171 (100%)	-1.05	0 100 100	47, 76, 106, 122	0
11	H	133/146 (91%)	-0.84	0 100 100	91, 130, 165, 175	0
12	I	119/122 (97%)	-0.87	0 100 100	63, 122, 153, 191	0
13	J	65/70 (92%)	-1.10	0 100 100	37, 69, 113, 118	0
14	K	114/120 (95%)	-1.11	0 100 100	37, 75, 104, 118	0
15	L	46/70 (65%)	-0.88	0 100 100	73, 127, 160, 168	0
All	All	3951/4601 (85%)	-0.99	0 100 100	20, 84, 156, 195	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
16	ZN	A	1734	1/1	1.00	0.02	73,73,73,73	0
16	ZN	A	1735	1/1	1.00	0.01	36,36,36,36	0
16	ZN	B	1307	1/1	1.00	0.01	31,31,31,31	0
16	ZN	C	319	1/1	1.00	0.01	28,28,28,28	0
16	ZN	I	203	1/1	1.00	0.01	80,80,80,80	0
16	ZN	I	204	1/1	1.00	0.02	141,141,141,141	0
16	ZN	J	101	1/1	1.00	0.02	45,45,45,45	0
16	ZN	L	105	1/1	1.00	0.01	90,90,90,90	0
17	MG	A	1736	1/1	1.00	0.02	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.