



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:53 AM UTC

PDB ID : 7ML4 / pdb_00007ml4
EMDB ID : EMD-23908
Title : RNA polymerase II initially transcribing complex (ITC)
Authors : Yang, C.; Fujiwara, R.; Kim, H.J.; Gorbea Colon, J.J.; Steimle, S.; Garcia, B.A.; Murakami, K.
Deposited on : 2021-04-27
Resolution : 3.10 Å(reported)
Based on initial model : 5OQJ

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

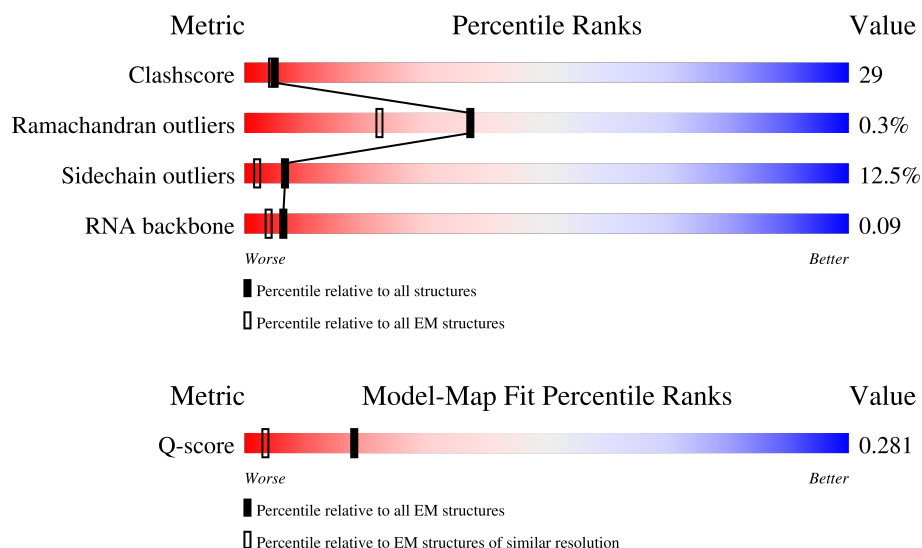
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	Q	735	
2	R	398	
3	D	221	

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Mol	Chain	Length	Quality of chain
4	G	171	
5	M	345	
6	A	1733	
7	B	1224	
8	C	318	
9	E	215	
10	F	155	
11	H	146	
12	I	122	
13	J	70	
14	K	120	
15	L	70	
16	3	321	
17	0	778	
18	4	338	
19	6	461	
20	1	543	
21	7	843	
22	5	72	
23	2	513	
24	X	328	
25	U	286	
26	V	122	
27	N	38	
28	T	148	

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Mol	Chain	Length	Quality of chain
29	O	240	
30	W	482	
31	P	5	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	SF4	0	801	-	-	X	-

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 62733 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Transcription initiation factor IIF subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Q	148	Total	C	N	O	S	0	0
			1141	731	195	212	3		

- Molecule 2 is a protein called Transcription initiation factor IIF subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	154	Total	C	N	O	S	0	0
			1039	652	190	193	4		

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	157	Total	C	N	O	S	0	0
			1253	779	220	252	2		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB7.

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

- Molecule 5 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	234	Total	C	N	O	S	0	0
			1805	1152	304	333	16		

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1405	Total	C	N	O	S	0	0
			11039	6962	1935	2081	61		

- Molecule 7 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	1114	Total	C	N	O	S	0	0
			8861	5610	1549	1647	55		

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB3.

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

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

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

- Molecule 10 is a protein called DNA-directed RNA polymerases I,II,and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	85	Total	C	N	O	S	0	0
			688	439	116	130	3		

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB9.

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

- Molecule 13 is a protein called DNA-directed RNA polymerases II subunit RPABC5.

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

- Molecule 14 is a protein called DNA-directed RNA polymerase II subunit RPB11.

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

- Molecule 15 is a protein called DNA-directed RNA polymerases II subunit RPABC4.

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

- Molecule 16 is a protein called BJ4_G0050160.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3	72	Total	C	N	O	S	0	0
			361	215	72	74			

- Molecule 17 is a protein called General transcription and DNA repair factor IIIH helicase subunit XPD.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	0	754	Total	C	N	O	S	0	0
			6108	3891	1032	1147	38		

- Molecule 18 is a protein called General transcription and DNA repair factor IIIH subunit TFB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	4	284	Total	C	N	O	S	0	0
			2041	1310	343	376	12		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	113	UNK	ASP	conflict	UNP A0A7I9C5C2
4	114	UNK	MET	conflict	UNP A0A7I9C5C2

- Molecule 19 is a protein called General transcription and DNA repair factor IIIH.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	6	351	Total	C	N	O	S	0	0
			2527	1590	454	456	27		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	412	UNK	ILE	conflict	UNP A0A7I9FQL5
6	413	UNK	LEU	conflict	UNP A0A7I9FQL5
6	414	UNK	LYS	conflict	UNP A0A7I9FQL5
6	415	UNK	ASN	conflict	UNP A0A7I9FQL5
6	416	UNK	HIS	conflict	UNP A0A7I9FQL5
6	417	UNK	LYS	conflict	UNP A0A7I9FQL5
6	418	UNK	ASN	conflict	UNP A0A7I9FQL5
6	419	UNK	ASP	conflict	UNP A0A7I9FQL5
6	420	UNK	LYS	conflict	UNP A0A7I9FQL5
6	421	UNK	LEU	conflict	UNP A0A7I9FQL5
6	422	UNK	LEU	conflict	UNP A0A7I9FQL5
6	423	UNK	THR	conflict	UNP A0A7I9FQL5
6	424	UNK	SER	conflict	UNP A0A7I9FQL5

- Molecule 20 is a protein called Tfb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	1	367	Total	C	N	O	S	0	0
			2411	1536	438	430	7		

- Molecule 21 is a protein called General transcription and DNA repair factor IIH helicase subunit XPB.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	7	634	Total	C	N	O	S	0	0
			4447	2722	827	874	24		

- Molecule 22 is a protein called General transcription and DNA repair factor IIH subunit TFB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	66	Total	C	N	O	S	0	0
			498	314	89	93	2		

- Molecule 23 is a protein called RNA polymerase II transcription factor B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	460	Total	C	N	O	S	0	0
			3011	1856	562	584	9		

- Molecule 24 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	149	Total	C	N	O	S	0	0
			921	569	168	180	4		

- Molecule 25 is a protein called Transcription initiation factor IIA large subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	46	Total	C	N	O	S	0	0
			383	242	67	71	3		

- Molecule 26 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	49	Total	C	N	O	S	0	0
			381	241	63	74	3		

- Molecule 27 is a DNA chain called non-template strand DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	N	38	Total	C	N	O	P	0	0
			791	376	161	216	38		

- Molecule 28 is a DNA chain called template strand DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	48	Total	C	N	O	P	0	0
			968	468	150	302	48		

- Molecule 29 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	O	180	Total	C	N	O	S	0	0
			1416	921	242	247	6		

- Molecule 30 is a protein called Transcription initiation factor IIE subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	191	Total	C	N	O	S	0	0
			1469	932	254	277	6		

- Molecule 31 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	P	5	Total	C	N	O	P	0	0
			110	50	25	31	4		

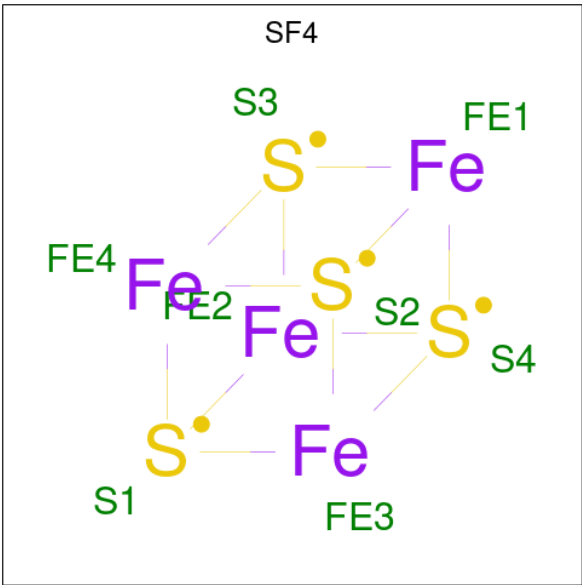
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	M	1	Total	Zn	0
			1	1	
32	A	2	Total	Zn	0
			2	2	
32	B	1	Total	Zn	0
			1	1	
32	C	1	Total	Zn	0
			1	1	
32	I	2	Total	Zn	0
			2	2	
32	J	1	Total	Zn	0
			1	1	
32	L	1	Total	Zn	0
			1	1	
32	4	1	Total	Zn	0
			1	1	
32	6	4	Total	Zn	0
			4	4	
32	W	1	Total	Zn	0
			1	1	

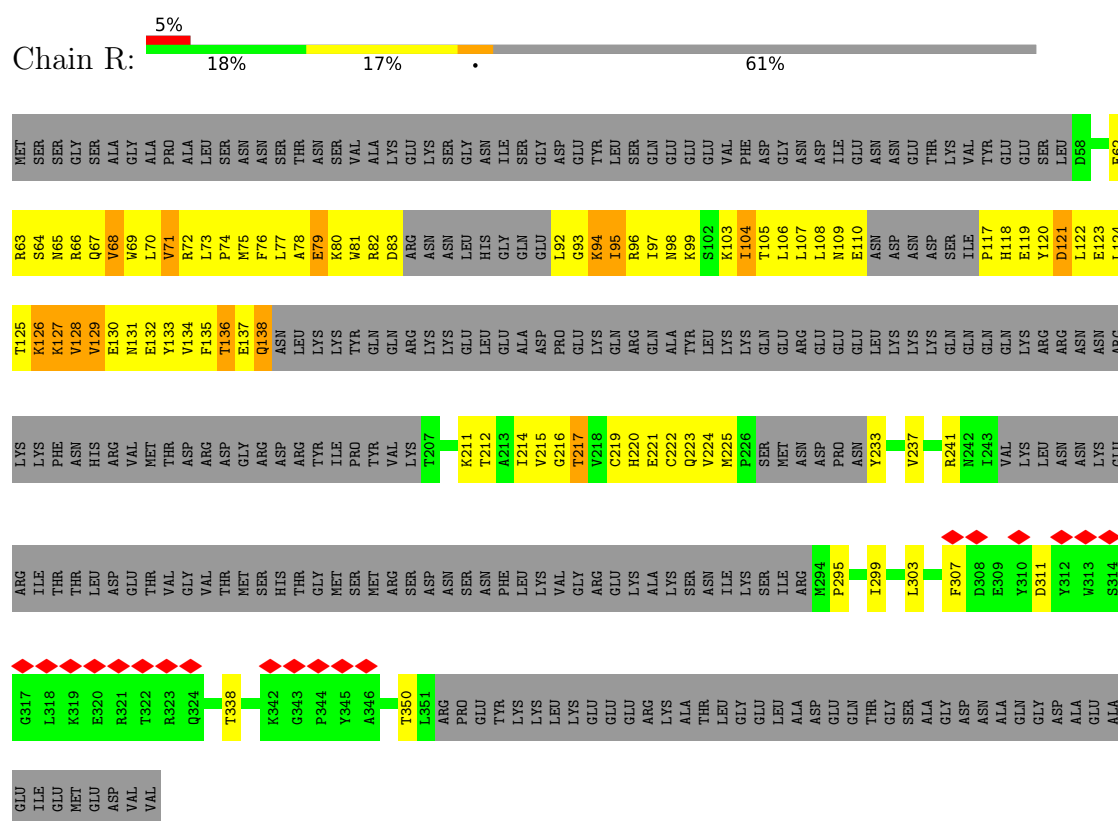
- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	A	1	Total	Mg	0
			1	1	

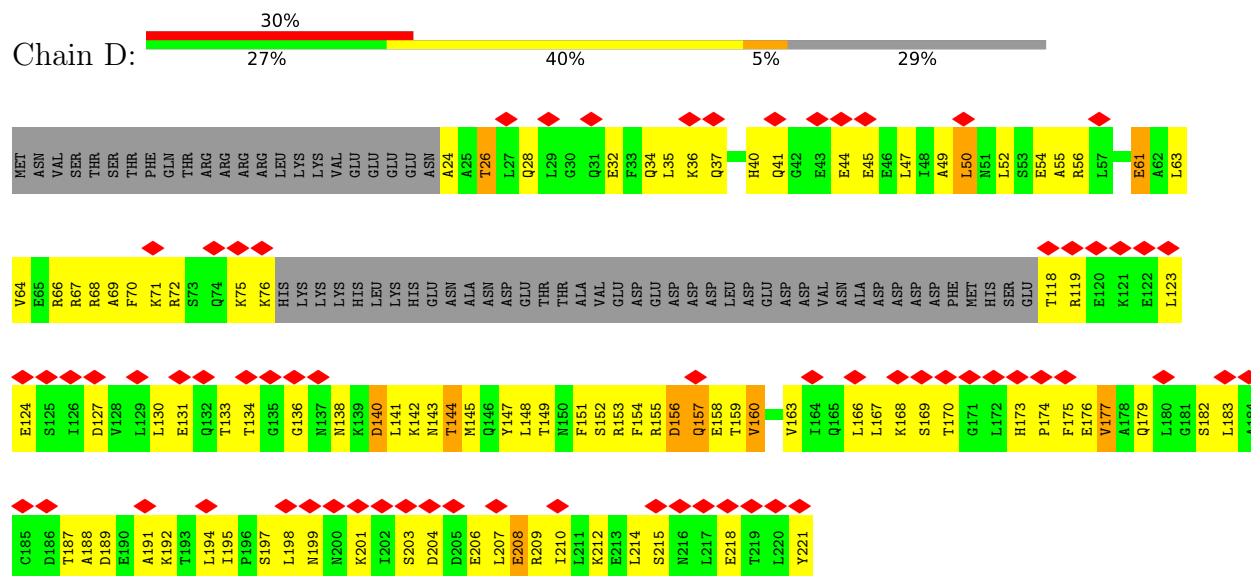
- Molecule 34 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



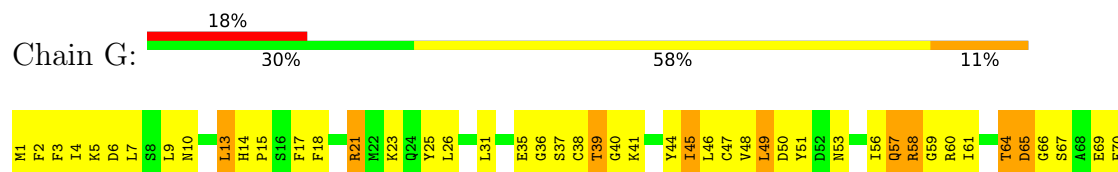
Mol	Chain	Residues	Atoms			AltConf
34	0	1	Total	Fe	S	0
			8	4	4	

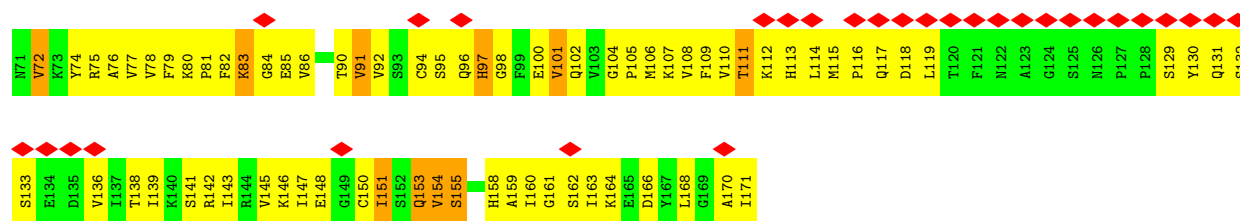


• Molecule 3: DNA-directed RNA polymerase II subunit RPB4

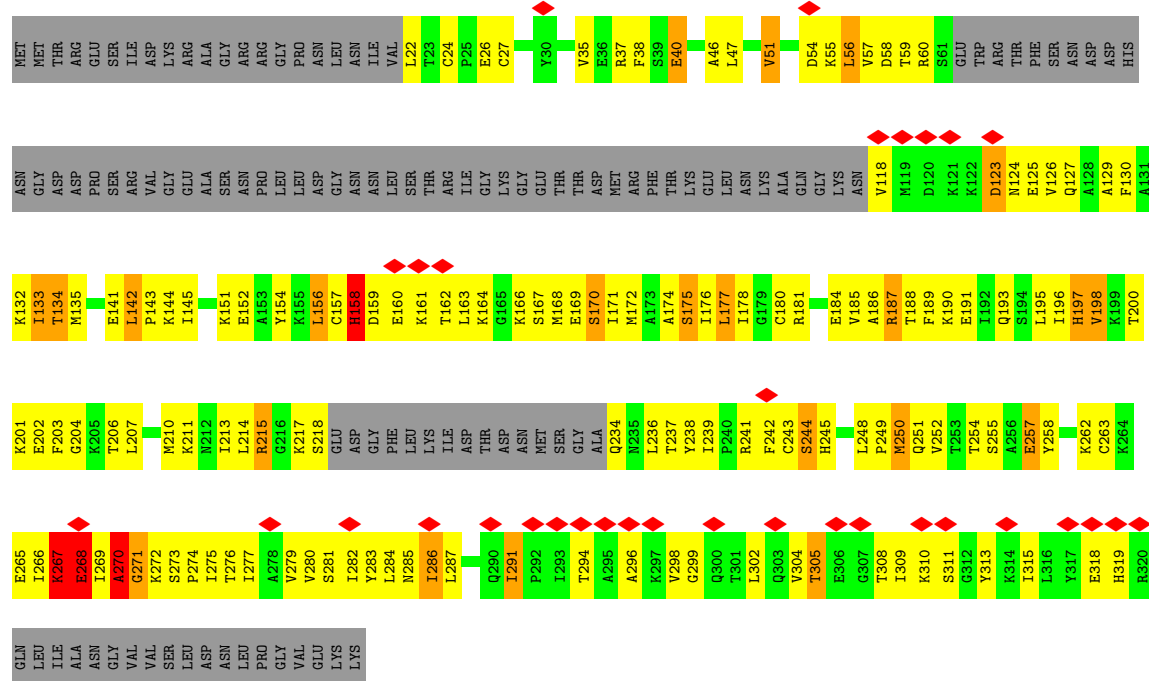
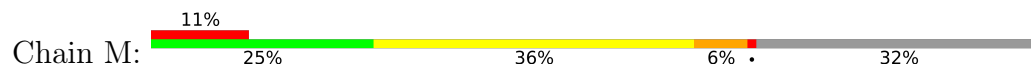


• Molecule 4: DNA-directed RNA polymerase II subunit RPB7

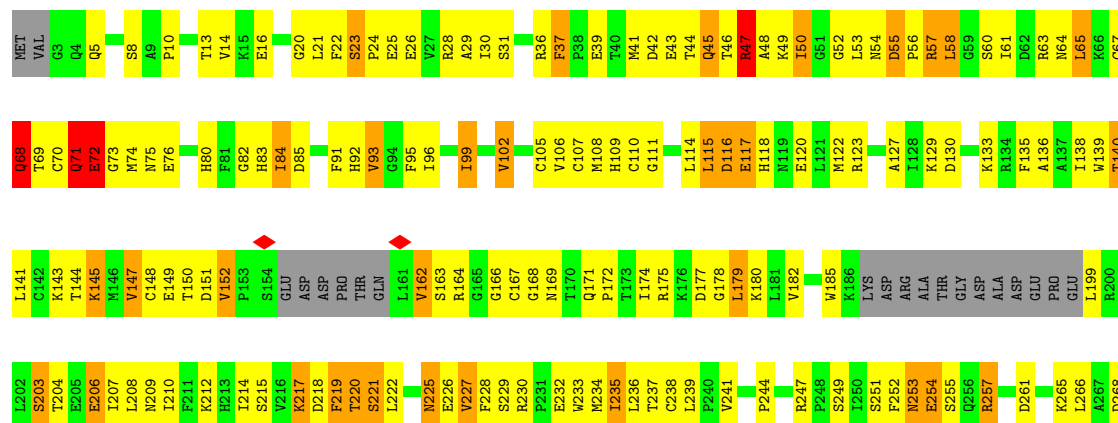




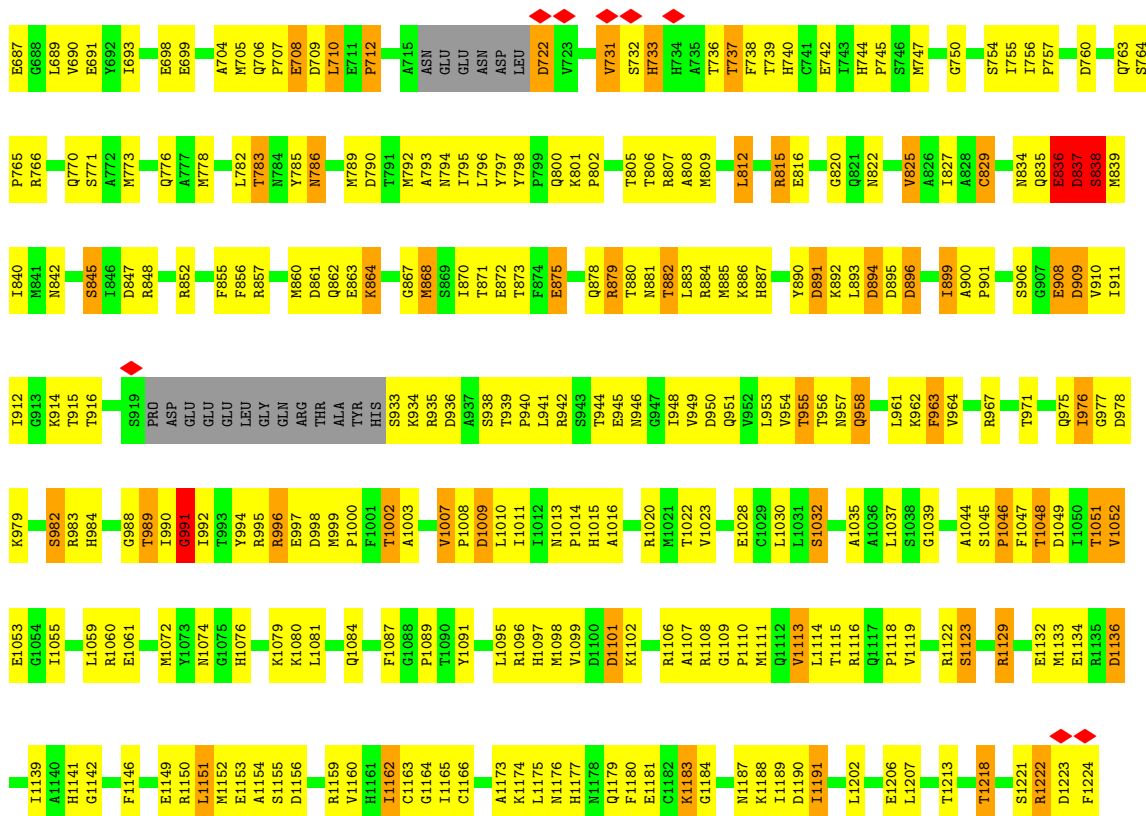
• Molecule 5: Transcription initiation factor IIB



• Molecule 6: DNA-directed RNA polymerase subunit

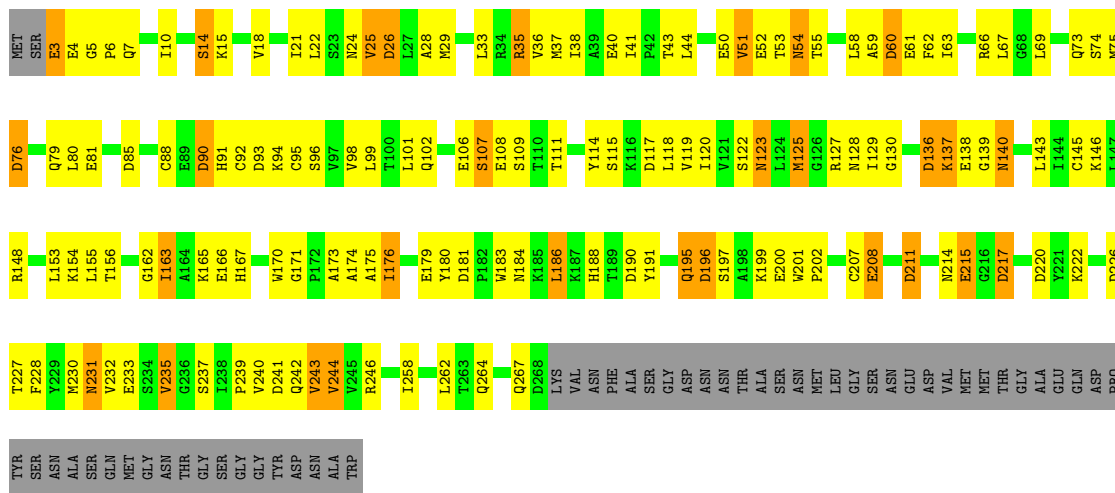






• Molecule 8: DNA-directed RNA polymerase II subunit RPB3

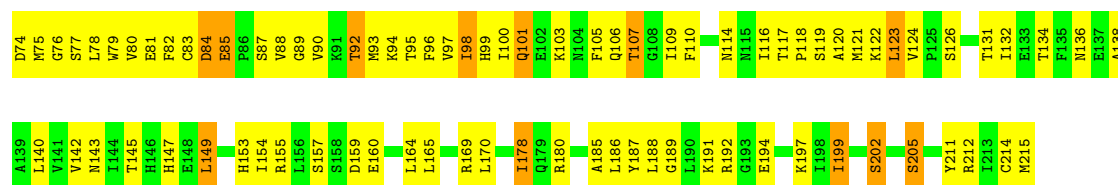
Chain C: 38% 37% 9% 16%



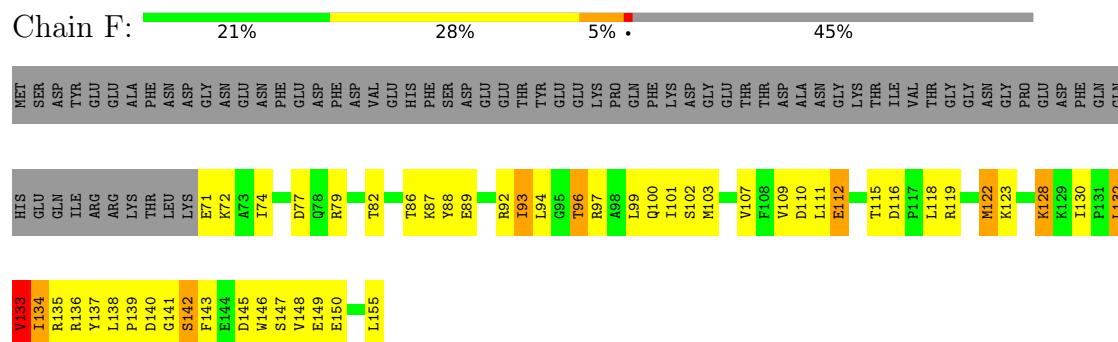
• Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 39% 51% 10%

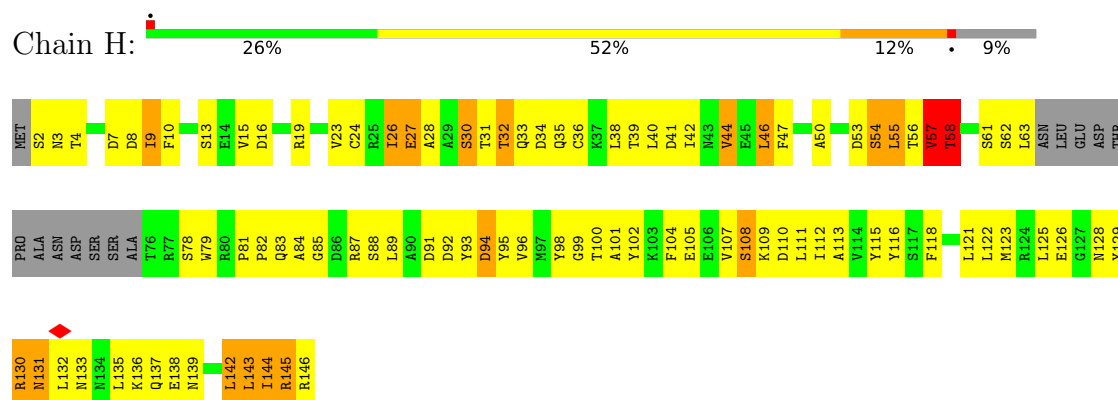




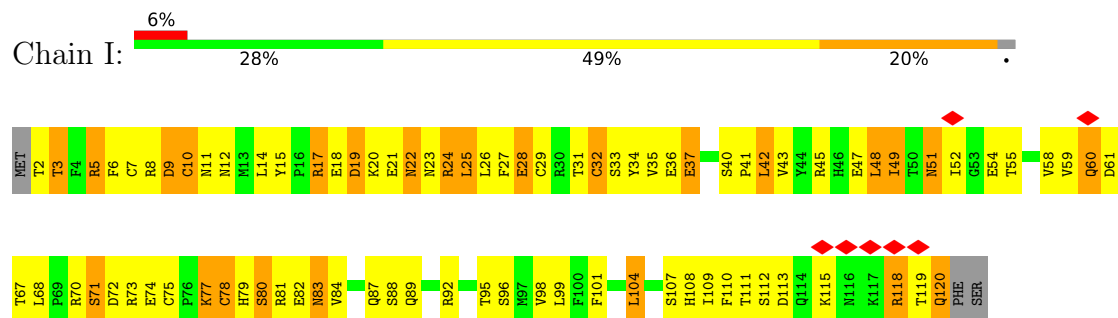
• Molecule 10: DNA-directed RNA polymerases I,II,and III subunit RPABC2



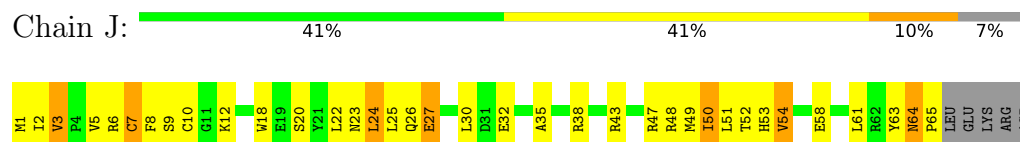
• Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC3

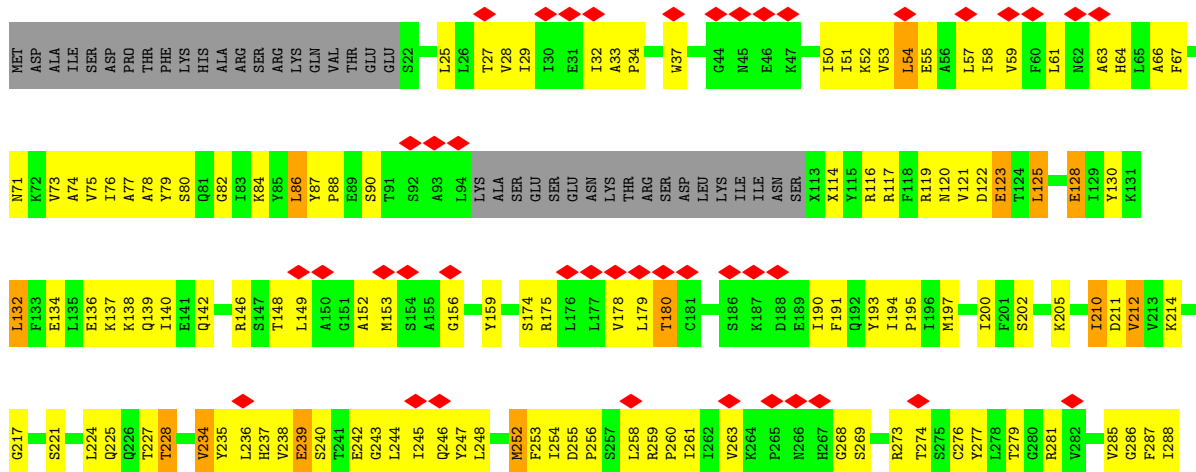


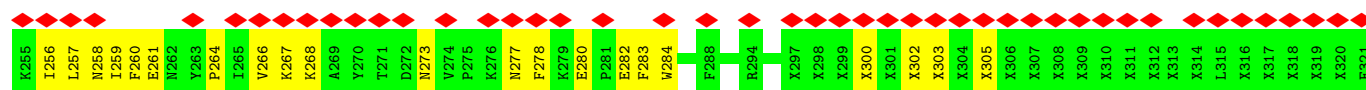
• Molecule 12: DNA-directed RNA polymerase II subunit RPB9

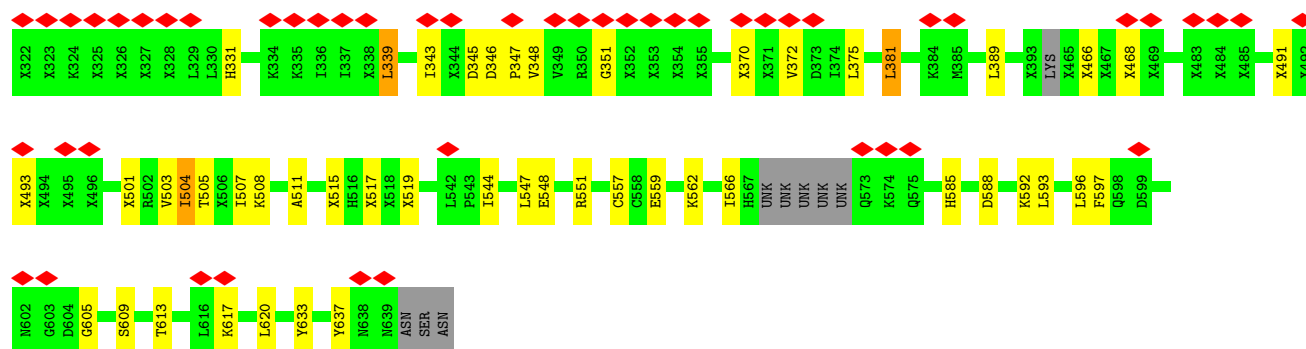


• Molecule 13: DNA-directed RNA polymerases II subunit RPABC5

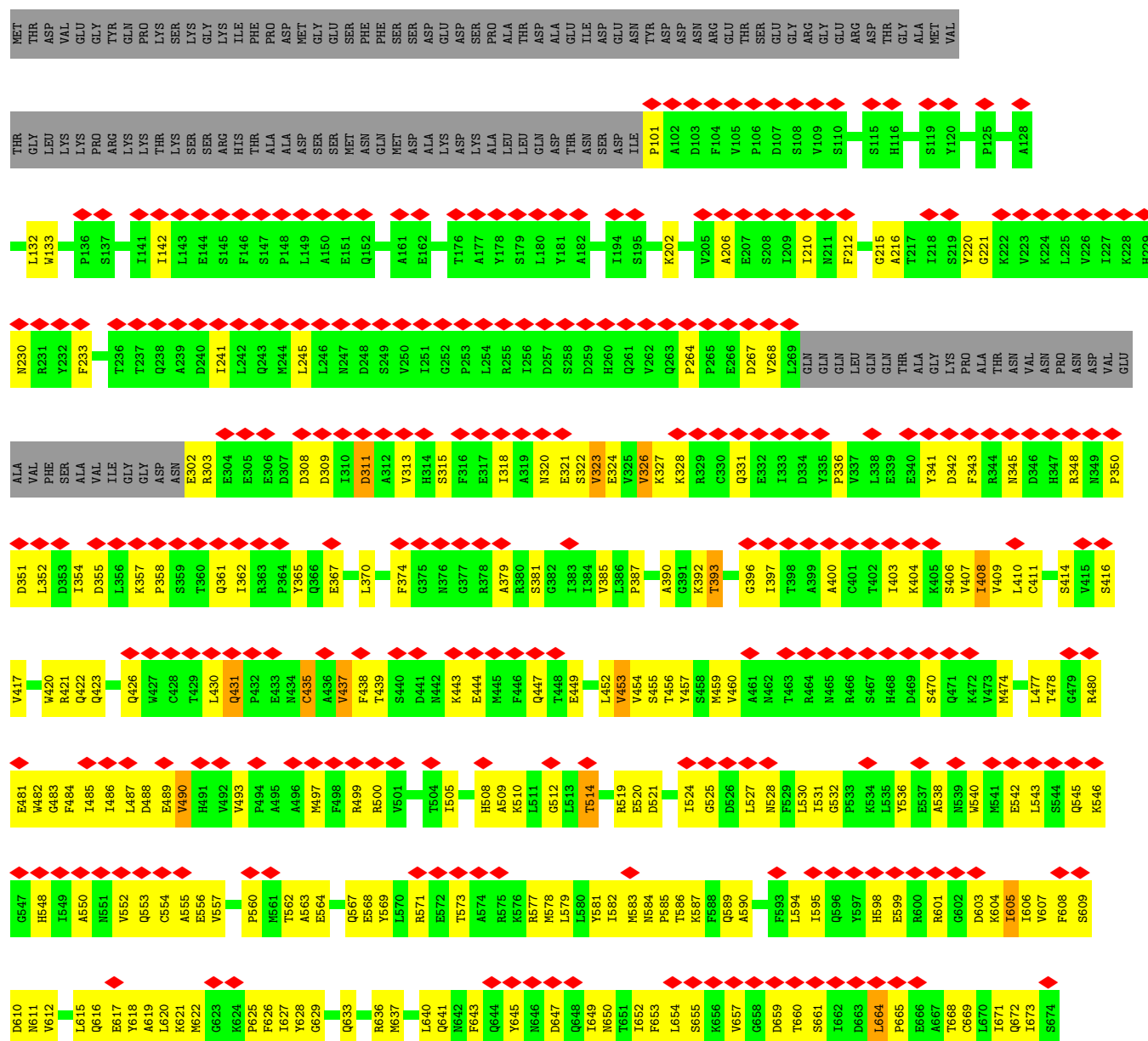






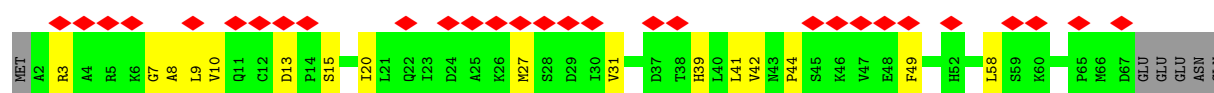
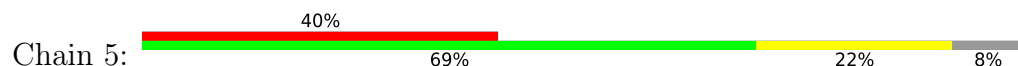


• Molecule 21: General transcription and DNA repair factor IIH helicase subunit XPB

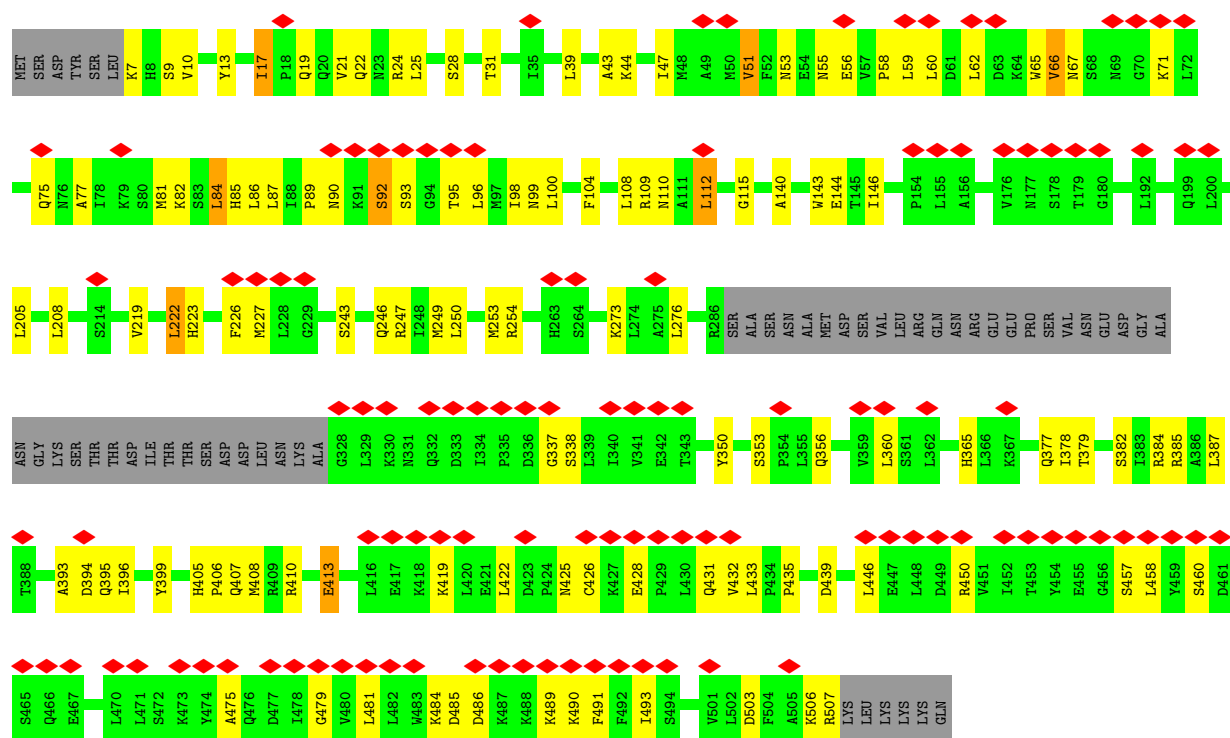




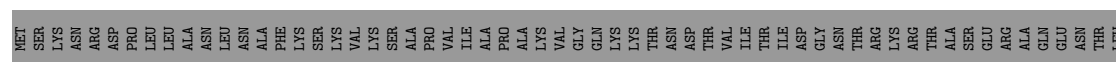
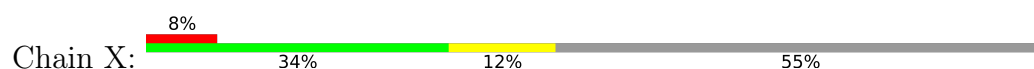
- Molecule 22: General transcription and DNA repair factor IIH subunit TFB5

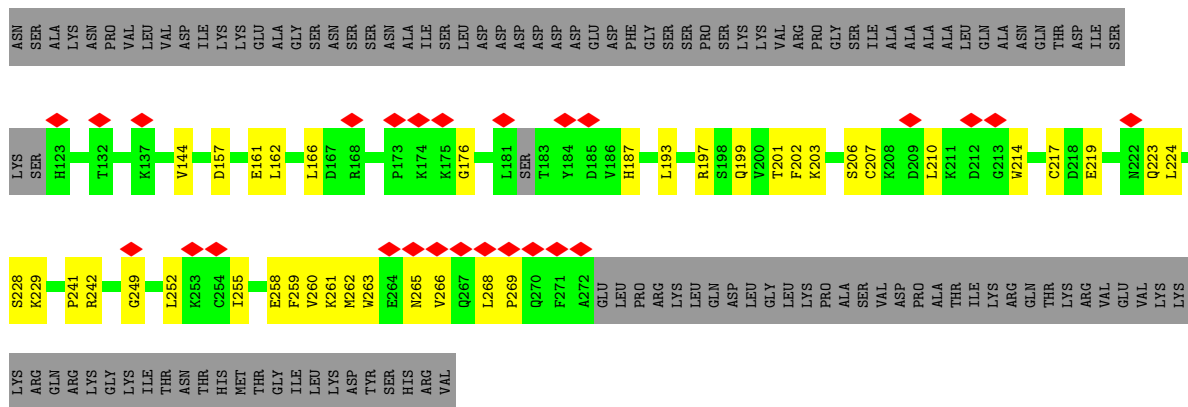


- Molecule 23: RNA polymerase II transcription factor B subunit 2

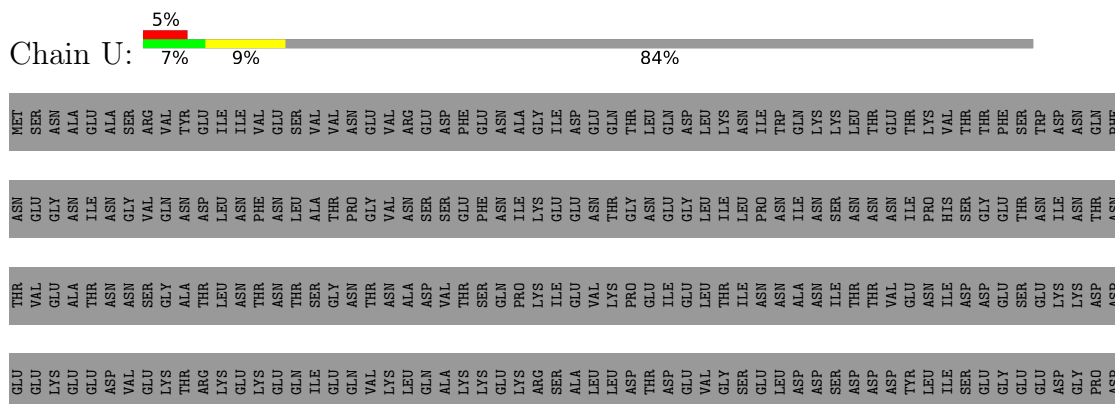


- Molecule 24: Transcription initiation factor IIE subunit beta

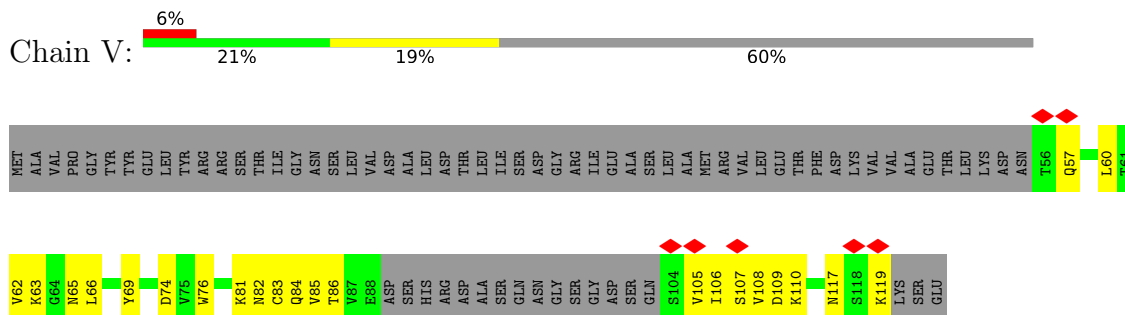




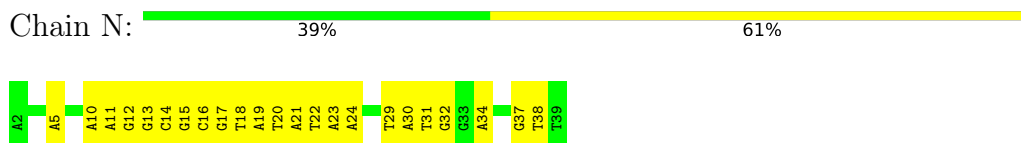
- Molecule 25: Transcription initiation factor IIA large subunit



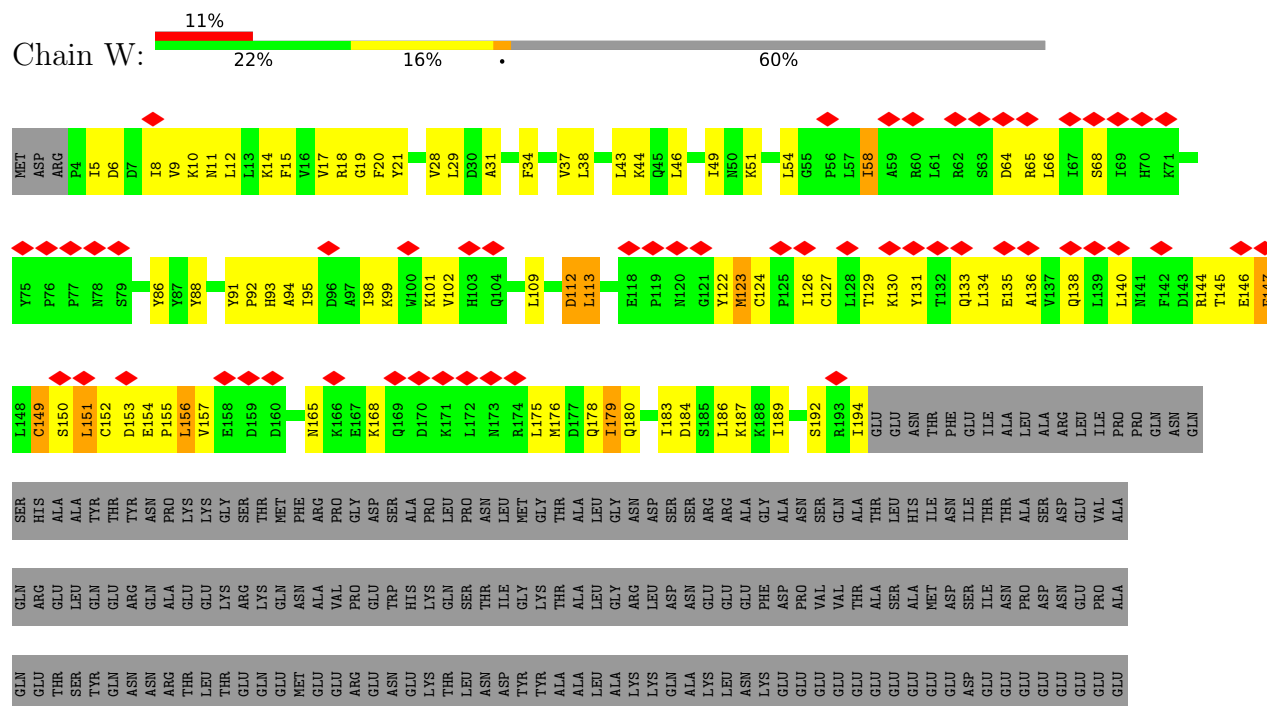
- Molecule 26: Transcription initiation factor IIA subunit 2



- Molecule 27: non-template strand DNA



- Molecule 28: template strand DNA



MET
GLY
ASP
VAL
SER
MET
ALA
ASP
ASP
ASN
GLU
THR
ALA
ARG
GLU
ASN
ALA
LEU
GLU
ASP
GLU
PHE
GLU
MET
ASP
VAL
THR
ASP
GLY
THR
ALA
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SER
GLY
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ALA
LYS
PRO
ASN
ASP
GLY
ASP
ASP
ASP
ASP
ASP
PHE
GLU
MET
MET
ILE
GLU
PHE
GLU
ASP
VAL

● Molecule 31: RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	254448	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.057	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	444.13998, 503.49997, 508.8	wwPDB
Map dimensions	419, 475, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, SF4

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	Q	0.42	0/1165	0.57	0/1576
2	R	0.30	0/1047	0.51	0/1422
3	D	0.28	0/1262	0.48	0/1693
4	G	0.50	0/1368	0.56	0/1844
5	M	0.37	0/1828	0.57	5/2459 (0.2%)
6	A	1.02	2/11237 (0.0%)	0.82	11/15195 (0.1%)
7	B	1.10	1/9033 (0.0%)	0.80	4/12181 (0.0%)
8	C	0.98	0/2133	0.74	0/2891
9	E	0.91	0/1788	0.69	0/2406
10	F	1.14	0/700	0.91	0/945
11	H	0.90	0/1086	0.84	3/1470 (0.2%)
12	I	0.72	0/989	0.67	0/1331
13	J	1.12	0/541	0.88	0/727
14	K	0.97	0/937	0.66	0/1265
15	L	0.78	0/365	0.84	0/485
16	3	0.13	0/360	0.30	0/501
17	0	0.14	0/6226	0.37	1/8407 (0.0%)
18	4	0.16	0/2062	0.41	2/2805 (0.1%)
19	6	0.14	0/2506	0.36	0/3402
20	1	0.13	0/1896	0.32	0/2543
21	7	0.13	0/4521	0.34	0/6036
22	5	0.12	0/502	0.30	0/677
23	2	0.12	0/3057	0.34	0/4071
24	X	0.15	0/929	0.41	0/1272
25	U	0.15	0/389	0.40	0/523
26	V	0.16	0/384	0.30	0/518
27	N	0.34	0/893	1.02	0/1377
28	T	0.37	0/1076	1.15	2/1654 (0.1%)
29	O	0.19	0/1443	0.38	0/1942
30	W	0.18	0/1490	0.41	0/2014
31	P	0.54	0/124	1.37	1/193 (0.5%)
All	All	0.71	3/63337 (0.0%)	0.65	29/85825 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Q	0	1
4	G	0	1
5	M	0	3
6	A	0	9
7	B	0	5
10	F	0	1
11	H	0	3
All	All	0	23

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	687	GLU	CA-C	-8.99	1.40	1.52
6	A	786	HIS	CA-C	-8.31	1.37	1.52
6	A	512	VAL	C-N	-5.70	1.21	1.33

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	P	9	G	N9-C1'-C2'	6.36	121.54	112.00
6	A	1123	GLY	CA-C-N	6.28	133.01	121.70
6	A	1123	GLY	C-N-CA	6.28	133.01	121.70
5	M	268	GLU	CA-C-N	6.28	133.27	121.97
5	M	268	GLU	C-N-CA	6.28	133.27	121.97
6	A	1444	MET	CA-C-N	6.14	132.76	121.70
6	A	1444	MET	C-N-CA	6.14	132.76	121.70
11	H	57	VAL	N-CA-C	6.02	116.54	107.75
6	A	1444	MET	N-CA-C	5.91	119.05	110.42
7	B	649	LYS	CA-C-N	-5.89	110.32	121.63
7	B	649	LYS	C-N-CA	-5.89	110.32	121.63
18	4	298	ILE	CA-C-N	5.88	123.95	120.24
18	4	298	ILE	C-N-CA	5.88	123.95	120.24
6	A	609	ASP	N-CA-C	-5.84	98.37	110.80
11	H	46	LEU	CA-C-N	-5.80	117.17	122.28
11	H	46	LEU	C-N-CA	-5.80	117.17	122.28
6	A	1442	ASP	N-CA-C	5.74	118.85	108.69
6	A	1442	ASP	CB-CA-C	-5.57	99.90	109.65
6	A	1441	PHE	N-CA-C	5.53	115.86	108.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	T	138	DG	O3'-P-O5'	-5.50	95.75	104.00
7	B	829	CYS	CA-C-N	-5.39	114.22	121.71
7	B	829	CYS	C-N-CA	-5.39	114.22	121.71
6	A	566	ILE	N-CA-C	-5.16	108.10	113.10
6	A	466	SER	N-CA-C	5.13	121.73	110.80
17	0	35	GLY	N-CA-C	5.11	117.34	111.36
5	M	271	GLY	N-CA-C	5.09	125.24	113.18
28	T	18	DA	O3'-P-O5'	-5.06	96.41	104.00
5	M	156	LEU	CA-C-N	-5.00	114.75	121.71
5	M	156	LEU	C-N-CA	-5.00	114.75	121.71

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	A	1441	PHE	Peptide
6	A	1443	VAL	Peptide
6	A	47	ARG	Peptide
6	A	524	VAL	Peptide
6	A	55	ASP	Peptide
6	A	568	PRO	Peptide
6	A	65	LEU	Peptide
6	A	71	GLN	Peptide
6	A	957	PRO	Peptide
7	B	648	HIS	Peptide
7	B	836	GLU	Peptide
7	B	837	ASP	Peptide
7	B	838	SER	Peptide
7	B	991	GLY	Peptide
10	F	133	VAL	Peptide
4	G	56	ILE	Peptide
11	H	131	ASN	Peptide
11	H	54	SER	Peptide
11	H	57	VAL	Peptide
5	M	267	LYS	Peptide
5	M	268	GLU	Peptide
5	M	270	ALA	Peptide
1	Q	125	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	1141	0	1027	133	0
2	R	1039	0	857	128	0
3	D	1253	0	1275	103	0
4	G	1340	0	1357	119	0
5	M	1805	0	1895	122	0
6	A	11039	0	11122	785	0
7	B	8861	0	8884	525	0
8	C	2095	0	2051	118	0
9	E	1752	0	1776	122	0
10	F	688	0	707	78	0
11	H	1068	0	1040	129	0
12	I	971	0	927	101	0
13	J	532	0	542	32	0
14	K	919	0	929	49	0
15	L	363	0	389	53	0
16	3	361	0	150	4	0
17	0	6108	0	6167	278	0
18	4	2041	0	1954	111	0
19	6	2527	0	2321	99	0
20	1	2411	0	1881	58	0
21	7	4447	0	3905	200	0
22	5	498	0	506	12	0
23	2	3011	0	2600	84	0
24	X	921	0	650	34	0
25	U	383	0	384	25	0
26	V	381	0	388	22	0
27	N	791	0	426	40	0
28	T	968	0	552	55	0
29	O	1416	0	1493	153	0
30	W	1469	0	1433	91	0
31	P	110	0	56	13	0
32	4	1	0	0	0	0
32	6	4	0	0	0	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	C	1	0	0	0	0
32	I	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	J	1	0	0	0	0
32	L	1	0	0	0	0
32	M	1	0	0	0	0
32	W	1	0	0	0	0
33	A	1	0	0	0	0
34	0	8	0	0	2	0
All	All	62733	0	59644	3536	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 29.

All (3536) 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)
6:A:68:GLN:NE2	6:A:80:HIS:ND1	1.92	1.16
11:H:55:LEU:H	11:H:146:ARG:HA	1.12	1.10
6:A:1444:MET:HA	10:F:133:VAL:HA	1.19	1.09
6:A:68:GLN:NE2	6:A:80:HIS:CE1	2.23	1.07
6:A:68:GLN:HE22	6:A:80:HIS:CG	1.74	1.05
6:A:68:GLN:NE2	6:A:80:HIS:CG	2.27	1.01
17:0:191:CYS:HB3	34:0:801:SF4:S3	2.00	1.00
15:L:31:CYS:SG	15:L:34:CYS:N	2.34	0.99
6:A:1423:GLY:O	6:A:1427:ASN:ND2	1.99	0.95
5:M:271:GLY:HA2	5:M:277:ILE:HG13	1.48	0.95
7:B:757:PRO:HD3	7:B:983:ARG:HE	1.32	0.94
18:4:228:THR:HG21	18:4:235:TYR:HB2	1.48	0.93
9:E:99:HIS:O	9:E:103:LYS:NZ	2.02	0.93
11:H:128:ASN:O	11:H:131:ASN:ND2	2.02	0.93
1:Q:98:TYR:HA	2:R:98:ASN:HA	1.49	0.92
11:H:55:LEU:N	11:H:146:ARG:HA	1.83	0.92
21:7:411:CYS:H	21:7:456:THR:HA	1.33	0.92
7:B:195:CYS:HG	7:B:783:THR:HG1	1.18	0.91
8:C:66:ARG:NH2	13:J:3:VAL:O	2.02	0.91
7:B:188:ASP:OD1	7:B:188:ASP:N	2.00	0.91
1:Q:377:SER:HB3	1:Q:385:THR:H	1.35	0.91
6:A:43:GLU:O	6:A:45:GLN:NE2	2.03	0.90
9:E:41:ASP:OD1	9:E:41:ASP:N	2.01	0.89
6:A:57:ARG:O	6:A:68:GLN:HG2	1.69	0.89
6:A:68:GLN:HE22	6:A:80:HIS:CD2	1.89	0.89
12:I:19:ASP:HB3	12:I:24:ARG:H	1.37	0.89
6:A:985:ASP:OD1	6:A:985:ASP:N	2.04	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:838:SER:OG	7:B:989:THR:N	2.05	0.89
6:A:68:GLN:HE21	6:A:80:HIS:CE1	1.88	0.88
12:I:78:CYS:SG	12:I:79:HIS:N	2.46	0.88
5:M:141:GLU:OE1	7:B:103:ASN:ND2	2.07	0.86
6:A:49:LYS:NZ	6:A:55:ASP:O	2.08	0.86
9:E:56:LYS:HE2	9:E:84:ASP:HB2	1.57	0.86
8:C:211:ASP:OD1	8:C:211:ASP:N	2.07	0.86
7:B:668:ASP:N	7:B:668:ASP:OD1	2.05	0.86
8:C:3:GLU:O	8:C:7:GLN:NE2	2.08	0.86
11:H:54:SER:HB3	11:H:146:ARG:HB3	1.56	0.86
30:W:43:LEU:HG	30:W:54:LEU:HD11	1.56	0.85
6:A:1232:ASN:ND2	6:A:1233:ASP:OD1	2.09	0.85
7:B:229:ALA:O	7:B:261:ARG:NH2	2.09	0.85
15:L:50:ASP:OD1	15:L:50:ASP:N	2.08	0.85
3:D:206:GLU:HG2	3:D:209:ARG:HE	1.41	0.85
8:C:76:ASP:N	8:C:76:ASP:OD1	2.08	0.85
6:A:1334:ASP:N	6:A:1334:ASP:OD1	2.07	0.85
8:C:148:ARG:NH1	13:J:64:ASN:O	2.11	0.84
6:A:767:GLN:NE2	6:A:768:GLN:O	2.10	0.84
12:I:32:CYS:SG	12:I:33:SER:N	2.50	0.84
6:A:290:GLU:OE1	6:A:290:GLU:N	2.09	0.84
6:A:383:TYR:HB3	10:F:115:THR:HG23	1.58	0.84
6:A:71:GLN:O	6:A:73:GLY:N	2.10	0.83
6:A:853:ASP:OD1	6:A:853:ASP:N	2.11	0.83
6:A:362:ASP:OD2	6:A:459:ARG:NH1	2.11	0.83
6:A:1197:LEU:HD11	6:A:1238:ILE:HD11	1.60	0.83
11:H:131:ASN:O	11:H:133:ASN:N	2.12	0.83
30:W:149:CYS:SG	30:W:150:SER:N	2.52	0.83
6:A:567:LYS:HB2	11:H:96:VAL:H	1.44	0.82
7:B:837:ASP:OD1	7:B:837:ASP:N	2.09	0.82
7:B:167:ILE:HD11	7:B:453:ILE:HD12	1.60	0.82
5:M:215:ARG:HB3	29:O:181:THR:HG23	1.61	0.82
29:O:68:GLN:H	29:O:162:GLY:HA2	1.45	0.82
6:A:1151:GLU:OE2	12:I:45:ARG:NH1	2.13	0.82
2:R:63:ARG:HE	2:R:65:ASN:HB3	1.43	0.82
6:A:1158:PRO:HB3	6:A:1188:GLN:HE22	1.45	0.81
9:E:40:GLU:OE1	9:E:40:GLU:N	2.13	0.81
6:A:674:PRO:O	6:A:677:ARG:NH1	2.14	0.81
29:O:206:ILE:HG12	29:O:212:ILE:HG23	1.62	0.81
21:7:490:VAL:HB	21:7:519:ARG:HH22	1.43	0.81
23:2:71:LYS:NZ	23:2:75:GLN:OE1	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:N:23:DA:H2''	29:O:158:GLN:HB3	1.62	0.81
6:A:49:LYS:NZ	6:A:55:ASP:OD2	2.12	0.81
6:A:120:GLU:OE2	6:A:123:ARG:NH1	2.13	0.81
6:A:1443:VAL:HG21	10:F:93:ILE:HD11	1.62	0.81
7:B:979:LYS:NZ	31:P:9:G:O3'	2.14	0.81
6:A:25:GLU:OE1	6:A:25:GLU:N	2.10	0.81
6:A:446:ARG:HB2	6:A:487:MET:HE3	1.63	0.81
12:I:7:CYS:O	12:I:11:ASN:N	2.12	0.81
3:D:55:ALA:HB3	3:D:148:LEU:HD21	1.61	0.81
4:G:95:SER:O	4:G:130:TYR:OH	1.99	0.81
6:A:1173:HIS:CE1	6:A:1228:TRP:H	1.99	0.80
7:B:647:GLY:HA3	7:B:648:HIS:HB3	1.62	0.80
6:A:46:THR:O	6:A:48:ALA:N	2.14	0.80
6:A:127:ALA:O	6:A:129:LYS:NZ	2.14	0.80
6:A:567:LYS:O	6:A:569:LYS:N	2.14	0.80
9:E:54:GLN:OE1	9:E:57:MET:N	2.15	0.80
13:J:10:CYS:SG	13:J:43:ARG:NH2	2.52	0.80
6:A:37:PHE:HB2	6:A:39:GLU:HG2	1.63	0.80
7:B:848:ARG:NH1	13:J:8:PHE:O	2.15	0.80
7:B:891:ASP:N	7:B:891:ASP:OD1	2.10	0.80
2:R:138:GLN:NE2	2:R:138:GLN:H	1.79	0.80
18:4:285:VAL:HA	19:6:323:GLY:HA2	1.64	0.80
29:O:192:GLY:HA2	29:O:207:PHE:HA	1.64	0.80
9:E:67:GLU:OE1	9:E:67:GLU:N	2.15	0.79
11:H:135:LEU:O	11:H:137:GLN:NE2	2.13	0.79
3:D:192:LYS:HG2	3:D:199:ASN:HA	1.64	0.79
12:I:8:ARG:NH1	12:I:9:ASP:OD1	2.14	0.79
7:B:641:GLU:O	7:B:650:GLU:N	2.15	0.79
6:A:147:VAL:HG23	6:A:149:GLU:H	1.45	0.79
7:B:763:GLN:HG2	7:B:765:PRO:HD2	1.64	0.79
25:U:263:LYS:HZ2	25:U:278:LYS:HG2	1.44	0.79
7:B:708:GLU:OE1	7:B:708:GLU:N	2.15	0.79
6:A:1128:GLN:HG3	6:A:1284:MET:HE1	1.64	0.79
7:B:706:GLN:H	7:B:710:LEU:HD23	1.48	0.79
23:2:7:LYS:HG2	23:2:9:SER:H	1.48	0.79
1:Q:339:ALA:O	1:Q:343:ARG:N	2.14	0.79
6:A:590:ARG:NH1	6:A:592:ASP:OD1	2.16	0.79
6:A:1008:GLN:HB3	6:A:1012:ARG:HH22	1.47	0.79
7:B:199:MET:N	7:B:199:MET:SD	2.52	0.79
5:M:188:THR:HG22	5:M:190:LYS:H	1.48	0.78
6:A:1215:ARG:NH2	6:A:1272:THR:O	2.15	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:1218:THR:O	7:B:1218:THR:OG1	2.01	0.78
6:A:5:GLN:O	7:B:1159:ARG:NH2	2.16	0.78
6:A:1442:ASP:HB2	10:F:136:ARG:N	1.99	0.78
19:6:126:LEU:HD11	19:6:233:LEU:HB2	1.66	0.78
6:A:438:ASP:OD1	6:A:438:ASP:N	2.15	0.78
7:B:270:LYS:HB3	7:B:279:ASP:HB3	1.66	0.78
5:M:157:CYS:SG	5:M:158:HIS:N	2.54	0.78
7:B:1163:CYS:HB3	7:B:1166:CYS:SG	2.24	0.78
6:A:1162:VAL:HG11	12:I:41:PRO:HG3	1.65	0.78
6:A:926:GLN:NE2	6:A:930:ASP:OD1	2.17	0.78
6:A:219:PHE:HD1	6:A:220:THR:H	1.32	0.78
30:W:92:PRO:HA	30:W:95:ILE:HD12	1.66	0.78
6:A:152:VAL:O	6:A:162:VAL:N	2.15	0.77
3:D:123:LEU:HD11	3:D:145:MET:HB3	1.66	0.77
18:4:79:TYR:HB3	18:4:140:ILE:HG23	1.65	0.77
29:O:102:VAL:HB	29:O:115:ILE:HB	1.66	0.77
6:A:67:CYS:SG	6:A:80:HIS:CE1	2.78	0.77
7:B:997:GLU:OE2	7:B:997:GLU:N	2.12	0.77
17:O:356:PRO:HG2	17:O:413:GLU:HA	1.66	0.77
7:B:1084:GLN:NE2	8:C:190:ASP:O	2.17	0.77
7:B:957:ASN:OD1	7:B:958:GLN:N	2.17	0.77
20:1:557:CYS:SG	20:1:585:HIS:NE2	2.57	0.77
18:4:175:ARG:HE	18:4:256:PRO:HG3	1.47	0.77
6:A:278:THR:HA	6:A:281:HIS:NE2	1.99	0.77
3:D:151:PHE:O	3:D:153:ARG:NH1	2.18	0.77
8:C:14:SER:OG	8:C:15:LYS:N	2.14	0.77
2:R:99:LYS:O	2:R:103:LYS:N	2.18	0.76
5:M:281:SER:O	5:M:285:ASN:ND2	2.18	0.76
11:H:56:THR:O	11:H:144:ILE:N	2.18	0.76
27:N:23:DA:N6	28:T:143:DT:O4	2.18	0.76
7:B:135:ARG:NH1	7:B:136:THR:O	2.19	0.76
1:Q:337:GLU:OE2	1:Q:340:LYS:N	2.18	0.76
7:B:235:SER:OG	7:B:236:HIS:ND1	2.16	0.76
12:I:22:ASN:OD1	12:I:22:ASN:N	2.19	0.76
6:A:1208:THR:H	6:A:1211:GLN:CD	1.93	0.76
7:B:1187:ASN:HD21	7:B:1190:ASP:HB3	1.49	0.76
25:U:253:ARG:NH1	28:T:144:DA:OP1	2.19	0.76
6:A:1062:GLU:OE1	10:F:88:TYR:OH	2.04	0.76
7:B:1175:LEU:O	7:B:1176:ASN:ND2	2.18	0.76
6:A:118:HIS:HA	6:A:123:ARG:HH22	1.49	0.76
6:A:982:THR:N	6:A:985:ASP:OD2	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:1:MET:O	13:J:53:HIS:NE2	2.18	0.76
7:B:89:GLU:N	7:B:135:ARG:O	2.18	0.76
7:B:567:GLU:OE1	7:B:567:GLU:N	2.18	0.76
6:A:1215:ARG:O	6:A:1218:GLN:NE2	2.17	0.75
6:A:1215:ARG:O	6:A:1219:THR:OG1	2.04	0.75
9:E:20:LYS:NZ	9:E:34:GLU:O	2.15	0.75
9:E:3:GLN:O	9:E:6:GLU:N	2.19	0.75
17:O:134:ARG:NH2	17:O:303:GLU:O	2.19	0.75
29:O:191:PRO:HG2	29:O:207:PHE:HE1	1.51	0.75
5:M:24:CYS:SG	5:M:27:CYS:N	2.57	0.75
6:A:107:CYS:SG	6:A:110:CYS:N	2.59	0.75
12:I:17:ARG:O	12:I:26:LEU:N	2.18	0.75
25:U:262:LEU:HB2	25:U:279:ALA:HB3	1.68	0.75
4:G:64:THR:OG1	4:G:65:ASP:OD1	2.04	0.75
7:B:996:ARG:HH22	8:C:173:ALA:HB1	1.51	0.75
3:D:140:ASP:N	3:D:140:ASP:OD1	2.16	0.75
5:M:193:GLN:HE22	5:M:197:HIS:HA	1.51	0.75
18:4:136:GLU:HA	18:4:140:ILE:HG13	1.68	0.75
18:4:84:LYS:HB3	18:4:132:LEU:HD12	1.67	0.75
3:D:119:ARG:HD2	3:D:155:ARG:HH22	1.52	0.74
6:A:185:TRP:H	6:A:199:LEU:HD12	1.53	0.74
7:B:864:LYS:HB3	7:B:872:GLU:H	1.51	0.74
1:Q:132:ASP:N	1:Q:132:ASP:OD1	2.21	0.74
4:G:46:LEU:HD12	4:G:77:VAL:HG12	1.70	0.74
15:L:48:CYS:O	15:L:52:GLY:N	2.17	0.74
6:A:1005:GLU:N	6:A:1005:GLU:OE1	2.19	0.74
7:B:529:GLU:HA	7:B:533:CYS:HB2	1.69	0.74
8:C:61:GLU:OE1	8:C:61:GLU:N	2.18	0.74
2:R:75:MET:N	2:R:75:MET:SD	2.60	0.74
17:O:618:ARG:NH1	17:O:676:TYR:O	2.20	0.74
1:Q:120:LYS:O	1:Q:395:PHE:N	2.15	0.74
8:C:60:ASP:OD1	8:C:60:ASP:N	2.15	0.74
19:6:132:CYS:HB2	19:6:175:ARG:HG2	1.68	0.74
28:T:144:DA:N3	29:O:69:ASN:ND2	2.35	0.74
17:O:74:ARG:NH1	17:O:239:ASN:OD1	2.21	0.74
20:1:214:ILE:HG13	20:1:215:PRO:HD3	1.70	0.74
29:O:73:THR:HG22	29:O:122:VAL:HG22	1.70	0.74
7:B:867:GLY:HA3	7:B:870:ILE:HB	1.70	0.74
6:A:795:GLU:N	6:A:795:GLU:OE1	2.20	0.73
7:B:642:ASP:OD1	7:B:642:ASP:N	2.18	0.73
7:B:982:SER:OG	7:B:983:ARG:N	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:F:149:GLU:N	10:F:149:GLU:OE2	2.20	0.73
30:W:123:MET:HA	30:W:130:LYS:HA	1.70	0.73
2:R:74:PRO:HD2	2:R:224:VAL:HB	1.70	0.73
7:B:326:ASP:O	7:B:329:THR:OG1	2.06	0.73
6:A:711:ARG:NH1	12:I:95:THR:O	2.21	0.73
6:A:821:ARG:HH12	7:B:527:THR:HG21	1.53	0.73
12:I:27:PHE:N	12:I:36:GLU:O	2.21	0.73
6:A:1147:THR:HA	6:A:1197:LEU:HA	1.71	0.73
7:B:195:CYS:SG	7:B:783:THR:OG1	2.43	0.73
9:E:48:ASP:OD1	9:E:52:ARG:N	2.22	0.73
17:O:37:ASN:HB2	17:O:477:THR:HG22	1.70	0.73
6:A:951:GLU:O	6:A:954:TRP:NE1	2.20	0.73
7:B:739:THR:OG1	7:B:740:HIS:ND1	2.20	0.73
9:E:52:ARG:HD3	9:E:53:PRO:HD2	1.70	0.73
6:A:232:GLU:OE1	6:A:232:GLU:N	2.21	0.73
29:O:183:SER:HB3	29:O:193:LEU:HD11	1.69	0.73
6:A:939:ASP:OD2	6:A:1023:ARG:NH1	2.22	0.73
6:A:1157:ASP:OD1	6:A:1160:SER:N	2.21	0.73
3:D:32:GLU:O	4:G:5:LYS:NZ	2.17	0.73
7:B:886:LYS:HE3	7:B:940:PRO:HD3	1.70	0.73
6:A:1426:GLU:OE1	6:A:1426:GLU:N	2.22	0.73
21:7:411:CYS:HA	21:7:488:ASP:HB2	1.71	0.73
4:G:57:GLN:OE1	4:G:57:GLN:N	2.22	0.72
5:M:157:CYS:HB3	5:M:210:MET:HE1	1.69	0.72
6:A:1278:ASN:HD22	6:A:1312:ASN:HB2	1.54	0.72
10:F:130:ILE:HG22	10:F:132:LEU:HD23	1.71	0.72
12:I:87:GLN:O	12:I:89:GLN:NE2	2.22	0.72
21:7:381:SER:HB3	21:7:509:ALA:HB1	1.70	0.72
6:A:1197:LEU:HD12	6:A:1236:LEU:HB3	1.71	0.72
9:E:66:GLU:O	9:E:69:ILE:N	2.22	0.72
15:L:47:ARG:NH2	15:L:52:GLY:O	2.22	0.72
17:O:140:GLN:NE2	17:O:386:ARG:O	2.21	0.72
6:A:1167:GLU:O	6:A:1171:GLN:NE2	2.17	0.72
3:D:119:ARG:NH1	3:D:152:SER:O	2.21	0.72
11:H:83:GLN:O	11:H:87:ARG:NH1	2.21	0.72
6:A:399:HIS:O	6:A:401:GLY:N	2.22	0.72
11:H:56:THR:HA	11:H:145:ARG:NH1	2.04	0.72
11:H:94:ASP:OD1	11:H:94:ASP:N	2.21	0.72
1:Q:375:LEU:HB3	1:Q:387:ILE:HB	1.71	0.72
17:O:41:GLU:HB2	17:O:466:LEU:HD21	1.71	0.72
17:O:350:HIS:HA	17:O:422:PRO:HD3	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:7:601:ARG:O	21:7:696:ARG:NH2	2.22	0.72
2:R:127:LYS:HD3	2:R:220:HIS:CE1	2.25	0.72
6:A:47:ARG:HG2	6:A:257:ARG:HH12	1.54	0.72
6:A:359:LEU:O	6:A:471:ASN:ND2	2.22	0.72
12:I:19:ASP:OD2	12:I:22:ASN:N	2.22	0.72
19:6:262:LYS:HG3	19:6:287:PHE:HB3	1.70	0.72
23:2:82:LYS:HE2	23:2:89:PRO:HG3	1.72	0.72
7:B:816:GLU:OE1	7:B:816:GLU:N	2.23	0.72
9:E:67:GLU:CD	9:E:67:GLU:H	1.97	0.72
11:H:57:VAL:HA	11:H:144:ILE:CA	2.19	0.72
29:O:195:TYR:HB3	29:O:204:LEU:HB2	1.71	0.72
5:M:244:SER:HB3	7:B:108:VAL:HG13	1.71	0.72
14:K:108:GLU:O	14:K:111:LEU:HB2	1.90	0.71
29:O:196:ARG:HG2	29:O:203:VAL:HG13	1.71	0.71
6:A:434:ARG:NH2	6:A:440:ASP:OD2	2.23	0.71
7:B:486:TYR:OH	7:B:794:ASN:ND2	2.23	0.71
10:F:92:ARG:O	10:F:96:THR:OG1	2.07	0.71
19:6:141:LEU:HD23	19:6:145:ARG:HA	1.70	0.71
6:A:152:VAL:N	6:A:162:VAL:O	2.20	0.71
7:B:67:SER:HB2	7:B:92:PHE:HD2	1.56	0.71
17:0:446:ILE:HG21	17:0:473:LEU:HB3	1.72	0.71
29:O:193:LEU:O	29:O:206:ILE:N	2.21	0.71
30:W:38:LEU:HD21	30:W:43:LEU:HD22	1.72	0.71
6:A:488:ASN:OD1	6:A:488:ASN:N	2.18	0.71
7:B:1028:GLU:O	7:B:1032:SER:OG	2.08	0.71
7:B:310:MET:HG3	7:B:386:LEU:HD12	1.73	0.71
21:7:603:ASP:OD1	21:7:696:ARG:NH1	2.24	0.71
6:A:918:GLU:OE1	6:A:918:GLU:N	2.17	0.71
9:E:66:GLU:OE1	9:E:66:GLU:N	2.23	0.71
17:0:66:HIS:ND1	17:0:229:ASP:O	2.23	0.71
30:W:127:CYS:HB2	30:W:151:LEU:HD12	1.71	0.71
2:R:106:LEU:N	2:R:120:TYR:O	2.22	0.71
12:I:6:PHE:HA	12:I:12:ASN:O	1.91	0.71
29:O:104:MET:HB3	29:O:113:ALA:HB3	1.71	0.71
7:B:708:GLU:CD	7:B:709:ASP:H	1.98	0.71
29:O:65:PRO:HA	29:O:164:CYS:HB3	1.73	0.71
6:A:385:ILE:O	6:A:389:THR:OG1	2.08	0.70
27:N:34:DA:H2	28:T:132:DT:H3	1.36	0.70
29:O:133:LYS:HD2	29:O:137:ARG:HH21	1.55	0.70
6:A:1444:MET:HE2	10:F:133:VAL:HG13	1.74	0.70
8:C:5:GLY:O	8:C:24:ASN:ND2	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:2:SER:N	11:H:61:SER:HG	1.89	0.70
6:A:107:CYS:HA	6:A:171:GLN:HE22	1.57	0.70
6:A:788:SER:OG	6:A:789:LYS:N	2.22	0.70
7:B:499:ASN:OD1	7:B:500:THR:N	2.23	0.70
11:H:2:SER:OG	11:H:3:ASN:N	2.21	0.70
4:G:84:GLY:N	4:G:147:ILE:O	2.24	0.70
7:B:957:ASN:N	7:B:961:LEU:O	2.21	0.70
6:A:273:ASN:ND2	6:A:277:GLU:OE2	2.25	0.70
6:A:560:ILE:N	11:H:78:SER:OG	2.17	0.70
7:B:641:GLU:N	7:B:650:GLU:O	2.25	0.70
3:D:56:ARG:HH21	3:D:152:SER:HB3	1.55	0.70
6:A:1121:GLU:OE2	6:A:1124:HIS:ND1	2.24	0.70
6:A:1442:ASP:HA	10:F:134:ILE:C	2.17	0.70
9:E:59:SER:OG	9:E:82:PHE:N	2.23	0.70
9:E:159:ASP:N	9:E:159:ASP:OD1	2.19	0.70
19:6:117:PRO:HB3	19:6:384:MET:HA	1.74	0.70
5:M:130:PHE:O	5:M:134:THR:OG1	2.09	0.70
6:A:496:GLU:OE1	6:A:496:GLU:N	2.22	0.70
30:W:149:CYS:SG	30:W:151:LEU:N	2.65	0.70
4:G:45:ILE:HA	4:G:78:VAL:HG12	1.71	0.70
8:C:53:THR:HG22	8:C:154:LYS:HB3	1.74	0.70
11:H:126:GLU:O	11:H:130:ARG:NH2	2.25	0.70
12:I:74:GLU:OE2	12:I:79:HIS:ND1	2.25	0.70
14:K:108:GLU:HA	14:K:111:LEU:HD13	1.74	0.70
6:A:1199:ARG:O	6:A:1203:ASN:ND2	2.23	0.70
8:C:123:ASN:ND2	8:C:125:MET:SD	2.65	0.70
19:6:165:PRO:HG2	19:6:375:HIS:HA	1.72	0.70
21:7:355:ASP:H	21:7:431:GLN:HE22	1.40	0.70
3:D:214:LEU:O	3:D:218:GLU:N	2.25	0.69
3:D:56:ARG:HB2	3:D:148:LEU:HD22	1.74	0.69
3:D:167:LEU:O	3:D:170:THR:OG1	2.08	0.69
6:A:41:MET:SD	6:A:42:ASP:N	2.65	0.69
6:A:268:ASP:HB3	6:A:299:HIS:NE2	2.08	0.69
6:A:775:ILE:O	6:A:797:LYS:NZ	2.25	0.69
23:2:462:PHE:HB2	23:2:489:LYS:HB3	1.74	0.69
1:Q:375:LEU:N	1:Q:387:ILE:O	2.21	0.69
6:A:618:GLU:OE1	6:A:619:LYS:N	2.25	0.69
7:B:896:ASP:N	7:B:896:ASP:OD1	2.23	0.69
9:E:40:GLU:HA	9:E:43:LYS:HE2	1.72	0.69
10:F:147:SER:N	10:F:150:GLU:OE2	2.23	0.69
6:A:935:GLN:NE2	6:A:939:ASP:OD1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:0:259:ARG:NH2	17:0:397:THR:OG1	2.25	0.69
2:R:94:LYS:NZ	2:R:107:LEU:O	2.24	0.69
3:D:148:LEU:O	3:D:152:SER:N	2.25	0.69
9:E:92:THR:O	9:E:95:THR:OG1	2.10	0.69
21:7:557:VAL:HB	21:7:708:LEU:HA	1.75	0.69
26:V:84:GLN:HA	26:V:107:SER:HA	1.74	0.69
6:A:1174:PHE:H	6:A:1174:PHE:HD1	1.40	0.69
3:D:127:ASP:HB3	3:D:142:LYS:HD2	1.74	0.69
6:A:1030:ARG:NH2	6:A:1035:TYR:OH	2.25	0.69
6:A:1173:HIS:CG	6:A:1227:ILE:HG23	2.28	0.69
19:6:136:MET:HA	19:6:145:ARG:HD2	1.75	0.69
7:B:245:GLU:HG2	7:B:246:LYS:HG2	1.73	0.69
9:E:101:GLN:H	9:E:101:GLN:CD	1.99	0.69
9:E:136:ASN:OD1	9:E:138:ALA:N	2.26	0.69
10:F:133:VAL:O	10:F:134:ILE:HG13	1.92	0.69
12:I:9:ASP:OD1	12:I:9:ASP:N	2.24	0.69
17:0:727:PRO:HG3	19:6:289:LYS:HA	1.75	0.69
19:6:269:GLN:HG3	19:6:288:TYR:HE2	1.57	0.69
8:C:75:MET:O	8:C:246:ARG:NH2	2.20	0.69
11:H:98:TYR:OH	11:H:138:GLU:OE2	2.07	0.69
21:7:587:LYS:HD3	21:7:673:ILE:HD12	1.74	0.69
6:A:23:SER:OG	6:A:26:GLU:N	2.22	0.69
6:A:219:PHE:HD1	6:A:220:THR:N	1.91	0.69
7:B:63:ILE:O	7:B:65:GLU:N	2.25	0.69
6:A:56:PRO:HB2	6:A:57:ARG:NH1	2.08	0.68
6:A:1376:THR:O	9:E:212:ARG:NH2	2.26	0.68
7:B:585:VAL:O	7:B:587:HIS:ND1	2.26	0.68
29:O:186:GLU:O	29:O:190:PHE:N	2.26	0.68
5:M:263:CYS:HA	5:M:266:ILE:HG22	1.75	0.68
6:A:1161:THR:HG21	6:A:1166:ASP:HB2	1.74	0.68
7:B:223:VAL:HG22	7:B:384:ARG:HH21	1.58	0.68
17:0:571:VAL:HG11	20:1:375:LEU:HD22	1.75	0.68
21:7:582:ILE:HG21	21:7:611:ASN:HD21	1.58	0.68
7:B:311:LEU:HA	7:B:314:LEU:HD12	1.74	0.68
9:E:197:LYS:HE2	9:E:199:ILE:HD11	1.74	0.68
1:Q:99:ASN:HB3	2:R:97:ILE:HB	1.73	0.68
1:Q:121:PHE:HB2	2:R:131:ASN:HD21	1.58	0.68
6:A:1134:ILE:O	6:A:1137:ALA:N	2.26	0.68
7:B:185:THR:N	7:B:188:ASP:OD2	2.24	0.68
7:B:326:ASP:OD1	7:B:327:ARG:N	2.26	0.68
7:B:975:GLN:N	7:B:978:ASP:OD2	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:69:TRP:CD1	2:R:219:CYS:HB3	2.29	0.68
5:M:59:THR:H	5:M:60:ARG:HH11	1.41	0.68
6:A:55:ASP:OD1	6:A:58:LEU:N	2.26	0.68
6:A:1386:ARG:NE	6:A:1404:GLU:OE2	2.24	0.68
7:B:800:GLN:OE1	7:B:822:ASN:ND2	2.22	0.68
21:7:489:GLU:OE1	21:7:685:GLN:NE2	2.26	0.68
6:A:746:MET:HE3	7:B:1015:HIS:CD2	2.29	0.68
7:B:1097:HIS:NE2	31:P:9:G:H4'	2.09	0.68
15:L:66:GLN:OE1	15:L:67:PHE:N	2.26	0.68
15:L:68:GLU:OE2	15:L:70:ARG:NH1	2.26	0.68
6:A:871:ASP:OD1	6:A:873:MET:N	2.17	0.68
7:B:516:ASN:N	7:B:516:ASN:OD1	2.21	0.68
9:E:26:ARG:NH1	9:E:188:LEU:O	2.27	0.68
11:H:110:ASP:O	11:H:128:ASN:HB2	1.94	0.68
7:B:990:ILE:HG22	7:B:991:GLY:H	1.59	0.68
8:C:136:ASP:OD2	8:C:139:GLY:N	2.26	0.68
12:I:7:CYS:HB2	12:I:29:CYS:HB2	1.75	0.68
12:I:73:ARG:O	12:I:83:ASN:ND2	2.26	0.68
4:G:90:THR:O	4:G:102:GLN:N	2.24	0.68
6:A:150:THR:HA	6:A:166:GLY:O	1.94	0.68
8:C:196:ASP:OD2	8:C:199:LYS:N	2.22	0.68
11:H:35:GLN:OE1	11:H:35:GLN:N	2.20	0.68
6:A:526:ASP:HB2	7:B:835:GLN:OE1	1.93	0.68
7:B:1122:ARG:N	28:T:23:DC:OP1	2.26	0.68
3:D:118:THR:OG1	3:D:119:ARG:N	2.27	0.67
6:A:25:GLU:H	6:A:25:GLU:CD	2.02	0.67
6:A:1396:ALA:N	6:A:1419:ASP:OD2	2.26	0.67
18:4:53:VAL:HG13	18:4:179:LEU:HD23	1.76	0.67
12:I:5:ARG:HB2	12:I:14:LEU:HB2	1.75	0.67
21:7:487:LEU:HB2	21:7:512:GLY:HA2	1.74	0.67
1:Q:99:ASN:N	2:R:97:ILE:O	2.26	0.67
5:M:170:SER:HB3	5:M:206:THR:HG21	1.75	0.67
8:C:3:GLU:N	8:C:6:PRO:O	2.27	0.67
21:7:615:LEU:HD11	21:7:653:PHE:HB3	1.76	0.67
3:D:67:ARG:HA	3:D:70:PHE:HB3	1.76	0.67
4:G:129:SER:OG	4:G:131:GLN:NE2	2.26	0.67
8:C:92:CYS:SG	8:C:94:LYS:N	2.62	0.67
6:A:898:ARG:O	6:A:1029:ARG:NH1	2.27	0.67
7:B:466:TRP:N	7:B:476:ARG:O	2.27	0.67
6:A:287:HIS:ND1	6:A:290:GLU:OE2	2.28	0.67
6:A:624:SER:O	6:A:624:SER:OG	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:881:GLN:NE2	6:A:957:PRO:O	2.28	0.67
6:A:1148:ILE:HB	6:A:1196:GLU:HG2	1.74	0.67
17:0:500:GLY:HA3	17:0:521:ASN:HD21	1.60	0.67
21:7:553:GLN:HB3	21:7:734:LYS:HE2	1.76	0.67
7:B:760:ASP:N	7:B:760:ASP:OD1	2.26	0.67
23:2:458:LEU:HD11	23:2:490:LYS:HB3	1.77	0.67
6:A:1445:ILE:H	10:F:133:VAL:HG23	1.60	0.67
18:4:289:CYS:SG	18:4:290:SER:N	2.68	0.67
4:G:146:LYS:NZ	4:G:148:GLU:OE1	2.25	0.66
8:C:26:ASP:OD2	8:C:29:MET:N	2.22	0.66
8:C:92:CYS:O	8:C:96:SER:OG	2.13	0.66
21:7:499:ARG:NH2	21:7:525:GLY:O	2.27	0.66
6:A:874:ASP:OD1	6:A:875:ALA:N	2.28	0.66
7:B:328:GLU:OE1	7:B:328:GLU:N	2.24	0.66
29:O:93:GLU:O	29:O:103:ILE:N	2.18	0.66
2:R:68:VAL:O	2:R:219:CYS:N	2.27	0.66
3:D:154:PHE:CE2	3:D:163:VAL:HG21	2.31	0.66
4:G:96:GLN:H	30:W:145:THR:HB	1.60	0.66
18:4:175:ARG:NH1	18:4:252:MET:O	2.28	0.66
29:O:162:GLY:O	29:O:214:LEU:N	2.23	0.66
4:G:101:VAL:N	4:G:108:VAL:O	2.28	0.66
5:M:186:ALA:HB3	5:M:241:ARG:HD2	1.76	0.66
5:M:201:LYS:HE3	27:N:19:DA:H3'	1.76	0.66
6:A:56:PRO:O	6:A:57:ARG:NH1	2.28	0.66
6:A:1329:THR:OG1	6:A:1330:ASN:N	2.25	0.66
7:B:178:ASN:O	7:B:178:ASN:ND2	2.29	0.66
11:H:142:LEU:HG	11:H:143:LEU:N	2.10	0.66
15:L:30:ILE:HG23	15:L:36:SER:O	1.95	0.66
17:0:288:LYS:O	17:0:291:GLN:NE2	2.28	0.66
17:0:496:ILE:HD12	17:0:686:PHE:HB3	1.78	0.66
21:7:606:ILE:O	21:7:671:ILE:N	2.26	0.66
2:R:98:ASN:OD1	2:R:99:LYS:N	2.23	0.66
4:G:110:VAL:HG13	4:G:162:SER:HA	1.76	0.66
6:A:76:GLU:OE2	7:B:1159:ARG:NH1	2.28	0.66
17:0:112:LYS:NZ	17:0:123:GLU:O	2.28	0.66
19:6:209:SER:OG	19:6:212:ASN:ND2	2.22	0.66
20:1:174:LEU:O	20:1:181:GLN:NE2	2.26	0.66
21:7:420:TRP:NE1	21:7:661:SER:OG	2.20	0.66
7:B:365:THR:HG1	7:B:367:LEU:H	1.44	0.66
1:Q:343:ARG:NH2	1:Q:346:GLU:OE2	2.21	0.66
29:O:206:ILE:HD13	29:O:234:LEU:HD21	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:E:74:ASP:OD1	9:E:74:ASP:N	2.24	0.66
11:H:57:VAL:HA	11:H:144:ILE:HA	1.77	0.66
14:K:24:ASP:OD1	14:K:25:THR:N	2.29	0.66
17:0:69:ILE:HG23	17:0:231:ILE:HG23	1.77	0.66
21:7:579:LEU:HD22	21:7:611:ASN:HD22	1.60	0.66
24:X:187:HIS:HA	24:X:214:TRP:HB2	1.77	0.66
1:Q:104:ARG:HD2	2:R:92:LEU:HB3	1.77	0.66
6:A:215:SER:OG	6:A:217:LYS:N	2.28	0.66
6:A:1063:MET:SD	6:A:1436:ILE:HD12	2.36	0.66
6:A:1229:SER:N	6:A:1237:ILE:O	2.21	0.66
7:B:1139:ILE:O	7:B:1142:GLY:N	2.28	0.66
11:H:57:VAL:HG23	11:H:144:ILE:HA	1.78	0.66
21:7:560:PRO:HA	21:7:711:LYS:HE2	1.77	0.66
21:7:607:VAL:O	21:7:654:LEU:N	2.29	0.66
28:T:147:DT:O4	28:T:148:DA:N6	2.29	0.66
4:G:97:HIS:O	4:G:112:LYS:N	2.29	0.65
6:A:900:ASP:OD1	6:A:903:ASN:N	2.29	0.65
6:A:1287:TYR:OH	6:A:1307:GLU:OE2	2.10	0.65
7:B:137:TYR:HD1	7:B:137:TYR:H	1.44	0.65
7:B:705:MET:HE1	7:B:745:PRO:HB3	1.79	0.65
7:B:737:THR:O	7:B:737:THR:OG1	2.10	0.65
12:I:34:TYR:OH	12:I:36:GLU:OE2	2.13	0.65
27:N:37:DG:O6	28:T:128:DA:N6	2.29	0.65
5:M:234:GLN:NE2	29:O:173:GLU:OE2	2.27	0.65
7:B:1008:PRO:HB3	7:B:1087:PHE:HE1	1.60	0.65
2:R:73:LEU:HD12	2:R:74:PRO:HD2	1.78	0.65
2:R:98:ASN:HB3	2:R:103:LYS:O	1.96	0.65
4:G:36:GLY:N	4:G:45:ILE:O	2.30	0.65
29:O:163:SER:HA	29:O:213:VAL:HA	1.78	0.65
6:A:739:ASP:OD1	6:A:739:ASP:N	2.27	0.65
7:B:213:ILE:O	7:B:215:GLN:NE2	2.27	0.65
7:B:862:GLN:HB3	7:B:963:PHE:HB2	1.79	0.65
6:A:1436:ILE:O	6:A:1439:GLY:N	2.20	0.65
7:B:216:GLU:OE2	7:B:404:LYS:HG2	1.96	0.65
17:0:446:ILE:HG13	17:0:473:LEU:HD22	1.78	0.65
29:O:193:LEU:N	29:O:206:ILE:O	2.29	0.65
1:Q:352:MET:N	1:Q:352:MET:SD	2.70	0.65
9:E:29:PHE:HB2	9:E:65:THR:HG22	1.78	0.65
19:6:124:ARG:NH2	19:6:231:GLU:OE1	2.29	0.65
21:7:456:THR:HG23	21:7:459:MET:H	1.61	0.65
29:O:136:SER:HB2	29:O:152:PHE:HE1	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:83:LYS:HD2	4:G:83:LYS:H	1.62	0.65
6:A:16:GLU:OE2	7:B:1221:SER:N	2.23	0.65
6:A:821:ARG:NH1	7:B:527:THR:HG21	2.12	0.65
7:B:253:THR:O	7:B:253:THR:OG1	2.12	0.65
7:B:802:PRO:HG2	7:B:805:THR:HG22	1.78	0.65
27:N:19:DA:H2''	27:N:20:DT:H5'	1.79	0.65
6:A:362:ASP:OD1	6:A:362:ASP:N	2.22	0.65
18:4:255:ASP:O	18:4:259:ARG:NH1	2.29	0.65
1:Q:380:ASP:OD1	1:Q:380:ASP:N	2.27	0.65
7:B:825:VAL:HG23	7:B:1010:LEU:HB3	1.78	0.65
9:E:191:LYS:N	9:E:194:GLU:OE1	2.25	0.65
23:2:350:TYR:N	23:2:407:GLN:OE1	2.25	0.65
30:W:149:CYS:HB3	30:W:154:GLU:H	1.62	0.65
7:B:104:GLU:OE2	15:L:54:ARG:NE	2.30	0.64
7:B:280:ILE:HB	7:B:285:ILE:HD11	1.77	0.64
17:0:534:PRO:HD3	17:0:721:LEU:HD21	1.78	0.64
6:A:82:GLY:O	6:A:241:VAL:N	2.28	0.64
6:A:1443:VAL:N	10:F:134:ILE:O	2.29	0.64
8:C:36:VAL:HG23	8:C:40:GLU:HB2	1.79	0.64
12:I:45:ARG:NH2	12:I:47:GLU:OE2	2.29	0.64
23:2:87:LEU:HD12	23:2:98:ILE:HG23	1.80	0.64
23:2:387:LEU:HD11	23:2:393:ALA:HB2	1.79	0.64
29:O:76:LEU:HD22	29:O:150:ALA:HB1	1.79	0.64
2:R:62:GLU:OE1	2:R:62:GLU:N	2.28	0.64
6:A:43:GLU:O	6:A:44:THR:OG1	2.16	0.64
6:A:609:ASP:OD1	6:A:610:GLY:N	2.31	0.64
17:0:580:SER:HB3	20:1:339:LEU:H	1.62	0.64
21:7:520:GLU:H	21:7:681:ARG:HH12	1.45	0.64
29:O:179:HIS:HB3	29:O:182:PHE:HD2	1.63	0.64
1:Q:104:ARG:CZ	1:Q:105:ALA:H	2.10	0.64
1:Q:116:THR:O	1:Q:117:HIS:ND1	2.31	0.64
6:A:1142:THR:O	6:A:1145:SER:OG	2.15	0.64
1:Q:373:TYR:H	2:R:82:ARG:NH2	1.96	0.64
5:M:60:ARG:H	5:M:60:ARG:HD2	1.62	0.64
6:A:401:GLY:O	6:A:435:HIS:ND1	2.31	0.64
7:B:69:LEU:HD13	7:B:429:PHE:HB2	1.80	0.64
8:C:5:GLY:O	8:C:7:GLN:NE2	2.31	0.64
17:0:293:LEU:HD13	17:0:319:GLU:HA	1.79	0.64
18:4:51:ILE:O	18:4:55:GLU:N	2.20	0.64
19:6:130:LEU:N	19:6:172:ILE:O	2.30	0.64
19:6:322:MET:HB2	19:6:369:MET:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:363:GLY:HA2	1:Q:395:PHE:HA	1.80	0.64
6:A:471:ASN:OD1	6:A:472:LEU:N	2.31	0.64
6:A:1297:GLU:OE1	6:A:1297:GLU:N	2.23	0.64
7:B:20:ASP:OD2	7:B:22:SER:N	2.31	0.64
7:B:618:ASP:OD1	7:B:621:GLU:N	2.29	0.64
8:C:90:ASP:OD1	8:C:91:HIS:ND1	2.31	0.64
11:H:58:THR:H	11:H:143:LEU:C	2.04	0.64
18:4:59:VAL:HB	18:4:245:ILE:HD11	1.78	0.64
25:U:281:VAL:HG22	26:V:62:VAL:HB	1.79	0.64
9:E:157:SER:OG	9:E:159:ASP:OD1	2.13	0.64
13:J:7:CYS:HA	13:J:49:MET:HE2	1.78	0.64
1:Q:140:HIS:NE2	1:Q:353:GLU:OE2	2.30	0.64
12:I:82:GLU:OE1	12:I:82:GLU:N	2.30	0.64
18:4:239:GLU:HG2	18:4:242:GLU:HB2	1.79	0.64
30:W:144:ARG:HH12	30:W:146:GLU:HB3	1.63	0.64
1:Q:117:HIS:HB2	2:R:135:PHE:CE1	2.33	0.64
6:A:225:ASN:OD1	6:A:228:PHE:N	2.21	0.64
6:A:780:VAL:N	7:B:699:GLU:OE1	2.29	0.64
6:A:1079:MET:HE3	6:A:1359:ASP:HB3	1.80	0.64
7:B:979:LYS:NZ	31:P:9:G:O2'	2.31	0.64
9:E:4:GLU:O	9:E:8:ASN:HB2	1.98	0.64
17:0:124:ARG:HH22	17:0:577:GLN:H	1.46	0.64
18:4:82:GLY:H	18:4:148:THR:HG21	1.63	0.64
30:W:65:ARG:HE	30:W:93:HIS:HB3	1.62	0.64
8:C:3:GLU:OE2	14:K:104:ASN:HB2	1.97	0.64
17:0:113:ASN:ND2	20:1:346:ASP:OD1	2.31	0.64
17:0:571:VAL:HG22	17:0:599:LEU:HD21	1.80	0.64
7:B:643:ASP:C	7:B:645:SER:H	2.07	0.63
7:B:1136:ASP:N	7:B:1136:ASP:OD1	2.27	0.63
7:B:1187:ASN:OD1	7:B:1188:LYS:N	2.31	0.63
11:H:32:THR:OG1	11:H:33:GLN:N	2.29	0.63
18:4:29:ILE:HD11	18:4:156:GLY:HA3	1.80	0.63
21:7:303:ARG:HA	21:7:320:ASN:HA	1.78	0.63
30:W:21:TYR:OH	30:W:64:ASP:OD2	2.16	0.63
6:A:316:GLN:O	6:A:318:SER:OG	2.14	0.63
6:A:1438:THR:O	10:F:92:ARG:NH1	2.30	0.63
7:B:882:THR:HA	7:B:934:LYS:O	1.98	0.63
17:0:507:SER:HG	17:0:685:ARG:HH22	1.43	0.63
19:6:142:ARG:HB2	19:6:143:PRO:HD3	1.79	0.63
24:X:255:ILE:HD13	30:W:178:GLN:HB3	1.79	0.63
1:Q:101:PHE:CZ	1:Q:382:GLY:HA3	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:109:GLU:OE1	1:Q:109:GLU:N	2.28	0.63
8:C:74:SER:OG	8:C:237:SER:OG	2.13	0.63
17:0:80:GLU:HA	17:0:83:LEU:HB2	1.80	0.63
19:6:173:ILE:HD12	19:6:175:ARG:HD2	1.79	0.63
20:1:593:LEU:O	20:1:597:PHE:N	2.30	0.63
1:Q:332:LEU:HB2	7:B:429:PHE:CZ	2.34	0.63
6:A:1234:GLU:OE1	6:A:1234:GLU:N	2.32	0.63
7:B:65:GLU:O	7:B:67:SER:N	2.31	0.63
7:B:864:LYS:HG2	7:B:871:THR:HA	1.79	0.63
9:E:46:TYR:CD1	9:E:58:MET:HG2	2.33	0.63
11:H:55:LEU:O	11:H:146:ARG:NE	2.31	0.63
17:0:343:LYS:HG2	17:0:347:LYS:HZ2	1.62	0.63
17:0:722:ARG:HA	19:6:267:SER:HB2	1.80	0.63
23:2:59:LEU:HD22	23:2:96:LEU:HD12	1.80	0.63
2:R:69:TRP:HD1	2:R:219:CYS:HB3	1.61	0.63
4:G:47:CYS:SG	4:G:48:VAL:N	2.72	0.63
4:G:49:LEU:HD21	4:G:77:VAL:HG23	1.81	0.63
6:A:21:LEU:HD12	6:A:229:SER:HB2	1.80	0.63
6:A:567:LYS:HB2	11:H:95:TYR:HA	1.80	0.63
6:A:1407:GLU:CD	6:A:1407:GLU:H	2.06	0.63
9:E:79:TRP:NE1	9:E:81:GLU:OE1	2.30	0.63
17:0:419:ILE:HG12	17:0:436:ARG:HB3	1.80	0.63
21:7:303:ARG:HB3	21:7:323:VAL:HG13	1.80	0.63
24:X:214:TRP:CD1	24:X:217:CYS:HG	2.16	0.63
1:Q:124:LYS:HG2	1:Q:126:LYS:HZ2	1.64	0.63
6:A:535:THR:HG21	6:A:617:VAL:H	1.64	0.63
7:B:135:ARG:HH12	7:B:138:GLU:HB2	1.62	0.63
7:B:332:ASP:O	7:B:348:ARG:NH1	2.32	0.63
7:B:977:GLY:HA3	7:B:1099:VAL:HG11	1.80	0.63
3:D:63:LEU:HB3	3:D:130:LEU:HD22	1.79	0.63
3:D:173:HIS:N	3:D:176:GLU:OE2	2.32	0.63
21:7:365:TYR:OH	21:7:390:ALA:O	2.15	0.63
6:A:1445:ILE:N	10:F:133:VAL:HG23	2.13	0.63
7:B:1002:THR:OG1	7:B:1003:ALA:N	2.32	0.63
17:0:436:ARG:HE	17:0:634:ILE:HG21	1.62	0.63
19:6:291:LEU:HA	19:6:296:HIS:CD2	2.33	0.63
21:7:302:GLU:HG3	21:7:321:GLU:HB3	1.80	0.63
21:7:483:GLY:HA2	21:7:508:HIS:HB2	1.80	0.63
7:B:46:GLN:OE1	7:B:47:GLN:N	2.32	0.63
7:B:282:ILE:O	7:B:285:ILE:N	2.31	0.63
21:7:599:GLU:HG2	21:7:650:ASN:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:2:246:GLN:O	23:2:250:LEU:N	2.26	0.63
29:O:129:GLU:OE1	29:O:220:ARG:NH2	2.32	0.63
29:O:171:ARG:N	29:O:237:PHE:O	2.26	0.63
1:Q:366:GLU:HB3	1:Q:392:VAL:HG13	1.80	0.62
6:A:65:LEU:O	6:A:67:CYS:N	2.30	0.62
6:A:136:ALA:O	6:A:140:THR:OG1	2.16	0.62
6:A:420:ARG:HB3	6:A:423:ASP:HB3	1.81	0.62
6:A:1147:THR:OG1	6:A:1196:GLU:O	2.16	0.62
7:B:895:ASP:N	7:B:895:ASP:OD1	2.32	0.62
7:B:1098:MET:N	7:B:1098:MET:SD	2.72	0.62
7:B:1153:GLU:OE1	7:B:1153:GLU:N	2.31	0.62
8:C:29:MET:HE1	14:K:97:LYS:HD2	1.81	0.62
19:6:217:ALA:HB1	19:6:232:VAL:HG21	1.80	0.62
4:G:148:GLU:HB2	4:G:160:ILE:HG22	1.81	0.62
7:B:37:PHE:HD2	7:B:38:PHE:N	1.97	0.62
4:G:60:ARG:O	4:G:69:GLU:N	2.31	0.62
5:M:255:SER:OG	5:M:285:ASN:OD1	2.14	0.62
6:A:1082:ASN:OD1	6:A:1083:THR:N	2.32	0.62
6:A:1123:GLY:HA3	6:A:1124:HIS:CG	2.34	0.62
7:B:792:MET:HE1	7:B:857:ARG:HH21	1.64	0.62
17:0:116:LEU:HD21	17:0:186:GLU:HA	1.81	0.62
17:0:666:LEU:HD22	17:0:679:MET:HB3	1.81	0.62
19:6:188:ASN:O	19:6:192:HIS:ND1	2.32	0.62
29:O:193:LEU:HB3	29:O:206:ILE:HB	1.80	0.62
1:Q:103:LEU:HD21	2:R:95:ILE:HG22	1.81	0.62
2:R:106:LEU:HB2	2:R:120:TYR:HB2	1.82	0.62
6:A:903:ASN:OD1	6:A:904:THR:N	2.32	0.62
11:H:55:LEU:O	11:H:145:ARG:HD2	1.98	0.62
11:H:142:LEU:O	11:H:143:LEU:HG	1.98	0.62
12:I:19:ASP:N	12:I:24:ARG:O	2.32	0.62
17:0:79:ILE:HG23	17:0:207:ILE:HG22	1.79	0.62
17:0:378:SER:OG	17:0:407:THR:OG1	2.17	0.62
5:M:37:ARG:HG3	6:A:416:ARG:HH21	1.64	0.62
6:A:67:CYS:H	6:A:71:GLN:HA	1.64	0.62
6:A:982:THR:OG1	6:A:985:ASP:OD1	2.07	0.62
7:B:432:MET:O	7:B:435:THR:OG1	2.14	0.62
7:B:757:PRO:HD3	7:B:983:ARG:NE	2.10	0.62
11:H:82:PRO:HA	11:H:87:ARG:HD2	1.81	0.62
23:2:81:MET:HE2	23:2:87:LEU:HD13	1.80	0.62
18:4:27:THR:HG22	18:4:74:ALA:HB3	1.80	0.62
21:7:308:ASP:OD1	21:7:309:ASP:N	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:214:TRP:HD1	24:X:217:CYS:HG	1.45	0.62
2:R:73:LEU:HD21	2:R:77:LEU:HG	1.81	0.62
2:R:138:GLN:H	2:R:138:GLN:HE21	1.45	0.62
8:C:214:ASN:ND2	8:C:217:ASP:OD1	2.32	0.62
12:I:19:ASP:HB3	12:I:24:ARG:N	2.12	0.62
15:L:61:THR:OG1	15:L:62:LYS:N	2.29	0.62
5:M:51:VAL:HG11	6:A:412:ARG:HB2	1.82	0.62
6:A:41:MET:O	6:A:49:LYS:HA	1.99	0.62
6:A:1442:ASP:OD2	10:F:135:ARG:HA	1.99	0.62
9:E:72:PHE:HB2	9:E:75:MET:HE2	1.80	0.62
12:I:92:ARG:O	12:I:95:THR:OG1	2.13	0.62
18:4:200:ILE:HG12	18:4:227:THR:HG23	1.80	0.62
18:4:212:VAL:HG21	18:4:224:LEU:HB3	1.80	0.62
1:Q:120:LYS:HB2	1:Q:394:LYS:HD2	1.82	0.62
1:Q:131:THR:OG1	1:Q:132:ASP:OD1	2.13	0.62
5:M:35:VAL:HG23	5:M:46:ALA:HB2	1.81	0.62
17:0:339:ILE:HD12	17:0:342:LEU:HD21	1.82	0.62
21:7:365:TYR:HB3	21:7:543:LEU:HD21	1.81	0.62
2:R:69:TRP:NE1	2:R:220:HIS:HB3	2.15	0.62
5:M:158:HIS:ND1	5:M:158:HIS:O	2.33	0.62
7:B:883:LEU:O	7:B:884:ARG:NE	2.33	0.62
18:4:29:ILE:HD13	18:4:153:MET:HA	1.82	0.62
20:1:547:LEU:O	20:1:551:ARG:N	2.33	0.62
3:D:63:LEU:HD22	3:D:130:LEU:HB3	1.82	0.61
5:M:267:LYS:HE2	29:O:240:MET:HB2	1.81	0.61
6:A:310:GLY:O	6:A:311:GLN:NE2	2.33	0.61
6:A:886:ILE:HD11	6:A:950:GLY:HA2	1.81	0.61
10:F:110:ASP:O	10:F:123:LYS:NZ	2.33	0.61
1:Q:119:LEU:HD12	2:R:133:TYR:HB2	1.82	0.61
6:A:1392:SER:OG	6:A:1393:ASN:N	2.32	0.61
8:C:262:LEU:HD11	14:K:87:LEU:HD23	1.80	0.61
18:4:273:ARG:HH11	19:6:373:SER:HB3	1.65	0.61
2:R:123:GLU:O	2:R:222:CYS:HB3	2.00	0.61
3:D:41:GLN:OE1	3:D:41:GLN:N	2.33	0.61
6:A:966:ASN:O	6:A:970:THR:OG1	2.15	0.61
11:H:110:ASP:OD1	11:H:110:ASP:N	2.31	0.61
18:4:289:CYS:HA	19:6:319:LEU:HD12	1.82	0.61
23:2:84:LEU:HD11	23:2:86:LEU:HD23	1.81	0.61
29:O:93:GLU:HB3	29:O:103:ILE:HB	1.82	0.61
29:O:235:SER:OG	29:O:238:ARG:NH2	2.33	0.61
2:R:73:LEU:HD23	2:R:78:ALA:HA	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:14:SER:HA	14:K:114:LEU:HD13	1.81	0.61
10:F:133:VAL:O	10:F:133:VAL:HG12	2.00	0.61
27:N:19:DA:H4'	29:O:189:LEU:HG	1.81	0.61
6:A:268:ASP:HB3	6:A:299:HIS:CD2	2.35	0.61
6:A:842:VAL:HG11	7:B:1136:ASP:OD2	2.01	0.61
7:B:838:SER:OG	7:B:989:THR:O	2.10	0.61
7:B:1180:PHE:HB3	7:B:1191:ILE:HD13	1.82	0.61
7:B:1187:ASN:OD1	7:B:1189:ILE:N	2.28	0.61
8:C:76:ASP:OD2	8:C:128:ASN:N	2.30	0.61
8:C:114:TYR:N	8:C:117:ASP:OD2	2.32	0.61
21:7:608:PHE:HB3	21:7:672:GLN:HA	1.83	0.61
6:A:68:GLN:HE22	6:A:80:HIS:CE1	2.06	0.61
29:O:207:PHE:HB2	29:O:211:LYS:HB2	1.82	0.61
1:Q:127:ILE:O	2:R:133:TYR:OH	2.18	0.61
1:Q:398:ARG:NH1	7:B:328:GLU:OE2	2.33	0.61
2:R:225:MET:N	2:R:225:MET:SD	2.74	0.61
6:A:130:ASP:O	6:A:133:LYS:N	2.33	0.61
7:B:385:LEU:HD23	7:B:386:LEU:HD23	1.82	0.61
11:H:57:VAL:HB	11:H:145:ARG:CB	2.30	0.61
18:4:202:SER:HA	18:4:205:LYS:HB3	1.82	0.61
1:Q:102:PRO:HA	2:R:93:GLY:O	2.01	0.61
2:R:105:THR:HA	2:R:121:ASP:HA	1.83	0.61
5:M:251:GLN:OE1	5:M:251:GLN:N	2.33	0.61
6:A:177:ASP:OD1	6:A:180:LYS:HB2	2.00	0.61
6:A:225:ASN:OD1	6:A:227:VAL:N	2.34	0.61
6:A:626:ASN:O	6:A:631:HIS:ND1	2.26	0.61
7:B:173:MET:O	7:B:176:SER:OG	2.12	0.61
7:B:911:ILE:HG13	7:B:912:ILE:HG13	1.81	0.61
17:0:315:ASP:OD1	17:0:315:ASP:N	2.29	0.61
17:0:372:LYS:HA	17:0:375:ARG:HD3	1.83	0.61
21:7:699:GLU:O	21:7:702:ASN:ND2	2.34	0.61
29:O:68:GLN:N	29:O:161:VAL:O	2.34	0.61
6:A:57:ARG:HB2	6:A:68:GLN:HB3	1.83	0.61
6:A:665:GLY:N	6:A:668:ASP:OD2	2.21	0.61
6:A:870:GLU:OE1	9:E:202:SER:HB2	2.01	0.61
6:A:1189:SER:OG	6:A:1256:GLU:OE1	2.17	0.61
6:A:1445:ILE:HB	10:F:133:VAL:HG23	1.83	0.61
7:B:722:ASP:OD1	7:B:722:ASP:N	2.34	0.61
21:7:607:VAL:HB	21:7:653:PHE:HA	1.82	0.61
30:W:122:TYR:N	30:W:131:TYR:O	2.33	0.61
2:R:69:TRP:CE2	2:R:220:HIS:HB3	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:37:PHE:HD2	7:B:38:PHE:H	1.49	0.61
7:B:786:ASN:N	7:B:786:ASN:OD1	2.24	0.61
17:0:159:HIS:NE2	17:0:303:GLU:OE2	2.34	0.61
17:0:673:LYS:NZ	17:0:737:SER:OG	2.34	0.61
29:O:179:HIS:O	29:O:183:SER:N	2.34	0.61
7:B:512:ARG:NH1	7:B:533:CYS:O	2.33	0.60
7:B:901:PRO:HG2	15:L:60:ARG:HA	1.82	0.60
12:I:71:SER:OG	12:I:72:ASP:N	2.32	0.60
17:0:593:GLY:HA2	19:6:272:ILE:HG21	1.83	0.60
18:4:29:ILE:HB	18:4:178:VAL:HG22	1.82	0.60
27:N:24:DA:N6	28:T:141:DT:O4	2.34	0.60
1:Q:401:TYR:CZ	12:I:32:CYS:HB2	2.36	0.60
4:G:97:HIS:HA	4:G:112:LYS:HD3	1.82	0.60
6:A:739:ASP:OD2	11:H:19:ARG:NE	2.34	0.60
7:B:365:THR:HG21	7:B:370:PHE:CD2	2.37	0.60
8:C:73:GLN:O	8:C:130:GLY:N	2.24	0.60
9:E:98:ILE:HA	9:E:101:GLN:HE22	1.66	0.60
12:I:59:VAL:HG23	12:I:61:ASP:H	1.66	0.60
17:0:114:LEU:HB3	17:0:192:PRO:HG2	1.83	0.60
3:D:189:ASP:HA	3:D:192:LYS:HE3	1.82	0.60
6:A:344:ARG:NH2	7:B:1118:PRO:O	2.33	0.60
7:B:241:ARG:HG2	7:B:253:THR:HB	1.83	0.60
8:C:43:THR:OG1	8:C:44:LEU:N	2.30	0.60
11:H:107:VAL:N	11:H:111:LEU:O	2.34	0.60
23:2:384:ARG:HA	23:2:387:LEU:HB2	1.82	0.60
2:R:67:GLN:C	2:R:219:CYS:HB2	2.27	0.60
5:M:243:CYS:HA	5:M:248:LEU:HD12	1.84	0.60
6:A:230:ARG:HD2	6:A:233:TRP:CH2	2.36	0.60
6:A:1199:ARG:NH2	6:A:1233:ASP:O	2.35	0.60
7:B:568:ASP:N	7:B:568:ASP:OD1	2.33	0.60
7:B:861:ASP:OD1	7:B:914:LYS:NZ	2.28	0.60
7:B:936:ASP:OD1	7:B:938:SER:N	2.34	0.60
18:4:119:ARG:O	18:4:123:GLU:N	2.27	0.60
19:6:349:CYS:HB3	19:6:352:CYS:SG	2.40	0.60
21:7:671:ILE:HG23	21:7:708:LEU:HD13	1.83	0.60
6:A:386:ASP:N	6:A:386:ASP:OD2	2.33	0.60
6:A:411:ASP:N	6:A:411:ASP:OD1	2.35	0.60
6:A:771:GLU:N	6:A:822:GLU:OE2	2.32	0.60
6:A:998:LEU:HA	6:A:1011:GLN:HE22	1.67	0.60
6:A:1140:HIS:HB2	6:A:1276:VAL:O	2.02	0.60
7:B:121:ASN:HA	7:B:207:GLY:HA3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:0:77:SER:OG	17:0:81:LYS:NZ	2.31	0.60
1:Q:121:PHE:HB2	2:R:131:ASN:ND2	2.17	0.60
1:Q:129:PRO:HG2	1:Q:132:ASP:HB2	1.84	0.60
6:A:208:LEU:O	6:A:212:LYS:HG3	2.02	0.60
7:B:680:THR:O	7:B:683:SER:OG	2.11	0.60
7:B:878:GLN:OE1	7:B:878:GLN:N	2.35	0.60
14:K:58:PHE:HB3	14:K:76:GLN:HB3	1.83	0.60
18:4:114:UNK:C	18:4:116:ARG:H	2.15	0.60
21:7:421:ARG:HH11	21:7:437:VAL:HG11	1.67	0.60
4:G:15:PRO:HA	4:G:18:PHE:CE1	2.37	0.60
6:A:148:CYS:H	6:A:169:ASN:H	1.49	0.60
6:A:175:ARG:N	6:A:182:VAL:O	2.33	0.60
6:A:206:GLU:O	6:A:210:ILE:HG12	2.00	0.60
6:A:517:ASN:O	6:A:517:ASN:ND2	2.35	0.60
6:A:587:HIS:NE2	6:A:969:GLN:HG3	2.17	0.60
7:B:1150:ARG:O	7:B:1154:ALA:HB3	2.01	0.60
8:C:241:ASP:OD1	8:C:242:GLN:N	2.33	0.60
14:K:18:LYS:NZ	14:K:38:GLU:OE2	2.26	0.60
18:4:190:ILE:HD12	18:4:277:TYR:HE1	1.66	0.60
20:1:259:ILE:HG22	20:1:266:VAL:HG11	1.82	0.60
21:7:664:LEU:HD12	21:7:690:ILE:HD13	1.84	0.60
1:Q:375:LEU:O	1:Q:387:ILE:N	2.23	0.60
4:G:97:HIS:HE1	30:W:146:GLU:HG3	1.66	0.60
19:6:130:LEU:HD23	19:6:235:VAL:HG21	1.84	0.60
6:A:475:THR:OG1	6:A:480:ALA:O	2.19	0.60
6:A:1092:LYS:O	6:A:1094:VAL:N	2.34	0.60
6:A:1342:GLU:OE2	9:E:212:ARG:NH1	2.34	0.60
7:B:801:LYS:O	13:J:52:THR:OG1	2.20	0.60
11:H:56:THR:HB	11:H:93:TYR:HB3	1.84	0.60
11:H:94:ASP:OD2	11:H:146:ARG:NH2	2.35	0.60
20:1:504:ILE:O	20:1:508:LYS:N	2.34	0.60
21:7:608:PHE:N	21:7:671:ILE:O	2.35	0.60
22:5:9:LEU:HD11	22:5:39:HIS:HB3	1.84	0.60
2:R:93:GLY:HA2	2:R:109:ASN:HB2	1.83	0.60
6:A:544:ASP:N	6:A:544:ASP:OD1	2.30	0.60
6:A:1035:TYR:HB3	6:A:1037:LEU:HD21	1.84	0.60
17:0:112:LYS:HG2	20:1:345:ASP:HB3	1.83	0.60
17:0:241:ASP:OD1	17:0:241:ASP:N	2.29	0.60
3:D:52:LEU:HD12	3:D:148:LEU:HD23	1.84	0.59
6:A:556:TRP:O	14:K:26:LYS:NZ	2.22	0.59
7:B:635:ARG:NH1	7:B:742:GLU:OE2	2.30	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:E:26:ARG:HH12	9:E:189:GLY:HA3	1.67	0.59
21:7:459:MET:O	21:7:470:SER:OG	2.14	0.59
6:A:830:LYS:HG3	6:A:1082:ASN:HB3	1.84	0.59
7:B:213:ILE:HG13	7:B:481:GLN:HE21	1.67	0.59
7:B:776:GLN:HB2	7:B:1095:LEU:HD22	1.82	0.59
17:0:346:MET:HG2	17:0:435:MET:HG2	1.84	0.59
1:Q:338:ASN:O	1:Q:342:LEU:N	2.28	0.59
3:D:195:ILE:HG22	3:D:198:LEU:H	1.66	0.59
6:A:56:PRO:HB2	6:A:57:ARG:HH12	1.67	0.59
7:B:1129:ARG:HD3	28:T:21:DC:OP1	2.01	0.59
8:C:215:GLU:OE1	8:C:215:GLU:N	2.33	0.59
17:0:20:GLU:HG2	17:0:43:PRO:HG2	1.84	0.59
17:0:61:MET:SD	17:0:93:ARG:NH1	2.75	0.59
24:X:259:PHE:HE1	30:W:109:LEU:HD11	1.66	0.59
26:V:66:LEU:HD21	26:V:69:TYR:HB3	1.83	0.59
2:R:63:ARG:HG2	2:R:65:ASN:H	1.67	0.59
5:M:177:LEU:O	5:M:181:ARG:HG2	2.02	0.59
5:M:187:ARG:O	5:M:238:TYR:OH	2.21	0.59
6:A:575:LYS:O	6:A:579:SER:OG	2.19	0.59
6:A:1214:GLU:O	6:A:1218:GLN:HG3	2.03	0.59
12:I:32:CYS:SG	12:I:34:TYR:N	2.62	0.59
30:W:144:ARG:NH1	30:W:146:GLU:O	2.36	0.59
6:A:596:THR:C	6:A:598:LEU:H	2.11	0.59
6:A:715:GLU:OE2	6:A:774:ARG:NE	2.32	0.59
6:A:1442:ASP:OD1	6:A:1443:VAL:N	2.35	0.59
11:H:8:ASP:OD1	11:H:9:ILE:N	2.34	0.59
13:J:32:GLU:OE1	13:J:32:GLU:N	2.22	0.59
21:7:714:GLN:HG2	21:7:718:TYR:HE2	1.67	0.59
29:O:206:ILE:HG23	29:O:212:ILE:HD12	1.85	0.59
6:A:219:PHE:O	6:A:222:LEU:HG	2.03	0.59
6:A:446:ARG:HG3	6:A:487:MET:HG2	1.83	0.59
7:B:486:TYR:CZ	7:B:1096:ARG:HD2	2.37	0.59
17:0:155:LEU:HD12	17:0:160:GLU:HG3	1.83	0.59
21:7:457:TYR:HB2	21:7:493:VAL:HG21	1.83	0.59
28:T:147:DT:H2'	28:T:148:DA:H5''	1.85	0.59
6:A:609:ASP:O	6:A:611:GLN:N	2.36	0.59
6:A:790:ASP:N	6:A:790:ASP:OD1	2.33	0.59
6:A:914:GLU:OE1	6:A:978:PRO:HB2	2.02	0.59
6:A:1151:GLU:HG2	12:I:45:ARG:HB2	1.84	0.59
6:A:1159:ARG:NH2	6:A:1175:SER:OG	2.26	0.59
7:B:345:LYS:HB3	7:B:347:LYS:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:0:170:TYR:HA	17:0:199:MET:HE1	1.84	0.59
20:1:208:GLU:OE1	20:1:208:GLU:N	2.33	0.59
21:7:101:PRO:O	21:7:331:GLN:NE2	2.35	0.59
21:7:324:GLU:HA	21:7:327:LYS:HE2	1.83	0.59
21:7:709:VAL:HG21	21:7:719:SER:HB3	1.83	0.59
24:X:261:LYS:O	24:X:265:ASN:ND2	2.35	0.59
6:A:42:ASP:OD2	6:A:47:ARG:NE	2.36	0.59
6:A:203:SER:N	6:A:206:GLU:OE2	2.35	0.59
7:B:118:ARG:NH1	7:B:209:GLU:OE2	2.33	0.59
7:B:304:ASP:OD1	7:B:306:ASN:ND2	2.32	0.59
7:B:480:SER:O	7:B:480:SER:OG	2.20	0.59
17:0:69:ILE:HD12	17:0:205:ILE:HB	1.85	0.59
17:0:440:LEU:HD22	17:0:638:ARG:HA	1.84	0.59
21:7:328:LYS:O	21:7:331:GLN:NE2	2.36	0.59
21:7:411:CYS:N	21:7:456:THR:HA	2.12	0.59
29:O:202:ILE:HD11	29:O:222:GLU:HB3	1.84	0.59
5:M:210:MET:HE2	5:M:214:LEU:HG	1.84	0.59
6:A:690:VAL:HG22	6:A:718:VAL:HG22	1.83	0.59
6:A:1153:TYR:CE1	6:A:1163:ILE:HD11	2.38	0.59
13:J:3:VAL:HG11	13:J:18:TRP:HB2	1.84	0.59
17:0:443:SER:HA	17:0:446:ILE:HB	1.85	0.59
18:4:261:ILE:HG13	23:2:66:VAL:HA	1.84	0.59
6:A:1106:ASN:N	6:A:1106:ASN:OD1	2.36	0.59
7:B:487:THR:O	7:B:490:SER:N	2.35	0.59
9:E:87:SER:H	9:E:114:ASN:HB2	1.67	0.59
14:K:77:THR:OG1	14:K:78:THR:O	2.20	0.59
17:0:353:SER:HB2	17:0:417:LEU:HD11	1.84	0.59
6:A:217:LYS:HG3	6:A:218:ASP:N	2.18	0.58
6:A:793:SER:O	6:A:796:SER:OG	2.18	0.58
11:H:57:VAL:HB	11:H:145:ARG:HB2	1.85	0.58
17:0:441:ASP:OD1	17:0:646:TYR:OH	2.21	0.58
21:7:556:GLU:HG2	21:7:707:SER:HB3	1.84	0.58
6:A:1386:ARG:O	6:A:1390:ASN:HB3	2.03	0.58
7:B:1037:LEU:O	13:J:47:ARG:NH2	2.33	0.58
26:V:86:THR:HG23	26:V:105:VAL:HG22	1.85	0.58
29:O:105:ARG:NE	29:O:112:THR:OG1	2.35	0.58
6:A:849:MET:HE1	6:A:1436:ILE:HA	1.85	0.58
6:A:949:ASP:OD1	6:A:950:GLY:N	2.36	0.58
11:H:50:ALA:N	11:H:53:ASP:OD2	2.21	0.58
17:0:468:MET:SD	17:0:471:ARG:NH1	2.77	0.58
4:G:60:ARG:HA	10:F:133:VAL:HG11	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:111:THR:HB	4:G:114:LEU:HD13	1.85	0.58
7:B:583:ASN:N	7:B:583:ASN:OD1	2.34	0.58
7:B:706:GLN:O	7:B:710:LEU:HB2	2.02	0.58
9:E:100:ILE:HG23	9:E:105:PHE:HB2	1.85	0.58
2:R:66:ARG:N	2:R:216:GLY:HA3	2.18	0.58
5:M:244:SER:HB3	7:B:108:VAL:HA	1.85	0.58
6:A:1229:SER:OG	6:A:1237:ILE:N	2.19	0.58
7:B:371:GLU:OE2	7:B:371:GLU:N	2.22	0.58
14:K:53:ASP:OD1	14:K:54:ARG:N	2.36	0.58
17:0:238:HIS:HB2	17:0:660:ARG:HD2	1.85	0.58
17:0:280:GLN:OE1	17:0:283:GLN:NE2	2.37	0.58
18:4:28:VAL:HB	18:4:75:VAL:HA	1.86	0.58
20:1:343:ILE:O	20:1:345:ASP:N	2.33	0.58
6:A:351:THR:HG22	6:A:352:VAL:H	1.69	0.58
6:A:1002:GLY:H	6:A:1007:ILE:HG21	1.69	0.58
7:B:216:GLU:OE1	7:B:500:THR:OG1	2.21	0.58
7:B:708:GLU:CD	7:B:708:GLU:H	2.09	0.58
9:E:165:LEU:HD13	9:E:170:LEU:HB2	1.84	0.58
11:H:27:GLU:OE1	11:H:28:ALA:N	2.36	0.58
17:0:286:TYR:O	17:0:326:ARG:NH1	2.37	0.58
21:7:416:SER:HG	21:7:661:SER:HG	1.48	0.58
21:7:417:VAL:HG12	21:7:437:VAL:HG12	1.85	0.58
21:7:595:ILE:HA	21:7:605:ILE:HD13	1.85	0.58
21:7:640:LEU:HA	21:7:643:PHE:HB3	1.85	0.58
4:G:6:ASP:OD1	4:G:75:ARG:NH1	2.37	0.58
5:M:171:ILE:O	5:M:175:SER:OG	2.22	0.58
6:A:406:ILE:HB	6:A:431:LYS:HB2	1.86	0.58
6:A:811:GLN:OE1	6:A:811:GLN:N	2.28	0.58
6:A:1438:THR:HG23	10:F:92:ARG:HB2	1.85	0.58
7:B:590:HIS:NE2	7:B:592:ASN:O	2.32	0.58
7:B:597:MET:HE1	7:B:615:MET:HB3	1.86	0.58
1:Q:405:THR:O	1:Q:409:ALA:N	2.25	0.58
2:R:62:GLU:OE1	2:R:214:ILE:N	2.36	0.58
6:A:203:SER:OG	6:A:204:THR:N	2.37	0.58
7:B:643:ASP:C	7:B:645:SER:N	2.62	0.58
7:B:880:THR:O	7:B:933:SER:OG	2.18	0.58
11:H:118:PHE:HB2	11:H:121:LEU:HB2	1.84	0.58
17:0:78:GLU:HA	17:0:81:LYS:HD2	1.86	0.58
6:A:329:LEU:HD21	7:B:1206:GLU:OE1	2.04	0.58
6:A:452:LYS:HB2	7:B:1141:HIS:CE1	2.39	0.58
6:A:1095:THR:HG22	6:A:1100:ARG:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1133:LEU:O	6:A:1136:SER:OG	2.16	0.58
7:B:277:LYS:NZ	7:B:333:PHE:O	2.27	0.58
7:B:639:ILE:HD11	7:B:691:GLU:HB2	1.84	0.58
9:E:169:ARG:HD3	10:F:140:ASP:OD2	2.03	0.58
4:G:111:THR:H	4:G:114:LEU:HD22	1.69	0.58
6:A:269:ILE:HG13	6:A:299:HIS:HB3	1.83	0.58
6:A:399:HIS:O	6:A:435:HIS:ND1	2.36	0.58
6:A:1148:ILE:O	12:I:48:LEU:HG	2.04	0.58
17:0:330:HIS:O	17:0:333:SER:OG	2.21	0.58
17:0:624:GLY:HA2	17:0:683:ASP:HB2	1.85	0.58
22:5:10:VAL:HG11	22:5:20:ILE:HG21	1.85	0.58
28:T:147:DT:H1'	29:O:207:PHE:CZ	2.38	0.58
1:Q:99:ASN:OD1	1:Q:100:GLU:N	2.37	0.57
6:A:949:ASP:OD1	6:A:951:GLU:N	2.37	0.57
7:B:861:ASP:OD1	7:B:862:GLN:N	2.36	0.57
17:0:395:ASP:OD1	17:0:395:ASP:N	2.30	0.57
18:4:273:ARG:NH1	19:6:373:SER:HB3	2.18	0.57
21:7:715:GLU:HA	21:7:718:TYR:HD2	1.68	0.57
28:T:21:DC:H2'	28:T:22:DT:C6	2.39	0.57
3:D:154:PHE:HE2	3:D:163:VAL:HG21	1.68	0.57
6:A:118:HIS:HA	6:A:123:ARG:NH2	2.19	0.57
12:I:60:GLN:OE1	12:I:60:GLN:N	2.20	0.57
12:I:101:PHE:HE1	12:I:112:SER:HB3	1.69	0.57
17:0:308:GLU:CD	17:0:308:GLU:H	2.12	0.57
21:7:481:GLU:HB3	21:7:508:HIS:NE2	2.19	0.57
30:W:184:ASP:OD1	30:W:187:LYS:NZ	2.37	0.57
2:R:338:THR:N	2:R:350:THR:O	2.37	0.57
4:G:158:HIS:CE1	30:W:138:GLN:HE22	2.22	0.57
5:M:262:LYS:HA	5:M:265:GLU:OE1	2.05	0.57
6:A:840:ARG:NH2	6:A:1106:ASN:OD1	2.37	0.57
7:B:739:THR:HG1	7:B:740:HIS:CE1	2.19	0.57
7:B:909:ASP:OD1	7:B:909:ASP:N	2.34	0.57
21:7:554:CYS:HB3	21:7:726:LEU:HD13	1.86	0.57
25:U:269:ILE:HG21	26:V:106:ILE:HG21	1.85	0.57
30:W:68:SER:O	30:W:88:TYR:N	2.33	0.57
6:A:107:CYS:SG	6:A:109:HIS:N	2.68	0.57
8:C:102:GLN:HG3	8:C:154:LYS:HG3	1.86	0.57
11:H:55:LEU:H	11:H:146:ARG:CA	2.01	0.57
15:L:44:ASP:OD2	15:L:46:VAL:N	2.26	0.57
18:4:221:SER:O	18:4:225:GLN:N	2.31	0.57
23:2:396:ILE:HD12	23:2:399:TYR:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:266:VAL:HG13	25:U:275:THR:HG22	1.86	0.57
7:B:756:ILE:HG12	7:B:770:GLN:HG2	1.86	0.57
7:B:1177:HIS:HB3	7:B:1179:GLN:NE2	2.18	0.57
18:4:245:ILE:HA	18:4:248:LEU:HB2	1.86	0.57
19:6:196:LEU:HA	19:6:199:ILE:HD12	1.87	0.57
3:D:154:PHE:HZ	3:D:214:LEU:HD22	1.70	0.57
4:G:91:VAL:HB	4:G:139:ILE:HA	1.86	0.57
6:A:1148:ILE:HA	12:I:49:ILE:HD11	1.86	0.57
9:E:123:LEU:O	9:E:126:SER:OG	2.20	0.57
20:1:503:VAL:O	20:1:507:ILE:N	2.37	0.57
21:7:604:LYS:H	21:7:668:THR:HB	1.70	0.57
22:5:31:VAL:HA	22:5:42:VAL:HG13	1.86	0.57
25:U:260:CYS:N	25:U:281:VAL:O	2.28	0.57
4:G:4:ILE:HA	4:G:77:VAL:HG22	1.87	0.57
5:M:188:THR:HG22	5:M:190:LYS:N	2.18	0.57
6:A:781:ASP:OD1	6:A:781:ASP:N	2.34	0.57
6:A:1210:GLY:O	6:A:1214:GLU:HG2	2.05	0.57
7:B:1048:THR:OG1	7:B:1049:ASP:N	2.30	0.57
11:H:7:ASP:OD1	11:H:8:ASP:N	2.37	0.57
21:7:267:ASP:O	21:7:348:ARG:NE	2.36	0.57
21:7:311:ASP:OD1	21:7:311:ASP:N	2.31	0.57
24:X:249:GLY:H	30:W:18:ARG:NH2	2.02	0.57
2:R:95:ILE:HD13	2:R:106:LEU:HG	1.85	0.57
3:D:175:PHE:O	3:D:179:GLN:HG2	2.04	0.57
4:G:142:ARG:HB3	4:G:171:ILE:HD12	1.87	0.57
6:A:567:LYS:HB2	11:H:96:VAL:N	2.18	0.57
6:A:635:ARG:HH11	6:A:635:ARG:HA	1.69	0.57
6:A:786:HIS:N	6:A:786:HIS:CD2	2.72	0.57
6:A:922:ASP:OD1	6:A:923:LEU:N	2.37	0.57
10:F:79:ARG:NH1	10:F:145:ASP:O	2.37	0.57
12:I:2:THR:OG1	12:I:3:THR:N	2.38	0.57
15:L:61:THR:HG1	15:L:63:ARG:HH11	1.52	0.57
6:A:147:VAL:HG22	6:A:149:GLU:OE2	2.04	0.57
6:A:741:ASN:ND2	6:A:744:LYS:H	2.03	0.57
7:B:60:GLN:OE1	7:B:95:ILE:HG22	2.05	0.57
7:B:324:ILE:HD11	7:B:333:PHE:HD2	1.69	0.57
7:B:650:GLU:OE2	7:B:651:LEU:N	2.36	0.57
7:B:942:ARG:HB2	7:B:945:GLU:HG2	1.87	0.57
11:H:83:GLN:HA	14:K:54:ARG:NH2	2.20	0.57
21:7:636:ARG:HH22	21:7:657:VAL:HG21	1.70	0.57
28:T:22:DT:O4	28:T:23:DC:N4	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:T:146:DA:OP1	29:O:68:GLN:NE2	2.37	0.57
30:W:109:LEU:HD12	30:W:175:LEU:HD22	1.87	0.57
6:A:997:LEU:O	6:A:1011:GLN:NE2	2.38	0.57
7:B:807:ARG:HG2	7:B:1045:SER:OG	2.05	0.57
8:C:92:CYS:SG	8:C:93:ASP:N	2.78	0.57
17:O:104:ARG:HH22	17:O:171:LEU:HB2	1.68	0.57
17:O:224:ASN:HA	17:O:227:SER:HB3	1.87	0.57
17:O:539:VAL:HG22	17:O:599:LEU:HA	1.86	0.57
18:4:52:LYS:HD3	18:4:243:GLY:HA2	1.86	0.57
25:U:276:PHE:HB3	26:V:60:LEU:HG	1.87	0.57
3:D:119:ARG:HD3	3:D:221:TYR:HB2	1.87	0.56
9:E:4:GLU:O	9:E:8:ASN:CB	2.53	0.56
12:I:11:ASN:O	12:I:12:ASN:ND2	2.38	0.56
17:O:351:VAL:HG21	17:O:633:ARG:HD2	1.86	0.56
20:1:501:UNK:HA	20:1:504:ILE:HB	1.87	0.56
29:O:204:LEU:HD13	29:O:230:ILE:HG12	1.87	0.56
31:P:7:A:H3'	31:P:8:G:O4'	2.05	0.56
5:M:187:ARG:HA	5:M:187:ARG:HE	1.69	0.56
6:A:28:ARG:NH2	6:A:85:ASP:OD1	2.26	0.56
6:A:1157:ASP:OD1	6:A:1159:ARG:N	2.37	0.56
8:C:51:VAL:HA	8:C:155:LEU:HB3	1.87	0.56
17:O:104:ARG:NH1	17:O:171:LEU:O	2.39	0.56
21:7:499:ARG:HH12	21:7:525:GLY:H	1.52	0.56
24:X:263:TRP:HZ3	30:W:179:ILE:HD11	1.70	0.56
3:D:191:ALA:O	3:D:195:ILE:N	2.25	0.56
3:D:197:SER:O	3:D:201:LYS:NZ	2.29	0.56
4:G:94:CYS:SG	4:G:95:SER:N	2.78	0.56
5:M:249:PRO:HB2	5:M:251:GLN:HE22	1.70	0.56
6:A:1239:ARG:HH12	6:A:1241:ARG:HH12	1.50	0.56
7:B:955:THR:OG1	7:B:956:THR:N	2.37	0.56
7:B:1099:VAL:O	7:B:1102:LYS:N	2.20	0.56
9:E:54:GLN:HE22	9:E:56:LYS:H	1.53	0.56
12:I:7:CYS:SG	12:I:10:CYS:N	2.71	0.56
13:J:48:ARG:O	13:J:52:THR:HG22	2.04	0.56
17:O:196:VAL:HA	17:O:199:MET:HB2	1.87	0.56
18:4:79:TYR:O	18:4:148:THR:OG1	2.15	0.56
21:7:585:PRO:HG2	21:7:756:ARG:HG2	1.87	0.56
28:T:145:DT:H4'	29:O:68:GLN:HE21	1.69	0.56
2:R:63:ARG:HD3	2:R:66:ARG:HG3	1.86	0.56
2:R:69:TRP:HA	2:R:220:HIS:O	2.05	0.56
2:R:124:LEU:HD13	2:R:127:LYS:HD2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:6:ASP:HA	4:G:75:ARG:HA	1.86	0.56
6:A:767:GLN:NE2	6:A:798:GLY:O	2.38	0.56
7:B:259:TYR:HE2	7:B:270:LYS:HB2	1.69	0.56
7:B:590:HIS:NE2	7:B:591:ARG:O	2.38	0.56
9:E:47:CYS:HA	9:E:53:PRO:HA	1.86	0.56
11:H:113:ALA:HA	11:H:125:LEU:O	2.05	0.56
28:T:25:DC:H2'	28:T:26:DG:C8	2.41	0.56
1:Q:371:ASP:OD1	1:Q:372:SER:N	2.35	0.56
6:A:915:SER:O	6:A:919:ILE:HG12	2.05	0.56
7:B:335:GLY:HA3	7:B:348:ARG:HH21	1.69	0.56
7:B:577:ALA:HB1	7:B:589:VAL:HB	1.88	0.56
10:F:140:ASP:OD1	10:F:141:GLY:N	2.39	0.56
11:H:57:VAL:C	11:H:143:LEU:HB2	2.31	0.56
17:0:430:VAL:HG12	30:W:18:ARG:HH12	1.70	0.56
21:7:554:CYS:HA	21:7:705:PHE:HB3	1.88	0.56
23:2:377:GLN:O	23:2:382:SER:OG	2.24	0.56
29:O:202:ILE:HG21	29:O:214:LEU:HD23	1.86	0.56
30:W:28:VAL:HG13	30:W:43:LEU:HD21	1.86	0.56
3:D:26:THR:OG1	3:D:28:GLN:NE2	2.39	0.56
6:A:253:ASN:ND2	6:A:255:SER:H	2.03	0.56
7:B:371:GLU:H	7:B:371:GLU:CD	2.08	0.56
7:B:629:ASP:OD1	7:B:630:ALA:N	2.39	0.56
7:B:647:GLY:C	7:B:649:LYS:H	2.11	0.56
8:C:3:GLU:C	8:C:7:GLN:HE22	2.13	0.56
12:I:10:CYS:SG	12:I:31:THR:OG1	2.63	0.56
17:0:310:PRO:HG3	17:0:404:THR:HG23	1.86	0.56
17:0:576:ALA:HB2	20:1:343:ILE:HD11	1.88	0.56
23:2:43:ALA:HB2	23:2:77:ALA:HB1	1.86	0.56
29:O:105:ARG:HG2	29:O:112:THR:HA	1.87	0.56
7:B:272:THR:OG1	7:B:279:ASP:OD1	2.19	0.56
8:C:174:ALA:HB1	8:C:233:GLU:HG2	1.87	0.56
9:E:25:ASP:OD2	9:E:187:TYR:OH	2.16	0.56
9:E:124:VAL:HA	9:E:132:ILE:HD11	1.86	0.56
19:6:163:GLN:OE1	19:6:378:ARG:NH1	2.38	0.56
2:R:66:ARG:HD2	2:R:215:VAL:HG13	1.87	0.56
4:G:84:GLY:HA2	4:G:146:LYS:HZ3	1.70	0.56
4:G:113:HIS:O	4:G:164:LYS:NZ	2.22	0.56
6:A:42:ASP:OD1	6:A:47:ARG:NH2	2.39	0.56
6:A:1442:ASP:CG	10:F:135:ARG:HA	2.31	0.56
7:B:98:THR:OG1	7:B:99:LYS:N	2.38	0.56
7:B:834:ASN:HB2	7:B:839:MET:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:58:THR:N	11:H:143:LEU:O	2.38	0.56
12:I:51:ASN:N	12:I:51:ASN:OD1	2.35	0.56
23:2:338:SER:O	23:2:356:GLN:NE2	2.39	0.56
3:D:131:GLU:HG3	3:D:136:GLY:HA2	1.88	0.56
7:B:839:MET:HB2	7:B:1011:ILE:O	2.06	0.56
18:4:254:ILE:HG22	18:4:259:ARG:HA	1.88	0.56
30:W:140:LEU:HB2	30:W:147:PHE:CD1	2.41	0.56
10:F:135:ARG:HD2	10:F:143:PHE:CE1	2.41	0.56
18:4:225:GLN:NE2	18:4:268:GLY:O	2.39	0.56
26:V:81:LYS:HE2	26:V:110:LYS:HG3	1.87	0.56
29:O:171:ARG:HB2	29:O:237:PHE:HB3	1.87	0.56
29:O:178:SER:HB3	29:O:237:PHE:HZ	1.70	0.56
1:Q:373:TYR:OH	2:R:72:ARG:NH1	2.39	0.55
5:M:157:CYS:O	5:M:159:ASP:N	2.39	0.55
6:A:91:PHE:HA	6:A:235:ILE:HG22	1.88	0.55
6:A:1166:ASP:HB3	6:A:1239:ARG:HD2	1.87	0.55
6:A:1443:VAL:HG12	10:F:132:LEU:O	2.07	0.55
7:B:996:ARG:HD2	7:B:1007:VAL:HG11	1.87	0.55
17:0:198:ARG:NH1	17:0:199:MET:SD	2.80	0.55
17:0:251:ASP:OD1	17:0:436:ARG:NH1	2.35	0.55
17:0:537:MET:SD	17:0:567:LYS:NZ	2.77	0.55
18:4:82:GLY:N	18:4:148:THR:HG21	2.21	0.55
22:5:31:VAL:HG22	22:5:42:VAL:HG22	1.87	0.55
1:Q:99:ASN:O	2:R:97:ILE:N	2.38	0.55
1:Q:336:ASP:OD1	1:Q:337:GLU:N	2.39	0.55
2:R:74:PRO:HB2	2:R:76:PHE:CD1	2.41	0.55
3:D:215:SER:HA	3:D:218:GLU:HB2	1.87	0.55
5:M:213:ILE:O	5:M:217:LYS:HG2	2.06	0.55
6:A:351:THR:HG22	6:A:352:VAL:N	2.21	0.55
6:A:1199:ARG:HE	6:A:1236:LEU:HD21	1.70	0.55
7:B:232:SER:O	7:B:261:ARG:NH1	2.39	0.55
11:H:87:ARG:NE	11:H:87:ARG:HA	2.20	0.55
29:O:205:LEU:HB2	29:O:213:VAL:HB	1.87	0.55
1:Q:138:ARG:HH22	1:Q:355:PHE:HB3	1.70	0.55
6:A:47:ARG:HG2	6:A:257:ARG:NH1	2.21	0.55
7:B:1134:GLU:N	7:B:1134:GLU:OE1	2.33	0.55
17:0:162:LEU:HD12	17:0:166:GLU:HG2	1.88	0.55
17:0:499:LYS:HB3	17:0:503:GLN:HA	1.87	0.55
18:4:59:VAL:O	18:4:63:ALA:N	2.30	0.55
18:4:75:VAL:HG12	18:4:86:LEU:HD23	1.87	0.55
21:7:221:GLY:H	21:7:336:PRO:HG2	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:7:407:VAL:HB	21:7:452:LEU:HD22	1.87	0.55
4:G:96:GLN:N	30:W:145:THR:HB	2.21	0.55
6:A:445:ASN:N	6:A:445:ASN:OD1	2.38	0.55
6:A:1168:GLU:HA	6:A:1171:GLN:HG2	1.89	0.55
6:A:1295:THR:OG1	6:A:1297:GLU:OE2	2.21	0.55
6:A:1318:THR:O	9:E:14:ARG:NH2	2.38	0.55
6:A:1442:ASP:HA	10:F:135:ARG:N	2.22	0.55
7:B:512:ARG:NH2	7:B:531:GLN:O	2.39	0.55
21:7:457:TYR:HE1	21:7:487:LEU:HD22	1.71	0.55
2:R:66:ARG:NH1	2:R:215:VAL:O	2.37	0.55
5:M:161:LYS:O	5:M:164:LYS:HB2	2.06	0.55
6:A:803:SER:OG	6:A:805:LEU:N	2.36	0.55
7:B:708:GLU:N	7:B:708:GLU:CD	2.64	0.55
1:Q:120:LYS:HB3	1:Q:394:LYS:HZ2	1.71	0.55
1:Q:372:SER:OG	2:R:73:LEU:N	2.38	0.55
2:R:94:LYS:NZ	2:R:94:LYS:O	2.35	0.55
4:G:1:MET:N	4:G:80:LYS:O	2.35	0.55
6:A:567:LYS:HZ2	6:A:568:PRO:N	2.05	0.55
6:A:1329:THR:OG1	6:A:1331:SER:N	2.32	0.55
11:H:54:SER:HB3	11:H:146:ARG:CB	2.33	0.55
16:3:86:LYS:O	16:3:90:ASN:N	2.39	0.55
20:1:251:LEU:HB3	20:1:254:GLU:HB2	1.89	0.55
3:D:179:GLN:HB3	3:D:195:ILE:HD13	1.89	0.55
6:A:1154:TYR:HB2	6:A:1191:TRP:CZ3	2.41	0.55
6:A:1202:MET:HG3	6:A:1236:LEU:HD13	1.87	0.55
12:I:15:TYR:O	12:I:27:PHE:HA	2.07	0.55
12:I:29:CYS:SG	12:I:31:THR:OG1	2.59	0.55
23:2:140:ALA:O	23:2:144:GLU:N	2.37	0.55
25:U:259:LYS:HA	25:U:282:GLU:HG2	1.88	0.55
1:Q:362:VAL:O	1:Q:396:THR:N	2.35	0.55
2:R:211:LYS:H	2:R:211:LYS:HD2	1.71	0.55
4:G:13:LEU:HD11	4:G:17:PHE:HB2	1.89	0.55
6:A:107:CYS:HA	6:A:171:GLN:NE2	2.21	0.55
6:A:579:SER:HB3	6:A:611:GLN:HA	1.88	0.55
18:4:88:PRO:HB2	19:6:407:GLN:NE2	2.22	0.55
18:4:137:LYS:HG3	18:4:139:GLN:HG3	1.89	0.55
18:4:197:MET:HE2	19:6:377:ALA:HB2	1.89	0.55
19:6:122:ILE:HG21	19:6:379:SER:HB3	1.88	0.55
21:7:323:VAL:HA	21:7:326:VAL:HB	1.87	0.55
21:7:564:GLU:HA	21:7:567:GLN:HB2	1.89	0.55
30:W:31:ALA:HA	30:W:34:PHE:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:1:MET:HB3	4:G:82:PHE:HE2	1.71	0.55
6:A:980:ASP:OD2	6:A:1039:LYS:HB3	2.06	0.55
7:B:946:ASN:OD1	7:B:946:ASN:N	2.39	0.55
17:0:248:LEU:HB2	17:0:439:CYS:HB2	1.89	0.55
18:4:28:VAL:N	18:4:74:ALA:O	2.32	0.55
21:7:215:GLY:O	21:7:220:TYR:N	2.28	0.55
21:7:385:VAL:HG23	21:7:538:ALA:H	1.72	0.55
1:Q:121:PHE:N	2:R:131:ASN:OD1	2.39	0.55
6:A:878:ILE:HG21	6:A:955:PRO:HB2	1.90	0.55
7:B:61:ASP:N	7:B:61:ASP:OD1	2.34	0.55
8:C:93:ASP:N	8:C:93:ASP:OD1	2.40	0.55
11:H:47:PHE:HE1	11:H:94:ASP:HB2	1.72	0.55
26:V:69:TYR:HB2	26:V:76:TRP:CZ3	2.41	0.55
29:O:121:MET:HE1	29:O:136:SER:HB3	1.89	0.55
2:R:73:LEU:HD11	2:R:77:LEU:HD23	1.89	0.54
6:A:1116:LEU:HB2	6:A:1311:VAL:HG22	1.89	0.54
8:C:88:CYS:SG	8:C:92:CYS:HB3	2.47	0.54
17:0:496:ILE:HG13	17:0:706:LEU:HD13	1.90	0.54
1:Q:124:LYS:HG2	1:Q:126:LYS:NZ	2.21	0.54
1:Q:127:ILE:HG23	1:Q:129:PRO:HD3	1.88	0.54
3:D:40:HIS:HE1	4:G:74:TYR:O	1.91	0.54
7:B:331:LEU:HD23	7:B:352:ALA:HB3	1.90	0.54
7:B:334:ILE:O	7:B:348:ARG:NE	2.41	0.54
18:4:75:VAL:H	18:4:88:PRO:HD3	1.71	0.54
18:4:292:CYS:HB2	18:4:308:CYS:SG	2.47	0.54
19:6:267:SER:HA	19:6:290:ILE:HD12	1.89	0.54
21:7:435:CYS:HA	21:7:453:VAL:HA	1.89	0.54
6:A:419:LYS:NZ	6:A:419:LYS:H	2.04	0.54
6:A:798:GLY:HA2	6:A:815:PHE:CD2	2.43	0.54
6:A:1090:ALA:HA	6:A:1093:LYS:HG3	1.89	0.54
6:A:1299:VAL:HG23	6:A:1300:LYS:O	2.07	0.54
10:F:110:ASP:OD1	10:F:110:ASP:N	2.38	0.54
17:0:280:GLN:HA	17:0:283:GLN:HG2	1.89	0.54
18:4:77:ALA:HB3	18:4:132:LEU:HD11	1.87	0.54
21:7:569:TYR:HA	21:7:577:ARG:HH11	1.71	0.54
21:7:617:GLU:O	21:7:621:LYS:NZ	2.40	0.54
4:G:85:GLU:HB3	4:G:147:ILE:HD12	1.88	0.54
6:A:1111:MET:HE1	6:A:1330:ASN:ND2	2.21	0.54
8:C:98:VAL:H	8:C:122:SER:HB3	1.73	0.54
11:H:58:THR:N	11:H:143:LEU:HB2	2.22	0.54
17:0:493:LEU:HB2	17:0:678:VAL:HG13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:0:516:PRO:HB2	21:7:358:PRO:HD2	1.89	0.54
30:W:9:VAL:HG11	30:W:91:TYR:HB3	1.90	0.54
30:W:149:CYS:SG	30:W:152:CYS:N	2.70	0.54
2:R:106:LEU:HD11	2:R:122:LEU:HB2	1.89	0.54
5:M:202:GLU:O	5:M:206:THR:OG1	2.22	0.54
6:A:57:ARG:HG3	6:A:68:GLN:HB3	1.88	0.54
6:A:298:PHE:O	6:A:302:THR:HG22	2.07	0.54
6:A:1197:LEU:HB2	6:A:1236:LEU:HD12	1.89	0.54
7:B:862:GLN:CB	7:B:963:PHE:HB2	2.36	0.54
11:H:128:ASN:O	11:H:128:ASN:ND2	2.41	0.54
19:6:128:LEU:HA	19:6:233:LEU:HB3	1.88	0.54
21:7:637:MET:HA	21:7:640:LEU:HB2	1.88	0.54
23:2:62:LEU:HA	23:2:65:TRP:HD1	1.72	0.54
26:V:83:CYS:O	26:V:108:VAL:N	2.34	0.54
29:O:215:THR:OG1	29:O:216:GLY:N	2.40	0.54
30:W:123:MET:HG2	30:W:157:VAL:HB	1.88	0.54
2:R:118:HIS:ND1	2:R:120:TYR:OH	2.39	0.54
5:M:157:CYS:C	5:M:159:ASP:H	2.15	0.54
6:A:923:LEU:O	6:A:927:VAL:HG12	2.08	0.54
7:B:355:ILE:HG22	7:B:356:LEU:HD23	1.90	0.54
7:B:954:VAL:HG22	7:B:964:VAL:HG22	1.89	0.54
12:I:77:LYS:HZ3	12:I:108:HIS:HB2	1.73	0.54
13:J:6:ARG:HA	13:J:12:LYS:O	2.08	0.54
14:K:82:ASP:OD2	14:K:85:ASP:N	2.36	0.54
17:0:729:ASP:O	17:0:731:LYS:NZ	2.40	0.54
18:4:234:VAL:HG11	18:4:252:MET:HG3	1.89	0.54
19:6:182:VAL:HG21	19:6:199:ILE:HD11	1.88	0.54
23:2:432:VAL:HG23	23:2:433:LEU:HD23	1.90	0.54
24:X:201:THR:HG22	30:W:34:PHE:HA	1.88	0.54
30:W:66:LEU:HA	30:W:94:ALA:HB2	1.89	0.54
2:R:237:VAL:O	2:R:241:ARG:N	2.39	0.54
5:M:143:PRO:HB2	5:M:145:ILE:HG22	1.90	0.54
6:A:215:SER:OG	6:A:218:ASP:OD1	2.23	0.54
6:A:590:ARG:NH2	6:A:621:THR:OG1	2.40	0.54
6:A:606:LEU:HD21	6:A:608:ILE:HD11	1.88	0.54
6:A:1110:ASN:OD1	6:A:1110:ASN:N	2.36	0.54
20:1:544:ILE:O	20:1:548:GLU:N	2.33	0.54
21:7:710:SER:O	21:7:713:THR:OG1	2.25	0.54
28:T:158:DT:H2''	28:T:159:DT:O4'	2.07	0.54
1:Q:372:SER:HG	2:R:73:LEU:H	1.55	0.54
4:G:118:ASP:OD2	4:G:132:SER:OG	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:204:GLY:O	5:M:207:LEU:HG	2.08	0.54
6:A:494:SER:OG	6:A:496:GLU:OE1	2.25	0.54
6:A:1148:ILE:N	6:A:1196:GLU:O	2.36	0.54
9:E:20:LYS:HE3	9:E:34:GLU:HG2	1.89	0.54
11:H:41:ASP:OD2	11:H:122:LEU:N	2.29	0.54
15:L:62:LYS:H	15:L:63:ARG:NH1	2.06	0.54
23:2:47:ILE:HD12	23:2:104:PHE:HE2	1.73	0.54
1:Q:120:LYS:HG2	2:R:132:GLU:OE1	2.08	0.54
6:A:257:ARG:H	6:A:257:ARG:HE	1.55	0.54
6:A:1021:LEU:O	6:A:1024:SER:OG	2.18	0.54
9:E:56:LYS:NZ	9:E:84:ASP:H	2.05	0.54
11:H:100:THR:HG23	11:H:138:GLU:HA	1.88	0.54
17:0:245:ILE:HA	17:0:439:CYS:HB3	1.90	0.54
20:1:511:ALA:O	20:1:515:UNK:N	2.40	0.54
24:X:199:GLN:HA	24:X:202:PHE:HB2	1.90	0.54
6:A:1043:ASP:N	6:A:1043:ASP:OD1	2.40	0.54
6:A:1161:THR:HG22	6:A:1163:ILE:N	2.23	0.54
6:A:1261:LYS:O	6:A:1264:GLU:HG3	2.08	0.54
6:A:1436:ILE:O	6:A:1437:GLY:C	2.51	0.54
7:B:345:LYS:HA	7:B:347:LYS:N	2.23	0.54
7:B:361:LEU:HB3	7:B:364:ILE:HG13	1.89	0.54
17:0:322:PRO:HB3	17:0:376:PHE:HB2	1.89	0.54
18:4:122:ASP:HA	18:4:125:LEU:HB2	1.90	0.54
21:7:637:MET:O	21:7:641:GLN:N	2.40	0.54
23:2:39:LEU:HD13	23:2:47:ILE:HG13	1.88	0.54
6:A:512:VAL:HA	6:A:519:PRO:HA	1.90	0.53
6:A:803:SER:HG	6:A:805:LEU:H	1.56	0.53
6:A:827:THR:O	6:A:831:THR:HG23	2.09	0.53
6:A:1348:LEU:HD23	6:A:1372:VAL:HG22	1.89	0.53
10:F:77:ASP:OD2	10:F:77:ASP:N	2.28	0.53
11:H:100:THR:HG1	11:H:138:GLU:HG2	1.73	0.53
29:O:130:ASP:OD1	29:O:133:LYS:NZ	2.33	0.53
1:Q:375:LEU:HD21	2:R:134:VAL:HG21	1.90	0.53
4:G:50:ASP:OD1	4:G:53:ASN:N	2.35	0.53
5:M:236:LEU:O	5:M:239:ILE:HG12	2.08	0.53
6:A:980:ASP:OD1	6:A:1039:LYS:N	2.36	0.53
7:B:808:ALA:O	7:B:812:LEU:HD22	2.09	0.53
20:1:303:UNK:O	20:1:305:UNK:N	2.42	0.53
4:G:84:GLY:HA2	4:G:146:LYS:NZ	2.23	0.53
6:A:31:SER:HB2	6:A:83:HIS:HB3	1.91	0.53
6:A:668:ASP:OD1	6:A:742:ASN:ND2	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:731:VAL:HG23	7:B:732:SER:H	1.74	0.53
9:E:97:VAL:O	9:E:101:GLN:NE2	2.41	0.53
9:E:143:ASN:OD1	9:E:145:THR:N	2.42	0.53
19:6:166:ILE:HG12	19:6:375:HIS:HB3	1.90	0.53
24:X:269:PRO:O	30:W:65:ARG:NH2	2.41	0.53
6:A:23:SER:HG	6:A:26:GLU:H	1.52	0.53
6:A:39:GLU:HG3	6:A:50:ILE:HD13	1.91	0.53
6:A:302:THR:HA	6:A:305:ASP:O	2.09	0.53
8:C:107:SER:OG	8:C:108:GLU:N	2.42	0.53
10:F:99:LEU:O	10:F:102:SER:OG	2.22	0.53
12:I:80:SER:HG	12:I:82:GLU:H	1.53	0.53
16:3:82:VAL:O	16:3:86:LYS:N	2.31	0.53
17:0:79:ILE:HD12	17:0:207:ILE:HG22	1.91	0.53
21:7:497:MET:HA	21:7:500:ARG:HE	1.73	0.53
27:N:16:DC:H2"	27:N:17:DG:N7	2.23	0.53
3:D:35:LEU:O	3:D:47:LEU:N	2.41	0.53
3:D:68:ARG:HG2	3:D:72:ARG:HH22	1.72	0.53
6:A:414:ASP:OD1	6:A:416:ARG:N	2.34	0.53
9:E:76:GLY:HA3	9:E:106:GLN:HB2	1.90	0.53
11:H:108:SER:OG	11:H:110:ASP:OD1	2.25	0.53
17:0:257:LEU:HD22	17:0:346:MET:HE2	1.90	0.53
17:0:422:PRO:HA	17:0:433:PRO:HB3	1.91	0.53
23:2:24:ARG:HB3	23:2:219:VAL:HG11	1.90	0.53
27:N:5:DA:H61	28:T:161:DT:H3	1.55	0.53
29:O:141:ARG:NH1	29:O:144:GLN:OE1	2.38	0.53
29:O:176:ALA:HA	29:O:183:SER:HB2	1.90	0.53
2:R:94:LYS:HE3	2:R:107:LEU:HG	1.91	0.53
3:D:144:THR:HG23	4:G:105:PRO:HD3	1.91	0.53
4:G:10:ASN:HA	4:G:70:PHE:O	2.08	0.53
6:A:1209:MET:N	6:A:1231:ASP:OD1	2.28	0.53
6:A:1444:MET:CG	10:F:133:VAL:HG22	2.39	0.53
12:I:107:SER:O	12:I:107:SER:OG	2.26	0.53
15:L:61:THR:OG1	15:L:63:ARG:NH1	2.42	0.53
15:L:63:ARG:NE	15:L:63:ARG:HA	2.22	0.53
17:0:342:LEU:O	17:0:346:MET:N	2.41	0.53
24:X:203:LYS:HA	30:W:46:LEU:HD13	1.90	0.53
29:O:81:ASP:HB3	29:O:84:THR:HB	1.89	0.53
3:D:127:ASP:O	3:D:142:LYS:NZ	2.32	0.53
6:A:557:ASP:O	14:K:26:LYS:HB3	2.08	0.53
6:A:924:LYS:HE3	6:A:984:LYS:HZ2	1.73	0.53
6:A:1301:GLU:HG3	6:A:1302:PRO:HD2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:408:LEU:HD11	7:B:545:ILE:HD12	1.89	0.53
29:O:68:GLN:O	29:O:127:LYS:NZ	2.31	0.53
6:A:1441:PHE:HZ	10:F:92:ARG:HB3	1.74	0.53
7:B:26:THR:N	7:B:29:ASP:OD2	2.42	0.53
9:E:38:PRO:HB2	9:E:41:ASP:OD1	2.09	0.53
9:E:101:GLN:N	9:E:101:GLN:OE1	2.42	0.53
12:I:7:CYS:O	12:I:9:ASP:N	2.41	0.53
17:O:208:TYR:HE2	17:O:213:LEU:HB2	1.73	0.53
18:4:54:LEU:O	18:4:58:ILE:N	2.42	0.53
21:7:552:VAL:HG21	21:7:731:TYR:HD2	1.74	0.53
21:7:647:ASP:O	21:7:650:ASN:ND2	2.42	0.53
1:Q:333:LYS:HB2	7:B:70:ILE:HD11	1.90	0.53
2:R:134:VAL:N	2:R:216:GLY:O	2.32	0.53
3:D:195:ILE:HG21	3:D:198:LEU:HD12	1.89	0.53
6:A:254:GLU:OE1	7:B:935:ARG:NH1	2.42	0.53
7:B:892:LYS:NZ	7:B:909:ASP:OD2	2.41	0.53
7:B:894:ASP:N	7:B:894:ASP:OD1	2.41	0.53
12:I:18:GLU:HB3	12:I:20:LYS:HD3	1.91	0.53
18:4:52:LYS:NZ	18:4:242:GLU:O	2.41	0.53
18:4:78:ALA:HB2	18:4:152:ALA:HB2	1.90	0.53
19:6:291:LEU:HD13	19:6:297:LEU:HB3	1.91	0.53
30:W:124:CYS:N	30:W:129:THR:O	2.22	0.53
4:G:115:MET:HE3	4:G:119:LEU:HD23	1.91	0.53
6:A:41:MET:O	6:A:50:ILE:HG13	2.07	0.53
6:A:53:LEU:HD12	6:A:54:ASN:H	1.73	0.53
6:A:420:ARG:NH2	6:A:423:ASP:OD2	2.27	0.53
6:A:549:MET:HE2	6:A:577:ILE:HG21	1.90	0.53
6:A:1166:ASP:O	6:A:1170:ILE:HG12	2.09	0.53
7:B:137:TYR:N	7:B:137:TYR:CD1	2.76	0.53
7:B:345:LYS:N	7:B:346:GLU:HB3	2.23	0.53
7:B:706:GLN:N	7:B:710:LEU:HD23	2.21	0.53
7:B:1175:LEU:C	7:B:1177:HIS:H	2.16	0.53
11:H:84:ALA:H	14:K:54:ARG:HH22	1.57	0.53
17:O:53:LEU:HD13	17:O:86:LEU:HB2	1.91	0.53
20:1:370:UNK:C	20:1:372:VAL:H	2.22	0.53
21:7:212:PHE:O	21:7:216:ALA:N	2.34	0.53
21:7:615:LEU:HD12	21:7:618:TYR:HD2	1.74	0.53
23:2:19:GLN:HE21	23:2:85:HIS:CE1	2.26	0.53
26:V:62:VAL:HA	26:V:84:GLN:O	2.09	0.53
1:Q:103:LEU:HA	1:Q:384:PHE:O	2.09	0.52
3:D:34:GLN:O	3:D:47:LEU:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:154:PHE:O	3:D:155:ARG:NE	2.42	0.52
4:G:138:THR:O	4:G:141:SER:OG	2.17	0.52
6:A:584:ASN:HA	6:A:610:GLY:HA3	1.89	0.52
6:A:884:ASP:OD1	6:A:884:ASP:N	2.37	0.52
7:B:1016:ALA:O	7:B:1020:ARG:HD2	2.09	0.52
8:C:235:VAL:HG21	13:J:6:ARG:NH2	2.24	0.52
12:I:25:LEU:O	12:I:37:GLU:HA	2.09	0.52
17:O:21:GLN:O	17:O:25:MET:N	2.29	0.52
29:O:172:LEU:HD13	29:O:193:LEU:HB2	1.90	0.52
30:W:44:LYS:HA	30:W:54:LEU:HD13	1.89	0.52
30:W:98:ILE:HB	30:W:186:LEU:HD21	1.90	0.52
2:R:71:VAL:HA	2:R:222:CYS:O	2.08	0.52
4:G:92:VAL:HG23	4:G:102:GLN:HB2	1.90	0.52
5:M:60:ARG:HD2	5:M:60:ARG:N	2.24	0.52
6:A:50:ILE:C	6:A:52:GLY:H	2.18	0.52
6:A:1212:VAL:O	6:A:1216:ILE:HG13	2.09	0.52
9:E:56:LYS:HZ1	9:E:84:ASP:H	1.56	0.52
12:I:7:CYS:H	12:I:12:ASN:H	1.58	0.52
17:O:137:THR:HA	17:O:142:LYS:HB3	1.91	0.52
1:Q:100:GLU:HA	2:R:95:ILE:O	2.10	0.52
1:Q:103:LEU:HD12	1:Q:384:PHE:HB2	1.90	0.52
1:Q:133:PHE:HE1	1:Q:359:ASN:HB2	1.74	0.52
4:G:60:ARG:HA	10:F:133:VAL:CG1	2.39	0.52
5:M:193:GLN:NE2	5:M:197:HIS:HA	2.22	0.52
6:A:218:ASP:N	6:A:218:ASP:OD1	2.42	0.52
6:A:1158:PRO:HB3	6:A:1188:GLN:NE2	2.22	0.52
6:A:1445:ILE:N	10:F:132:LEU:O	2.42	0.52
7:B:135:ARG:NH1	7:B:138:GLU:HB2	2.25	0.52
7:B:864:LYS:NZ	7:B:867:GLY:O	2.42	0.52
21:7:390:ALA:HB2	21:7:692:ARG:CZ	2.39	0.52
21:7:655:SER:HB2	21:7:657:VAL:HG22	1.91	0.52
29:O:67:LEU:HD13	29:O:70:ILE:HD11	1.91	0.52
29:O:160:ILE:N	29:O:217:ALA:O	2.41	0.52
6:A:60:SER:OG	6:A:65:LEU:O	2.24	0.52
6:A:287:HIS:HA	6:A:290:GLU:OE1	2.10	0.52
6:A:858:ASN:OD1	6:A:859:SER:N	2.43	0.52
6:A:1037:LEU:HD12	6:A:1042:PHE:HD1	1.74	0.52
27:N:10:DA:H2"	27:N:11:DA:N7	2.24	0.52
29:O:165:ASP:OD1	29:O:166:VAL:N	2.42	0.52
2:R:99:LYS:HB2	2:R:103:LYS:HE2	1.91	0.52
3:D:206:GLU:O	3:D:210:ILE:HG13	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:163:LEU:O	5:M:166:LYS:HG2	2.09	0.52
12:I:17:ARG:N	12:I:26:LEU:O	2.42	0.52
17:O:125:LYS:HE2	17:O:127:THR:HG23	1.92	0.52
17:O:703:ASP:HA	17:O:706:LEU:HD23	1.91	0.52
20:1:300:UNK:O	20:1:302:UNK:N	2.42	0.52
23:2:59:LEU:HB2	23:2:96:LEU:HB2	1.92	0.52
24:X:201:THR:HA	30:W:34:PHE:HB3	1.91	0.52
25:U:282:GLU:HB2	26:V:63:LYS:HG2	1.92	0.52
29:O:170:ILE:HG21	29:O:234:LEU:HD22	1.90	0.52
30:W:98:ILE:HG22	30:W:186:LEU:HD11	1.92	0.52
6:A:858:ASN:OD1	6:A:860:LEU:N	2.43	0.52
6:A:1129:GLU:O	6:A:1133:LEU:HG	2.10	0.52
6:A:1229:SER:HB3	6:A:1237:ILE:HD12	1.91	0.52
7:B:1097:HIS:CE1	31:P:9:G:H4'	2.45	0.52
11:H:56:THR:HA	11:H:145:ARG:HH11	1.72	0.52
24:X:207:CYS:HA	24:X:210:LEU:HD12	1.91	0.52
30:W:144:ARG:NH2	30:W:145:THR:H	2.07	0.52
4:G:9:LEU:O	4:G:72:VAL:N	2.42	0.52
5:M:271:GLY:HA2	5:M:277:ILE:CG1	2.33	0.52
6:A:72:GLU:O	6:A:76:GLU:HB3	2.09	0.52
6:A:1228:TRP:HA	6:A:1238:ILE:HA	1.91	0.52
7:B:600:LEU:HB3	7:B:615:MET:HE3	1.91	0.52
11:H:57:VAL:HB	11:H:145:ARG:N	2.24	0.52
11:H:116:TYR:HB2	11:H:123:MET:HE3	1.91	0.52
18:4:217:GLY:O	18:4:237:HIS:NE2	2.40	0.52
20:1:605:GLY:O	20:1:609:SER:OG	2.26	0.52
29:O:175:LEU:HD11	29:O:195:TYR:HE1	1.74	0.52
2:R:105:THR:OG1	2:R:119:GLU:OE2	2.14	0.52
3:D:63:LEU:HD13	3:D:130:LEU:HD13	1.92	0.52
6:A:353:ILE:HG13	6:A:482:PHE:HD1	1.75	0.52
6:A:860:LEU:HD11	6:A:1394:THR:HA	1.91	0.52
7:B:232:SER:O	7:B:261:ARG:NH2	2.42	0.52
7:B:950:ASP:OD2	7:B:967:ARG:NE	2.42	0.52
9:E:119:SER:O	9:E:122:LYS:HB2	2.10	0.52
11:H:57:VAL:HA	11:H:144:ILE:N	2.24	0.52
17:O:231:ILE:HA	17:O:455:SER:HB2	1.92	0.52
29:O:84:THR:O	29:O:88:HIS:ND1	2.43	0.52
6:A:244:PRO:O	6:A:247:ARG:N	2.40	0.52
6:A:821:ARG:HE	7:B:514:LEU:HB2	1.75	0.52
8:C:22:LEU:HG	8:C:25:VAL:HG21	1.91	0.52
14:K:12:LEU:HD11	14:K:18:LYS:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:0:657:ASP:O	17:0:661:HIS:ND1	2.35	0.52
17:0:719:GLN:OE1	17:0:722:ARG:NH1	2.43	0.52
19:6:352:CYS:HB3	19:6:366:CYS:SG	2.50	0.52
20:1:260:PHE:HE1	20:1:266:VAL:HG22	1.73	0.52
1:Q:381:ASP:OD1	1:Q:382:GLY:N	2.43	0.52
3:D:167:LEU:HA	3:D:170:THR:HG23	1.92	0.52
5:M:168:MET:O	5:M:172:MET:HG2	2.10	0.52
6:A:630:ILE:O	6:A:634:THR:OG1	2.28	0.52
7:B:46:GLN:OE1	7:B:47:GLN:HG2	2.10	0.52
7:B:936:ASP:OD1	7:B:938:SER:OG	2.14	0.52
7:B:1155:SER:OG	7:B:1156:ASP:N	2.43	0.52
9:E:81:GLU:HB3	9:E:110:PHE:HA	1.92	0.52
11:H:132:LEU:HB3	11:H:135:LEU:HD11	1.92	0.52
12:I:81:ARG:N	12:I:82:GLU:OE1	2.43	0.52
17:0:23:ASN:OD1	17:0:752:LYS:NZ	2.27	0.52
18:4:225:GLN:HE22	18:4:269:SER:HA	1.73	0.52
21:7:556:GLU:HA	21:7:707:SER:HB3	1.92	0.52
23:2:481:LEU:HA	23:2:493:ILE:HG21	1.92	0.52
26:V:85:VAL:N	26:V:106:ILE:O	2.29	0.52
3:D:130:LEU:HA	3:D:133:THR:HB	1.92	0.51
6:A:593:GLU:C	6:A:593:GLU:CD	2.77	0.51
6:A:900:ASP:O	6:A:907:THR:OG1	2.24	0.51
7:B:294:ASP:OD1	7:B:294:ASP:N	2.43	0.51
7:B:486:TYR:OH	7:B:1096:ARG:HB3	2.09	0.51
10:F:146:TRP:HE3	10:F:150:GLU:HG3	1.74	0.51
12:I:51:ASN:HB3	12:I:118:ARG:NH2	2.25	0.51
17:0:497:ILE:HB	17:0:682:ALA:HA	1.91	0.51
21:7:350:PRO:HD2	21:7:480:ARG:HH12	1.75	0.51
21:7:607:VAL:N	21:7:652:ILE:O	2.31	0.51
2:R:127:LYS:HA	2:R:220:HIS:ND1	2.25	0.51
2:R:129:VAL:HG11	2:R:220:HIS:HA	1.90	0.51
3:D:66:ARG:HH12	4:G:35:GLU:CD	2.18	0.51
6:A:709:THR:N	6:A:712:GLU:OE2	2.30	0.51
6:A:1173:HIS:NE2	6:A:1227:ILE:HA	2.25	0.51
7:B:245:GLU:H	7:B:245:GLU:CD	2.18	0.51
7:B:254:LEU:HG	7:B:255:GLN:N	2.24	0.51
8:C:75:MET:HE1	8:C:239:PRO:HG2	1.91	0.51
10:F:135:ARG:HD2	10:F:143:PHE:CZ	2.45	0.51
12:I:26:LEU:HD23	12:I:37:GLU:HA	1.93	0.51
17:0:124:ARG:HH12	17:0:577:GLN:HB2	1.75	0.51
1:Q:339:ALA:O	1:Q:343:ARG:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:367:ALA:HB3	7:B:369:GLY:O	2.10	0.51
2:R:303:LEU:O	2:R:307:PHE:N	2.32	0.51
5:M:280:VAL:HG12	5:M:309:ILE:HA	1.92	0.51
6:A:115:LEU:HD13	6:A:141:LEU:HB3	1.93	0.51
7:B:422:LYS:O	7:B:425:THR:OG1	2.26	0.51
12:I:75:CYS:SG	12:I:78:CYS:N	2.83	0.51
17:O:181:LEU:HG	17:O:192:PRO:HB3	1.93	0.51
4:G:98:GLY:HA3	4:G:110:VAL:O	2.11	0.51
6:A:67:CYS:SG	6:A:80:HIS:HE1	2.16	0.51
6:A:847:ASP:OD1	6:A:847:ASP:N	2.40	0.51
6:A:1217:LYS:O	6:A:1221:LYS:HG3	2.10	0.51
6:A:1359:ASP:OD1	6:A:1361:SER:N	2.42	0.51
6:A:1444:MET:SD	10:F:133:VAL:HG22	2.50	0.51
7:B:70:ILE:HD12	7:B:89:GLU:OE2	2.10	0.51
7:B:704:ALA:HB2	7:B:738:PHE:CD2	2.45	0.51
7:B:1000:PRO:HB2	7:B:1072:MET:HE2	1.92	0.51
9:E:45:LYS:HB3	9:E:46:TYR:CE2	2.45	0.51
27:N:12:DG:N2	28:T:155:DT:O2	2.43	0.51
29:O:115:ILE:HG12	29:O:121:MET:HG2	1.93	0.51
4:G:131:GLN:HG3	4:G:136:VAL:HG22	1.92	0.51
5:M:325:ASP:HB3	5:M:326:PRO:HD3	1.93	0.51
6:A:496:GLU:H	6:A:496:GLU:CD	2.17	0.51
9:E:83:CYS:SG	9:E:88:VAL:HG22	2.50	0.51
17:O:53:LEU:O	17:O:57:ILE:N	2.36	0.51
17:O:307:VAL:HG21	17:O:381:LEU:HB3	1.93	0.51
17:O:603:ARG:NH2	17:O:626:PRO:O	2.43	0.51
18:4:66:ALA:HA	18:4:117:ARG:NH2	2.25	0.51
18:4:84:LYS:HD3	18:4:132:LEU:HB2	1.93	0.51
21:7:264:PRO:O	21:7:268:VAL:N	2.43	0.51
23:2:92:SER:OG	23:2:93:SER:N	2.44	0.51
29:O:144:GLN:NE2	29:O:150:ALA:O	2.43	0.51
3:D:64:VAL:HG22	3:D:67:ARG:HH22	1.76	0.51
6:A:172:PRO:HB3	6:A:185:TRP:CD2	2.44	0.51
6:A:596:THR:O	6:A:598:LEU:N	2.44	0.51
7:B:102:VAL:O	7:B:109:THR:HA	2.10	0.51
12:I:19:ASP:OD2	12:I:21:GLU:N	2.35	0.51
17:O:154:GLU:N	17:O:154:GLU:OE1	2.43	0.51
17:O:694:PRO:HG2	17:O:697:ILE:HB	1.92	0.51
2:R:138:GLN:H	2:R:138:GLN:CD	2.15	0.51
3:D:69:ALA:HA	3:D:72:ARG:HB3	1.92	0.51
6:A:46:THR:C	6:A:48:ALA:H	2.17	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:771:GLU:O	6:A:773:LYS:N	2.39	0.51
8:C:6:PRO:HB2	14:K:101:LEU:HG	1.93	0.51
8:C:231:ASN:C	8:C:231:ASN:HD22	2.18	0.51
9:E:88:VAL:HB	9:E:116:ILE:HD13	1.92	0.51
9:E:117:THR:O	9:E:120:ALA:N	2.43	0.51
10:F:134:ILE:HG22	10:F:135:ARG:H	1.75	0.51
11:H:57:VAL:HB	11:H:145:ARG:CA	2.40	0.51
17:0:643:ARG:HH11	17:0:650:GLU:HG3	1.75	0.51
25:U:285:TRP:HZ3	29:O:110:LYS:HE3	1.76	0.51
5:M:274:PRO:HA	5:M:277:ILE:HG12	1.92	0.51
6:A:226:GLU:OE2	6:A:230:ARG:NH2	2.42	0.51
6:A:727:ASP:OD1	6:A:727:ASP:N	2.42	0.51
6:A:851:HIS:O	6:A:854:ASN:N	2.43	0.51
6:A:857:ARG:HD3	6:A:861:GLY:O	2.11	0.51
11:H:95:TYR:O	11:H:143:LEU:HD23	2.10	0.51
15:L:61:THR:OG1	15:L:63:ARG:HG2	2.11	0.51
17:0:123:GLU:OE1	17:0:125:LYS:N	2.43	0.51
17:0:275:ARG:NH2	17:0:329:GLU:OE2	2.43	0.51
21:7:520:GLU:N	21:7:681:ARG:HH12	2.09	0.51
30:W:112:ASP:HB2	30:W:168:LYS:HG3	1.93	0.51
4:G:101:VAL:HG13	4:G:143:ILE:HD13	1.93	0.51
8:C:226:ASP:OD1	8:C:227:THR:OG1	2.25	0.51
12:I:8:ARG:CZ	12:I:8:ARG:HB3	2.40	0.51
17:0:72:CYS:HB3	17:0:210:TYR:CD1	2.46	0.51
3:D:37:GLN:CD	4:G:5:LYS:HZ1	2.18	0.51
6:A:335:ARG:HD2	7:B:1202:LEU:HD23	1.92	0.51
6:A:603:ASN:N	6:A:603:ASN:OD1	2.39	0.51
9:E:90:VAL:HA	9:E:120:ALA:HB2	1.93	0.51
14:K:60:ALA:O	14:K:73:LEU:HD12	2.10	0.51
17:0:502:ASP:OD1	17:0:521:ASN:ND2	2.44	0.51
18:4:58:ILE:HD12	18:4:125:LEU:HD13	1.93	0.51
19:6:120:ARG:HG2	19:6:309:PRO:HG3	1.92	0.51
19:6:159:GLU:O	19:6:163:GLN:NE2	2.44	0.51
20:1:501:UNK:O	20:1:505:THR:N	2.32	0.51
21:7:626:PHE:HB2	21:7:653:PHE:CD1	2.46	0.51
23:2:95:THR:OG1	23:2:96:LEU:N	2.44	0.51
4:G:23:LYS:HA	4:G:26:LEU:HB2	1.93	0.50
6:A:737:LEU:HD13	6:A:741:ASN:ND2	2.26	0.50
7:B:652:LYS:HE3	7:B:689:LEU:HD23	1.92	0.50
8:C:35:ARG:HD3	14:K:41:THR:OG1	2.11	0.50
17:0:120:VAL:HG12	17:0:129:VAL:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:175:LEU:HD12	29:O:179:HIS:HB2	1.93	0.50
1:Q:133:PHE:CE1	1:Q:359:ASN:HB2	2.46	0.50
1:Q:337:GLU:CD	1:Q:340:LYS:H	2.16	0.50
6:A:862:ASN:OD1	6:A:862:ASN:N	2.41	0.50
6:A:1441:PHE:C	6:A:1441:PHE:CD2	2.90	0.50
7:B:487:THR:O	7:B:488:TYR:C	2.54	0.50
7:B:647:GLY:H	7:B:648:HIS:C	2.19	0.50
7:B:1221:SER:C	7:B:1222:ARG:HE	2.18	0.50
18:4:202:SER:HB3	19:6:448:LEU:HD21	1.92	0.50
18:4:260:PRO:O	23:2:67:ASN:ND2	2.43	0.50
23:2:25:LEU:HD21	23:2:226:PHE:HE2	1.75	0.50
6:A:1228:TRP:HB3	6:A:1238:ILE:HG23	1.92	0.50
15:L:38:LEU:HD23	15:L:39:SER:N	2.26	0.50
17:0:495:MET:HB2	17:0:680:VAL:HA	1.91	0.50
18:4:50:ILE:O	18:4:54:LEU:N	2.38	0.50
18:4:193:TYR:HE2	18:4:274:THR:HG21	1.77	0.50
18:4:302:GLY:HA2	19:6:319:LEU:HD22	1.94	0.50
21:7:477:LEU:HB3	21:7:505:ILE:HG12	1.94	0.50
21:7:619:ALA:HB3	21:7:626:PHE:CG	2.47	0.50
23:2:457:SER:N	23:2:493:ILE:O	2.41	0.50
27:N:11:DA:C5	27:N:12:DG:C6	2.99	0.50
4:G:97:HIS:CE1	30:W:146:GLU:HA	2.46	0.50
6:A:587:HIS:HA	6:A:607:ILE:O	2.11	0.50
7:B:882:THR:O	7:B:935:ARG:HA	2.11	0.50
7:B:1107:ALA:O	7:B:1108:ARG:HB3	2.12	0.50
8:C:79:GLN:OE1	8:C:79:GLN:N	2.44	0.50
17:0:310:PRO:HB2	17:0:408:LEU:HD21	1.93	0.50
17:0:515:ASP:N	17:0:515:ASP:OD1	2.45	0.50
17:0:555:GLN:HE22	17:0:564:TRP:HZ2	1.60	0.50
18:4:286:GLY:N	19:6:322:MET:O	2.44	0.50
19:6:137:LEU:HG	19:6:204:PRO:HG2	1.93	0.50
21:7:564:GLU:OE2	21:7:756:ARG:HB2	2.11	0.50
1:Q:409:ALA:HB1	7:B:323:VAL:CG1	2.42	0.50
6:A:75:ASN:HA	7:B:1116:ARG:HH12	1.77	0.50
6:A:164:ARG:O	6:A:166:GLY:N	2.42	0.50
7:B:93:GLY:N	7:B:131:ASP:O	2.42	0.50
9:E:55:ARG:HA	9:E:58:MET:HE2	1.94	0.50
11:H:84:ALA:HA	11:H:87:ARG:HG2	1.94	0.50
17:0:237:ALA:N	17:0:460:SER:OG	2.45	0.50
18:4:258:LEU:HB3	18:4:260:PRO:HD3	1.93	0.50
19:6:266:LEU:HA	19:6:291:LEU:HG	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:7:385:VAL:HG12	21:7:514:THR:HB	1.93	0.50
28:T:144:DA:H4'	29:O:125:GLY:HA2	1.93	0.50
29:O:133:LYS:HD3	29:O:155:PHE:CE2	2.47	0.50
3:D:67:ARG:HH11	3:D:130:LEU:HD21	1.76	0.50
6:A:43:GLU:OE1	6:A:43:GLU:N	2.36	0.50
6:A:1254:ALA:HB1	6:A:1256:GLU:HG3	1.93	0.50
7:B:327:ARG:O	7:B:331:LEU:HD12	2.11	0.50
7:B:497:ARG:HG2	7:B:498:THR:H	1.76	0.50
11:H:47:PHE:CE1	11:H:94:ASP:HB2	2.46	0.50
15:L:28:LYS:HG2	15:L:29:TYR:CE2	2.46	0.50
17:O:166:GLU:HG3	17:O:198:ARG:HH21	1.76	0.50
18:4:180:THR:OG1	18:4:214:LYS:NZ	2.35	0.50
19:6:427:TYR:N	19:6:436:PHE:O	2.44	0.50
21:7:536:TYR:OH	21:7:542:GLU:OE1	2.30	0.50
24:X:162:LEU:O	24:X:166:LEU:N	2.45	0.50
28:T:151:DC:H2''	28:T:152:DG:H8	1.77	0.50
29:O:162:GLY:N	29:O:214:LEU:O	2.44	0.50
29:O:178:SER:HB3	29:O:237:PHE:CZ	2.46	0.50
2:R:76:PHE:HZ	2:R:120:TYR:HE2	1.59	0.50
4:G:100:GLU:HA	4:G:109:PHE:HA	1.94	0.50
5:M:57:VAL:HG11	7:B:1113:VAL:HG13	1.93	0.50
6:A:1130:GLN:HA	6:A:1133:LEU:HD12	1.93	0.50
7:B:878:GLN:C	7:B:879:ARG:HE	2.20	0.50
8:C:145:CYS:SG	8:C:146:LYS:N	2.85	0.50
9:E:79:TRP:HD1	9:E:96:PHE:HE1	1.58	0.50
14:K:14:GLU:OE1	14:K:14:GLU:N	2.45	0.50
15:L:40:LEU:HG	15:L:41:SER:O	2.11	0.50
17:O:349:LEU:HD23	17:O:349:LEU:H	1.77	0.50
17:O:360:LEU:HD11	17:O:410:SER:HA	1.93	0.50
18:4:244:LEU:O	18:4:248:LEU:N	2.34	0.50
19:6:269:GLN:HG3	19:6:288:TYR:CE2	2.44	0.50
19:6:403:CYS:SG	19:6:404:PHE:N	2.84	0.50
29:O:73:THR:HG23	29:O:158:GLN:HG3	1.93	0.50
4:G:166:ASP:O	4:G:168:LEU:HG	2.12	0.50
5:M:250:MET:HE2	15:L:52:GLY:HA3	1.94	0.50
5:M:267:LYS:NZ	29:O:239:LYS:HB2	2.27	0.50
7:B:299:GLU:OE2	7:B:572:HIS:N	2.33	0.50
7:B:1051:THR:OG1	7:B:1053:GLU:N	2.45	0.50
9:E:95:THR:O	9:E:98:ILE:HG22	2.11	0.50
11:H:145:ARG:NH1	11:H:146:ARG:NH2	2.59	0.50
12:I:98:VAL:HG11	12:I:113:ASP:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:6:152:TYR:HD1	19:6:298:LYS:HD3	1.76	0.50
21:7:594:LEU:O	21:7:598:HIS:ND1	2.45	0.50
21:7:627:ILE:HG12	21:7:636:ARG:HG3	1.94	0.50
23:2:10:VAL:HG12	23:2:205:LEU:HD11	1.94	0.50
1:Q:116:THR:O	1:Q:390:ASP:HB3	2.12	0.50
7:B:37:PHE:C	7:B:39:ARG:H	2.20	0.50
7:B:137:TYR:O	7:B:140:ILE:HG13	2.11	0.50
17:0:509:ARG:HH11	17:0:685:ARG:HD3	1.77	0.50
23:2:51:VAL:HG13	23:2:109:ARG:HD2	1.94	0.50
23:2:108:LEU:HG	23:2:112:LEU:HD13	1.94	0.50
30:W:6:ASP:O	30:W:10:LYS:HG3	2.12	0.50
3:D:194:LEU:HD22	4:G:86:VAL:HG11	1.93	0.49
4:G:35:GLU:OE2	4:G:48:VAL:N	2.39	0.49
4:G:79:PHE:HE2	4:G:106:MET:HG2	1.77	0.49
5:M:273:SER:O	5:M:276:THR:HG22	2.12	0.49
6:A:249:SER:O	6:A:249:SER:OG	2.27	0.49
6:A:269:ILE:HD11	6:A:300:VAL:HA	1.94	0.49
6:A:390:GLN:O	6:A:393:ARG:HB3	2.12	0.49
6:A:1364:ASN:OD1	6:A:1365:TYR:N	2.45	0.49
7:B:363:HIS:CG	7:B:363:HIS:O	2.64	0.49
7:B:1074:ASN:HB2	7:B:1081:LEU:HD21	1.94	0.49
7:B:1179:GLN:HB3	7:B:1181:GLU:OE2	2.12	0.49
9:E:60:PHE:CZ	9:E:80:VAL:HG21	2.47	0.49
11:H:23:VAL:HA	11:H:42:ILE:O	2.11	0.49
12:I:19:ASP:OD2	12:I:23:ASN:N	2.34	0.49
12:I:80:SER:OG	12:I:82:GLU:OE1	2.23	0.49
15:L:47:ARG:HH22	15:L:54:ARG:CZ	2.25	0.49
17:0:239:ASN:OD1	17:0:664:GLN:NE2	2.45	0.49
17:0:586:TYR:OH	17:0:616:TYR:O	2.28	0.49
21:7:302:GLU:HG2	21:7:322:SER:HB2	1.94	0.49
21:7:759:LEU:O	21:7:763:VAL:HG23	2.12	0.49
1:Q:124:LYS:O	1:Q:126:LYS:NZ	2.28	0.49
4:G:151:ILE:HB	4:G:158:HIS:HB2	1.93	0.49
6:A:408:ASP:O	6:A:409:SER:OG	2.20	0.49
6:A:1163:ILE:HG22	6:A:1165:GLU:H	1.76	0.49
6:A:1205:LYS:O	6:A:1274:ARG:NH1	2.45	0.49
9:E:76:GLY:H	9:E:106:GLN:HG2	1.77	0.49
9:E:79:TRP:HB2	9:E:105:PHE:CD2	2.47	0.49
15:L:47:ARG:HH12	15:L:54:ARG:NE	2.10	0.49
21:7:589:GLN:HB3	21:7:745:ILE:HD11	1.94	0.49
21:7:684:ALA:HB2	21:7:725:PHE:HZ	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:2:208:LEU:HD13	23:2:222:LEU:HD21	1.93	0.49
23:2:405:HIS:O	23:2:408:MET:N	2.45	0.49
4:G:35:GLU:CD	4:G:47:CYS:HA	2.37	0.49
6:A:594:GLY:O	6:A:596:THR:HG23	2.12	0.49
6:A:943:LEU:O	6:A:946:VAL:N	2.45	0.49
6:A:1441:PHE:C	6:A:1441:PHE:HD2	2.20	0.49
7:B:183:GLU:OE1	7:B:184:ALA:N	2.44	0.49
7:B:576:ASP:OD1	7:B:576:ASP:N	2.42	0.49
8:C:264:GLN:O	8:C:267:GLN:HB3	2.12	0.49
17:0:270:ARG:CZ	17:0:390:VAL:HA	2.42	0.49
17:0:564:TRP:CD2	20:1:239:PRO:HG3	2.46	0.49
18:4:239:GLU:CD	18:4:239:GLU:H	2.20	0.49
21:7:595:ILE:HD13	21:7:622:MET:HE3	1.95	0.49
27:N:12:DG:C5	27:N:13:DG:C6	3.00	0.49
30:W:140:LEU:HB2	30:W:147:PHE:HD1	1.76	0.49
2:R:98:ASN:OD1	2:R:103:LYS:HE3	2.12	0.49
3:D:24:ALA:N	3:D:28:GLN:HB2	2.27	0.49
4:G:14:HIS:HB3	4:G:17:PHE:HE1	1.77	0.49
4:G:108:VAL:HG22	4:G:159:ALA:HB3	1.94	0.49
6:A:607:ILE:HG23	6:A:612:ILE:HA	1.94	0.49
6:A:917:SER:OG	6:A:918:GLU:N	2.46	0.49
9:E:101:GLN:CD	9:E:101:GLN:N	2.70	0.49
12:I:77:LYS:HG3	12:I:108:HIS:CD2	2.47	0.49
18:4:55:GLU:HA	18:4:58:ILE:HB	1.93	0.49
1:Q:343:ARG:NE	1:Q:343:ARG:HA	2.27	0.49
1:Q:405:THR:O	1:Q:408:GLU:N	2.46	0.49
6:A:425:GLN:O	6:A:427:GLN:NE2	2.45	0.49
6:A:463:ILE:HD11	6:A:469:ARG:HG3	1.95	0.49
6:A:810:PRO:HG3	7:B:1047:PHE:CD1	2.47	0.49
6:A:982:THR:OG1	6:A:983:ILE:N	2.44	0.49
7:B:994:TYR:HB2	7:B:999:MET:SD	2.52	0.49
9:E:78:LEU:HD12	9:E:107:THR:O	2.12	0.49
12:I:99:LEU:HB2	12:I:112:SER:HB3	1.95	0.49
15:L:28:LYS:HG2	15:L:29:TYR:CD2	2.47	0.49
17:0:619:THR:HG22	17:0:678:VAL:HB	1.94	0.49
21:7:406:SER:HB3	21:7:482:TRP:CE3	2.48	0.49
26:V:60:LEU:HA	26:V:86:THR:O	2.12	0.49
29:O:185:TYR:CG	29:O:187:PRO:HD3	2.48	0.49
29:O:204:LEU:HD23	29:O:214:LEU:HD11	1.92	0.49
1:Q:120:LYS:HE2	1:Q:394:LYS:HZ2	1.78	0.49
3:D:61:GLU:O	3:D:64:VAL:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:46:LEU:HD21	4:G:79:PHE:HB3	1.94	0.49
5:M:189:PHE:N	29:O:188:GLU:OE1	2.37	0.49
6:A:515:GLN:HG2	6:A:516:SER:OG	2.12	0.49
6:A:766:GLY:HA2	6:A:799:PHE:CE1	2.47	0.49
6:A:873:MET:HE2	6:A:957:PRO:HB3	1.94	0.49
7:B:908:GLU:OE1	7:B:908:GLU:N	2.45	0.49
7:B:1101:ASP:N	7:B:1101:ASP:OD1	2.42	0.49
11:H:9:ILE:HD11	11:H:31:THR:HG21	1.95	0.49
11:H:84:ALA:H	14:K:54:ARG:HH12	1.59	0.49
12:I:54:GLU:OE1	12:I:120:GLN:HA	2.13	0.49
17:O:161:ASN:ND2	17:O:189:THR:O	2.46	0.49
21:7:606:ILE:HA	21:7:652:ILE:HG13	1.95	0.49
23:2:485:ASP:OD1	23:2:485:ASP:N	2.45	0.49
29:O:184:SER:H	29:O:193:LEU:HG	1.78	0.49
1:Q:116:THR:HA	2:R:136:THR:HG22	1.93	0.49
2:R:307:PHE:O	2:R:311:ASP:N	2.45	0.49
6:A:457:ALA:HB3	6:A:506:ALA:HA	1.93	0.49
7:B:27:ALA:O	7:B:30:SER:OG	2.29	0.49
9:E:33:GLU:C	9:E:33:GLU:CD	2.81	0.49
15:L:62:LYS:H	15:L:63:ARG:HH12	1.60	0.49
17:O:312:LEU:O	17:O:314:GLN:N	2.44	0.49
17:O:318:THR:H	17:O:375:ARG:HH11	1.60	0.49
17:O:564:TRP:CE2	20:1:239:PRO:HG3	2.47	0.49
21:7:564:GLU:O	21:7:568:GLU:N	2.42	0.49
3:D:49:ALA:O	3:D:50:LEU:HD23	2.13	0.49
4:G:65:ASP:OD1	4:G:65:ASP:N	2.46	0.49
5:M:126:VAL:HG13	5:M:154:TYR:HE2	1.76	0.49
6:A:870:GLU:O	9:E:205:SER:OG	2.14	0.49
7:B:643:ASP:OD2	7:B:654:ARG:NH2	2.29	0.49
17:O:211:HIS:O	17:O:215:ASP:N	2.38	0.49
21:7:438:PHE:HB3	21:7:459:MET:HG3	1.94	0.49
23:2:486:ASP:O	23:2:489:LYS:NZ	2.27	0.49
29:O:169:PRO:HA	29:O:208:VAL:O	2.13	0.49
4:G:65:ASP:O	4:G:67:SER:N	2.46	0.49
6:A:741:ASN:HD22	6:A:744:LYS:HB2	1.78	0.49
6:A:1218:GLN:O	6:A:1221:LYS:NZ	2.46	0.49
7:B:307:ASP:O	7:B:310:MET:N	2.45	0.49
9:E:185:ALA:O	9:E:189:GLY:N	2.46	0.49
14:K:10:PHE:HA	14:K:37:LYS:HB3	1.94	0.49
21:7:659:ASP:HB3	21:7:660:THR:HG22	1.95	0.49
25:U:253:ARG:HA	25:U:257:ARG:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:T:17:DG:H2'	28:T:18:DA:C4	2.47	0.49
4:G:7:LEU:HB2	4:G:74:TYR:CZ	2.48	0.49
5:M:180:CYS:SG	5:M:181:ARG:N	2.86	0.49
5:M:244:SER:CB	7:B:108:VAL:HA	2.43	0.49
6:A:36:ARG:O	6:A:270:LEU:HD21	2.12	0.49
6:A:316:GLN:O	6:A:318:SER:N	2.45	0.49
6:A:1217:LYS:C	6:A:1221:LYS:HG3	2.38	0.49
7:B:1122:ARG:HG3	7:B:1123:SER:N	2.26	0.49
8:C:91:HIS:HA	8:C:95:CYS:SG	2.53	0.49
9:E:67:GLU:O	9:E:70:SER:OG	2.25	0.49
19:6:129:THR:HG22	19:6:172:ILE:HD12	1.95	0.49
22:5:9:LEU:HD21	22:5:39:HIS:HD2	1.77	0.49
30:W:152:CYS:O	30:W:154:GLU:HG3	2.13	0.49
1:Q:337:GLU:OE1	1:Q:339:ALA:N	2.44	0.48
1:Q:377:SER:HB3	1:Q:385:THR:N	2.16	0.48
2:R:220:HIS:CG	2:R:221:GLU:N	2.81	0.48
6:A:1072:ILE:O	6:A:1075:PRO:HD2	2.13	0.48
6:A:1225:PHE:CE2	6:A:1227:ILE:HD11	2.48	0.48
8:C:81:GLU:HG3	8:C:85:ASP:HB2	1.95	0.48
12:I:113:ASP:OD2	12:I:115:LYS:N	2.46	0.48
17:0:294:HIS:ND1	17:0:383:LEU:HD12	2.28	0.48
17:0:473:LEU:HB2	17:0:475:PHE:CD1	2.48	0.48
27:N:15:DG:N2	28:T:152:DG:O4'	2.45	0.48
1:Q:120:LYS:HG3	1:Q:393:TYR:O	2.13	0.48
6:A:39:GLU:OE2	6:A:50:ILE:HG21	2.12	0.48
6:A:286:HIS:C	6:A:287:HIS:HD1	2.18	0.48
6:A:404:TYR:HB2	6:A:433:GLU:HG3	1.95	0.48
6:A:567:LYS:C	6:A:567:LYS:HD3	2.38	0.48
6:A:786:HIS:CD2	6:A:786:HIS:H	2.31	0.48
6:A:1198:ASP:OD2	6:A:1201:ALA:N	2.39	0.48
7:B:345:LYS:HA	7:B:347:LYS:H	1.78	0.48
12:I:18:GLU:O	12:I:20:LYS:HE3	2.14	0.48
17:0:512:ILE:O	17:0:513:ARG:NE	2.43	0.48
17:0:690:ARG:HG3	17:0:701:LEU:HD23	1.94	0.48
21:7:354:ILE:HD12	21:7:404:LYS:HA	1.95	0.48
26:V:82:ASN:HA	26:V:109:ASP:HA	1.93	0.48
29:O:196:ARG:HA	29:O:203:VAL:HA	1.95	0.48
1:Q:104:ARG:NH2	1:Q:105:ALA:HB3	2.28	0.48
3:D:159:THR:O	3:D:163:VAL:HG23	2.13	0.48
6:A:332:LYS:O	6:A:333:GLU:HB2	2.13	0.48
7:B:168:GLY:H	7:B:450:ALA:HB1	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:33:LEU:HG	8:C:37:MET:HE2	1.94	0.48
9:E:116:ILE:HB	9:E:121:MET:HE2	1.95	0.48
11:H:96:VAL:HG22	11:H:143:LEU:HD21	1.94	0.48
12:I:54:GLU:N	12:I:120:GLN:OE1	2.45	0.48
13:J:32:GLU:HA	13:J:35:ALA:HB3	1.95	0.48
17:O:76:MET:HB3	17:O:178:PHE:HE2	1.78	0.48
17:O:232:VAL:HG21	17:O:453:PHE:CD2	2.48	0.48
17:O:252:LEU:HB2	17:O:435:MET:HB2	1.95	0.48
23:2:475:ALA:O	23:2:479:GLY:N	2.43	0.48
27:N:21:DA:H4'	29:O:203:VAL:HG11	1.95	0.48
1:Q:375:LEU:HD21	2:R:68:VAL:HG21	1.94	0.48
5:M:129:ALA:O	5:M:133:ILE:HB	2.12	0.48
6:A:746:MET:HE1	7:B:1015:HIS:HA	1.95	0.48
6:A:1163:ILE:HD12	6:A:1163:ILE:H	1.78	0.48
7:B:40:GLU:OE2	7:B:681:TRP:HD1	1.96	0.48
7:B:643:ASP:O	7:B:645:SER:N	2.47	0.48
8:C:215:GLU:N	8:C:215:GLU:CD	2.71	0.48
10:F:135:ARG:HD2	10:F:143:PHE:CD1	2.48	0.48
11:H:34:ASP:OD2	11:H:34:ASP:N	2.45	0.48
17:O:190:LEU:HD12	17:O:195:ILE:HD11	1.94	0.48
21:7:414:SER:HB2	21:7:439:THR:HG23	1.95	0.48
21:7:555:ALA:N	21:7:705:PHE:O	2.46	0.48
23:2:53:ASN:ND2	23:2:55:ASN:OD1	2.47	0.48
29:O:114:LEU:HB2	29:O:122:VAL:HB	1.96	0.48
4:G:151:ILE:N	4:G:158:HIS:O	2.40	0.48
5:M:185:VAL:HG22	7:B:106:ASP:HB2	1.95	0.48
6:A:286:HIS:O	6:A:287:HIS:ND1	2.36	0.48
6:A:446:ARG:NH1	6:A:479:ASN:O	2.46	0.48
6:A:1445:ILE:CB	10:F:133:VAL:HG23	2.43	0.48
7:B:564:GLU:OE1	7:B:591:ARG:NE	2.46	0.48
11:H:58:THR:O	11:H:143:LEU:HD12	2.13	0.48
14:K:13:GLY:H	14:K:16:GLU:HB2	1.78	0.48
21:7:407:VAL:HG13	21:7:484:PHE:HB3	1.94	0.48
24:X:214:TRP:HD1	24:X:217:CYS:SG	2.37	0.48
3:D:71:LYS:O	3:D:75:LYS:HG3	2.13	0.48
4:G:102:GLN:HA	4:G:107:LYS:HA	1.94	0.48
5:M:241:ARG:O	5:M:245:HIS:ND1	2.47	0.48
5:M:267:LYS:HZ3	29:O:239:LYS:HB2	1.78	0.48
6:A:811:GLN:O	6:A:812:GLU:C	2.57	0.48
6:A:896:ARG:HD2	6:A:897:TYR:CE2	2.49	0.48
6:A:1012:ARG:HB2	6:A:1012:ARG:CZ	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1198:ASP:OD1	6:A:1200:ALA:N	2.46	0.48
7:B:556:THR:O	7:B:559:SER:OG	2.30	0.48
8:C:165:LYS:NZ	14:K:9:LEU:O	2.30	0.48
9:E:56:LYS:HZ3	9:E:83:CYS:HA	1.77	0.48
17:O:83:LEU:HB3	17:O:177:SER:HA	1.96	0.48
17:O:244:CYS:HB2	17:O:442:ALA:HB1	1.95	0.48
17:O:431:PRO:HG3	24:X:252:LEU:HG	1.96	0.48
17:O:496:ILE:HG12	17:O:701:LEU:HD11	1.96	0.48
21:7:579:LEU:HD22	21:7:611:ASN:ND2	2.28	0.48
23:2:223:HIS:O	23:2:227:MET:N	2.47	0.48
1:Q:398:ARG:HD3	7:B:326:ASP:OD2	2.13	0.48
4:G:21:ARG:HD2	4:G:25:TYR:CE2	2.48	0.48
5:M:211:LYS:NZ	29:O:176:ALA:HB1	2.29	0.48
5:M:277:ILE:HA	5:M:280:VAL:HG22	1.96	0.48
6:A:39:GLU:CG	6:A:50:ILE:HD13	2.43	0.48
6:A:130:ASP:CG	6:A:133:LYS:HB2	2.39	0.48
6:A:353:ILE:HG21	6:A:487:MET:SD	2.53	0.48
6:A:1435:PRO:HA	6:A:1439:GLY:O	2.14	0.48
7:B:405:ARG:O	7:B:406:LEU:HD23	2.14	0.48
7:B:586:TRP:NE1	7:B:588:GLY:O	2.34	0.48
7:B:1009:ASP:OD1	7:B:1009:ASP:N	2.34	0.48
11:H:33:GLN:HG3	11:H:129:TYR:CE1	2.49	0.48
11:H:81:PRO:O	11:H:83:GLN:N	2.47	0.48
17:O:537:MET:HB2	17:O:597:ILE:HG12	1.96	0.48
20:1:597:PHE:HE2	20:1:620:LEU:HD13	1.78	0.48
21:7:341:TYR:N	21:7:379:ALA:O	2.47	0.48
21:7:396:GLY:O	21:7:400:ALA:N	2.41	0.48
21:7:616:GLN:HE21	21:7:628:TYR:HD2	1.62	0.48
26:V:62:VAL:HG22	26:V:85:VAL:HG22	1.94	0.48
26:V:74:ASP:HB3	26:V:117:ASN:HB2	1.95	0.48
28:T:143:DT:O2	29:O:114:LEU:HD11	2.14	0.48
28:T:146:DA:H5'	29:O:68:GLN:CD	2.39	0.48
29:O:141:ARG:O	29:O:145:LYS:N	2.46	0.48
30:W:131:TYR:HD1	30:W:135:GLU:HB3	1.79	0.48
2:R:94:LYS:H	2:R:94:LYS:HZ3	1.61	0.48
3:D:50:LEU:O	4:G:2:PHE:HB2	2.14	0.48
3:D:153:ARG:HH22	3:D:182:SER:C	2.22	0.48
4:G:7:LEU:N	4:G:74:TYR:O	2.40	0.48
4:G:148:GLU:N	4:G:160:ILE:O	2.33	0.48
6:A:151:ASP:HB3	6:A:163:SER:HA	1.95	0.48
6:A:408:ASP:N	6:A:408:ASP:OD1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:678:GLU:HG2	6:A:732:LEU:HD13	1.96	0.48
6:A:1089:VAL:HG12	6:A:1091:SER:HB3	1.95	0.48
7:B:37:PHE:CD2	7:B:38:PHE:N	2.81	0.48
7:B:569:TYR:CE2	7:B:571:PRO:HG3	2.49	0.48
7:B:614:SER:C	7:B:615:MET:HG3	2.38	0.48
17:0:85:GLU:O	17:0:89:LEU:HD13	2.13	0.48
18:4:28:VAL:O	18:4:76:ILE:N	2.40	0.48
18:4:67:PHE:CE1	23:2:44:LYS:HB3	2.48	0.48
1:Q:364:SER:N	1:Q:394:LYS:O	2.46	0.48
4:G:114:LEU:HD23	4:G:161:GLY:O	2.13	0.48
6:A:408:ASP:H	6:A:430:TRP:CD1	2.32	0.48
6:A:1139:GLU:O	6:A:1275:GLY:HA3	2.13	0.48
6:A:1239:ARG:HH22	6:A:1241:ARG:HH22	1.60	0.48
6:A:1256:GLU:C	6:A:1258:HIS:H	2.22	0.48
7:B:275:TYR:O	7:B:276:ILE:HD13	2.14	0.48
7:B:647:GLY:C	7:B:649:LYS:N	2.70	0.48
7:B:1051:THR:O	7:B:1055:ILE:HG13	2.14	0.48
8:C:163:ILE:HG13	8:C:165:LYS:H	1.78	0.48
11:H:56:THR:HB	11:H:93:TYR:CD1	2.47	0.48
18:4:246:GLN:HG3	20:1:503:VAL:HG11	1.94	0.48
20:1:557:CYS:HG	20:1:585:HIS:CD2	2.29	0.48
23:2:17:ILE:O	23:2:22:GLN:NE2	2.46	0.48
24:X:266:VAL:HG21	30:W:101:LYS:HG2	1.96	0.48
25:U:285:TRP:CH2	29:O:105:ARG:HB3	2.49	0.48
27:N:22:DT:OP2	29:O:196:ARG:NH1	2.46	0.48
2:R:121:ASP:N	2:R:225:MET:O	2.36	0.48
3:D:40:HIS:CE1	4:G:74:TYR:N	2.82	0.48
6:A:118:HIS:C	6:A:123:ARG:HH12	2.22	0.48
6:A:483:ASP:O	31:P:10:A:H5"	2.13	0.48
6:A:926:GLN:NE2	6:A:926:GLN:O	2.46	0.48
7:B:128:LEU:HA	7:B:128:LEU:HD23	1.53	0.48
7:B:603:LEU:HD23	7:B:603:LEU:HA	1.58	0.48
8:C:186:LEU:HB3	8:C:188:HIS:CD2	2.49	0.48
9:E:59:SER:HG	9:E:82:PHE:H	1.56	0.48
17:0:346:MET:SD	17:0:433:PRO:HG2	2.54	0.48
17:0:369:ILE:HG21	17:0:374:LEU:HD13	1.95	0.48
28:T:24:DT:H4'	31:P:6:G:O6	2.13	0.48
1:Q:119:LEU:HD11	2:R:135:PHE:HB3	1.95	0.47
3:D:119:ARG:HB3	3:D:155:ARG:HH12	1.78	0.47
5:M:257:GLU:OE1	5:M:258:TYR:N	2.47	0.47
5:M:294:THR:O	5:M:296:ALA:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:346:ASP:OD1	6:A:346:ASP:N	2.46	0.47
6:A:784:LEU:HD23	6:A:784:LEU:HA	1.71	0.47
6:A:961:ARG:O	6:A:965:GLN:HG2	2.14	0.47
6:A:1134:ILE:HD13	6:A:1322:ILE:HG22	1.96	0.47
7:B:875:GLU:OE2	7:B:915:THR:OG1	2.18	0.47
8:C:99:LEU:HD13	8:C:120:ILE:HA	1.96	0.47
21:7:568:GLU:OE1	21:7:571:ARG:NH1	2.41	0.47
23:2:62:LEU:HA	23:2:65:TRP:CD1	2.48	0.47
30:W:11:ASN:HA	30:W:14:LYS:HD2	1.96	0.47
4:G:37:SER:O	4:G:44:TYR:HA	2.14	0.47
4:G:131:GLN:HG3	4:G:136:VAL:HG13	1.95	0.47
6:A:672:ASP:OD1	6:A:674:PRO:HD2	2.14	0.47
7:B:834:ASN:HB3	7:B:840:ILE:HG13	1.95	0.47
7:B:1164:GLY:HA3	7:B:1190:ASP:OD2	2.14	0.47
11:H:55:LEU:HB2	11:H:144:ILE:O	2.13	0.47
11:H:102:TYR:CZ	11:H:115:TYR:HB3	2.49	0.47
12:I:55:THR:H	12:I:120:GLN:CD	2.22	0.47
17:0:74:ARG:NH1	17:0:664:GLN:OE1	2.38	0.47
17:0:673:LYS:NZ	17:0:737:SER:O	2.40	0.47
18:4:71:ASN:OD1	18:4:71:ASN:N	2.44	0.47
21:7:303:ARG:HG3	21:7:320:ASN:C	2.39	0.47
21:7:609:SER:O	21:7:655:SER:HA	2.14	0.47
1:Q:139:LEU:HD23	2:R:212:THR:HG21	1.97	0.47
2:R:76:PHE:HZ	2:R:120:TYR:CE2	2.32	0.47
3:D:35:LEU:HG	3:D:36:LYS:HG3	1.96	0.47
3:D:147:TYR:HB2	4:G:104:GLY:HA2	1.95	0.47
5:M:242:PHE:HB3	5:M:302:LEU:HD21	1.96	0.47
6:A:567:LYS:CB	11:H:96:VAL:H	2.22	0.47
6:A:885:THR:O	6:A:940:ARG:NH1	2.42	0.47
6:A:1196:GLU:HA	6:A:1236:LEU:O	2.14	0.47
7:B:57:TYR:CD1	7:B:57:TYR:N	2.83	0.47
7:B:578:THR:HG23	7:B:622:LYS:C	2.40	0.47
7:B:770:GLN:HB2	7:B:984:HIS:O	2.14	0.47
7:B:899:ILE:HD11	7:B:911:ILE:HA	1.96	0.47
8:C:162:GLY:HA3	8:C:170:TRP:CE2	2.49	0.47
8:C:181:ASP:OD1	8:C:184:ASN:N	2.46	0.47
14:K:99:GLY:O	14:K:103:THR:HG23	2.15	0.47
17:0:726:GLN:HA	19:6:290:ILE:HG12	1.96	0.47
19:6:129:THR:N	19:6:233:LEU:O	2.44	0.47
20:1:184:LEU:HD21	20:1:216:LEU:HB3	1.97	0.47
20:1:222:LEU:O	20:1:226:GLN:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1:562:LYS:O	20:1:566:ILE:N	2.41	0.47
21:7:599:GLU:HG2	21:7:650:ASN:HD22	1.78	0.47
25:U:285:TRP:CZ3	29:O:110:LYS:HE3	2.50	0.47
29:O:159:ASN:ND2	29:O:161:VAL:HG22	2.29	0.47
1:Q:120:LYS:NZ	1:Q:366:GLU:OE2	2.47	0.47
3:D:156:ASP:N	3:D:156:ASP:OD1	2.46	0.47
3:D:158:GLU:OE1	3:D:158:GLU:N	2.42	0.47
6:A:1207:LEU:HA	6:A:1211:GLN:HE22	1.80	0.47
7:B:329:THR:O	7:B:332:ASP:HB3	2.14	0.47
7:B:790:ASP:OD1	7:B:790:ASP:N	2.44	0.47
7:B:1162:ILE:HA	7:B:1162:ILE:HD13	1.60	0.47
9:E:58:MET:HE3	9:E:82:PHE:CD2	2.49	0.47
15:L:28:LYS:HB3	15:L:39:SER:HA	1.97	0.47
17:0:333:SER:HB2	17:0:337:ARG:HH22	1.80	0.47
17:0:436:ARG:NE	17:0:634:ILE:HG21	2.28	0.47
17:0:687:SER:HA	17:0:706:LEU:HD12	1.96	0.47
20:1:593:LEU:HA	20:1:596:LEU:HB2	1.95	0.47
1:Q:123:SER:HB3	1:Q:361:TRP:CH2	2.50	0.47
3:D:140:ASP:HA	3:D:143:ASN:ND2	2.30	0.47
4:G:81:PRO:HG3	4:G:106:MET:SD	2.54	0.47
5:M:267:LYS:HA	5:M:270:ALA:HB3	1.96	0.47
6:A:122:MET:HE1	6:A:138:ILE:HG23	1.95	0.47
6:A:217:LYS:NZ	6:A:221:SER:OG	2.45	0.47
6:A:396:PRO:HG3	6:A:416:ARG:HG2	1.97	0.47
6:A:439:ASN:HA	6:A:459:ARG:HB3	1.96	0.47
7:B:955:THR:HB	15:L:55:ILE:HG22	1.96	0.47
9:E:78:LEU:HD11	9:E:109:ILE:HG12	1.97	0.47
12:I:51:ASN:HB3	12:I:118:ARG:CZ	2.44	0.47
13:J:53:HIS:CD2	13:J:54:VAL:H	2.32	0.47
17:0:325:ILE:HG22	17:0:331:PHE:HA	1.95	0.47
17:0:476:LYS:NZ	17:0:478:VAL:HG22	2.29	0.47
18:4:288:ILE:HD11	18:4:293:LEU:HD13	1.95	0.47
22:5:9:LEU:HD21	22:5:39:HIS:CD2	2.49	0.47
29:O:72:ALA:O	29:O:123:VAL:N	2.28	0.47
30:W:64:ASP:OD1	30:W:101:LYS:NZ	2.48	0.47
2:R:81:TRP:N	2:R:81:TRP:CD1	2.81	0.47
3:D:119:ARG:HD2	3:D:155:ARG:NH2	2.25	0.47
5:M:249:PRO:HB2	5:M:251:GLN:NE2	2.29	0.47
6:A:24:PRO:HD2	6:A:233:TRP:CD1	2.50	0.47
6:A:251:SER:HA	6:A:257:ARG:HA	1.96	0.47
6:A:446:ARG:HD2	6:A:480:ALA:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:585:VAL:HB	7:B:587:HIS:CE1	2.49	0.47
7:B:984:HIS:CD2	7:B:984:HIS:N	2.83	0.47
9:E:45:LYS:HB3	9:E:46:TYR:CD2	2.49	0.47
11:H:30:SER:HB3	11:H:36:CYS:O	2.15	0.47
12:I:51:ASN:HD22	12:I:118:ARG:HH12	1.62	0.47
17:O:37:ASN:ND2	17:O:476:LYS:O	2.47	0.47
17:O:643:ARG:HD2	17:O:650:GLU:HG3	1.97	0.47
19:6:171:ILE:HG21	19:6:196:LEU:HD11	1.95	0.47
20:1:491:UNK:O	20:1:493:UNK:N	2.47	0.47
21:7:206:ALA:O	21:7:210:ILE:N	2.32	0.47
21:7:510:LYS:HE3	21:7:531:ILE:HG12	1.96	0.47
21:7:527:LEU:HA	21:7:530:LEU:HB2	1.97	0.47
21:7:607:VAL:HA	21:7:671:ILE:HB	1.97	0.47
24:X:252:LEU:HB3	30:W:19:GLY:HA2	1.96	0.47
24:X:263:TRP:CZ3	30:W:179:ILE:HD11	2.49	0.47
27:N:17:DG:C4	27:N:18:DT:C4	3.03	0.47
1:Q:106:ILE:HD13	1:Q:385:THR:HG21	1.97	0.47
4:G:39:THR:HG1	4:G:41:LYS:H	1.60	0.47
4:G:64:THR:C	4:G:66:GLY:H	2.22	0.47
6:A:99:ILE:HG12	6:A:234:MET:HE2	1.97	0.47
6:A:525:GLN:OE1	7:B:836:GLU:N	2.47	0.47
6:A:1209:MET:HA	6:A:1212:VAL:HG23	1.95	0.47
6:A:1443:VAL:HG21	10:F:93:ILE:CD1	2.40	0.47
7:B:548:GLY:HA3	7:B:630:ALA:HB2	1.96	0.47
7:B:603:LEU:HB3	7:B:609:ILE:HG13	1.95	0.47
7:B:842:ASN:HB2	7:B:1009:ASP:HA	1.97	0.47
7:B:880:THR:O	7:B:880:THR:OG1	2.29	0.47
8:C:107:SER:OG	8:C:109:SER:N	2.48	0.47
9:E:77:SER:HG	9:E:105:PHE:HD1	1.60	0.47
10:F:93:ILE:HA	10:F:93:ILE:HD13	1.45	0.47
11:H:138:GLU:OE1	11:H:139:ASN:N	2.48	0.47
12:I:21:GLU:N	12:I:21:GLU:CD	2.73	0.47
17:O:627:PHE:HD1	17:O:654:LEU:HD12	1.80	0.47
18:4:175:ARG:NH2	18:4:211:ASP:OD2	2.48	0.47
18:4:236:LEU:HB3	18:4:238:VAL:HG13	1.96	0.47
19:6:211:GLN:HB3	19:6:243:ASP:HA	1.96	0.47
21:7:133:TRP:N	21:7:142:ILE:O	2.45	0.47
21:7:678:GLY:HA2	21:7:679:SER:HA	1.67	0.47
23:2:250:LEU:O	23:2:254:ARG:N	2.37	0.47
25:U:258:TRP:CE2	26:V:66:LEU:HD23	2.50	0.47
29:O:74:VAL:HB	29:O:121:MET:HE3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:141:ARG:HA	29:O:141:ARG:HD2	1.79	0.47
30:W:149:CYS:O	30:W:153:ASP:HA	2.14	0.47
1:Q:375:LEU:HA	1:Q:375:LEU:HD12	1.70	0.47
1:Q:377:SER:O	1:Q:384:PHE:HD1	1.98	0.47
2:R:223:GLN:HG2	2:R:224:VAL:N	2.30	0.47
5:M:299:GLY:HA2	5:M:304:VAL:HG22	1.97	0.47
6:A:567:LYS:HZ2	6:A:568:PRO:CD	2.27	0.47
6:A:668:ASP:CG	6:A:742:ASN:HD22	2.22	0.47
6:A:1257:ASP:N	6:A:1257:ASP:OD1	2.47	0.47
6:A:1271:ILE:HG22	6:A:1273:LEU:HD12	1.97	0.47
7:B:46:GLN:H	7:B:46:GLN:HG3	1.42	0.47
7:B:170:LEU:HD12	7:B:171:PRO:HD2	1.97	0.47
7:B:433:GLN:O	7:B:436:VAL:HG13	2.14	0.47
7:B:750:GLY:O	7:B:754:SER:OG	2.33	0.47
7:B:794:ASN:OD1	7:B:855:PHE:HD1	1.98	0.47
8:C:76:ASP:C	8:C:129:ILE:HD11	2.40	0.47
8:C:90:ASP:O	8:C:91:HIS:HB3	2.13	0.47
9:E:54:GLN:CD	9:E:54:GLN:C	2.82	0.47
9:E:147:HIS:CD2	9:E:149:LEU:H	2.32	0.47
12:I:36:GLU:HB3	12:I:37:GLU:OE2	2.15	0.47
12:I:74:GLU:HB2	12:I:81:ARG:NH1	2.30	0.47
17:O:12:PHE:HE2	17:O:14:TYR:HB2	1.78	0.47
17:O:104:ARG:CZ	17:O:170:TYR:HB2	2.45	0.47
17:O:271:ILE:HA	17:O:388:LEU:HD22	1.97	0.47
21:7:545:GLN:HA	21:7:550:ALA:HA	1.97	0.47
21:7:709:VAL:HG13	21:7:715:GLU:HB3	1.97	0.47
23:2:353:SER:HB2	23:2:356:GLN:HB2	1.97	0.47
30:W:144:ARG:NH1	30:W:155:PRO:HG3	2.29	0.47
1:Q:120:LYS:HD3	1:Q:394:LYS:HD2	1.95	0.47
2:R:80:LYS:HB3	2:R:81:TRP:HD1	1.79	0.47
3:D:130:LEU:O	3:D:134:THR:N	2.35	0.47
5:M:268:GLU:C	5:M:270:ALA:H	2.23	0.47
5:M:305:THR:HB	5:M:308:THR:H	1.80	0.47
6:A:178:GLY:C	6:A:179:LEU:HD13	2.40	0.47
6:A:871:ASP:OD1	6:A:872:GLY:N	2.48	0.47
6:A:1397:LEU:HB2	6:A:1426:GLU:HG3	1.96	0.47
17:O:581:LEU:O	17:O:585:THR:OG1	2.29	0.47
18:4:87:TYR:CE1	18:4:121:VAL:HG22	2.50	0.47
29:O:93:GLU:HG2	29:O:103:ILE:HD12	1.96	0.47
1:Q:117:HIS:ND1	1:Q:391:LYS:HB2	2.30	0.47
3:D:124:GLU:HA	3:D:127:ASP:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:286:ILE:HG13	5:M:291:ILE:HB	1.97	0.47
6:A:607:ILE:HG22	6:A:609:ASP:O	2.14	0.47
6:A:871:ASP:OD1	6:A:871:ASP:C	2.57	0.47
6:A:878:ILE:HD12	6:A:878:ILE:HG23	1.75	0.47
6:A:1034:GLU:O	6:A:1036:ARG:HG3	2.15	0.47
7:B:291:ILE:HD12	7:B:291:ILE:N	2.30	0.47
7:B:706:GLN:HB2	7:B:710:LEU:HD23	1.96	0.47
11:H:50:ALA:H	11:H:53:ASP:CG	2.15	0.47
11:H:125:LEU:HD12	11:H:125:LEU:HA	1.63	0.47
17:O:136:MET:HG3	17:O:154:GLU:HG2	1.97	0.47
19:6:176:ASN:HA	19:6:206:GLY:HA3	1.96	0.47
23:2:249:MET:O	23:2:253:MET:N	2.36	0.47
1:Q:106:ILE:HG13	1:Q:107:PRO:HD2	1.97	0.46
1:Q:142:LYS:O	1:Q:142:LYS:HG2	2.15	0.46
2:R:94:LYS:HZ1	2:R:107:LEU:C	2.19	0.46
6:A:20:GLY:O	7:B:1213:THR:OG1	2.31	0.46
6:A:172:PRO:HB3	6:A:185:TRP:CE2	2.50	0.46
6:A:525:GLN:CD	7:B:836:GLU:HG2	2.40	0.46
6:A:1121:GLU:O	6:A:1123:GLY:N	2.48	0.46
7:B:69:LEU:O	7:B:89:GLU:HA	2.15	0.46
7:B:547:VAL:N	7:B:612:GLU:OE2	2.45	0.46
7:B:1051:THR:OG1	7:B:1052:VAL:N	2.46	0.46
8:C:26:ASP:OD1	8:C:28:ALA:N	2.41	0.46
9:E:20:LYS:HE2	9:E:35:VAL:HA	1.96	0.46
15:L:47:ARG:HH22	15:L:54:ARG:NH1	2.13	0.46
17:O:416:PHE:HA	17:O:440:LEU:HG	1.97	0.46
18:4:130:TYR:O	18:4:134:GLU:N	2.48	0.46
18:4:303:ASN:N	18:4:303:ASN:OD1	2.48	0.46
21:7:582:ILE:O	21:7:587:LYS:HD2	2.15	0.46
29:O:175:LEU:HA	29:O:237:PHE:CD2	2.49	0.46
30:W:122:TYR:CD2	30:W:156:LEU:HB2	2.49	0.46
2:R:118:HIS:HB2	2:R:120:TYR:CE1	2.51	0.46
6:A:261:ASP:OD1	6:A:322:VAL:HG13	2.16	0.46
6:A:770:VAL:HA	6:A:822:GLU:OE1	2.15	0.46
6:A:1166:ASP:OD2	6:A:1194:ARG:NE	2.34	0.46
6:A:1174:PHE:CD1	6:A:1175:SER:N	2.79	0.46
6:A:1187:GLN:HE22	6:A:1188:GLN:NE2	2.13	0.46
7:B:805:THR:O	7:B:1044:ALA:N	2.35	0.46
7:B:990:ILE:HD12	7:B:990:ILE:HG23	1.65	0.46
7:B:1046:PRO:HB2	7:B:1047:PHE:CD2	2.50	0.46
15:L:27:LEU:HG	15:L:37:LYS:NZ	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:0:252:LEU:O	17:0:434:ILE:HA	2.16	0.46
17:0:534:PRO:HA	19:6:239:LEU:HG	1.97	0.46
18:4:64:HIS:O	18:4:71:ASN:ND2	2.31	0.46
21:7:422:GLN:HA	21:7:426:GLN:HE22	1.79	0.46
23:2:81:MET:HG2	23:2:86:LEU:HD11	1.97	0.46
25:U:253:ARG:HD3	25:U:255:LYS:H	1.80	0.46
25:U:269:ILE:O	25:U:272:ASN:ND2	2.48	0.46
29:O:175:LEU:HD11	29:O:195:TYR:CE1	2.51	0.46
1:Q:373:TYR:H	2:R:82:ARG:HH21	1.60	0.46
5:M:188:THR:HG23	29:O:188:GLU:CD	2.41	0.46
6:A:1406:VAL:HG13	6:A:1407:GLU:OE1	2.16	0.46
7:B:302:CYS:SG	7:B:307:ASP:HB3	2.55	0.46
7:B:586:TRP:C	7:B:586:TRP:CD1	2.91	0.46
7:B:1221:SER:O	7:B:1222:ARG:NE	2.40	0.46
8:C:60:ASP:O	8:C:63:ILE:N	2.48	0.46
17:0:694:PRO:O	17:0:698:ALA:N	2.31	0.46
18:4:194:ILE:HB	18:4:195:PRO:HD3	1.96	0.46
21:7:303:ARG:HB2	21:7:323:VAL:H	1.79	0.46
29:O:82:LEU:HD11	29:O:117:ALA:HB2	1.97	0.46
30:W:65:ARG:NE	30:W:93:HIS:HB3	2.30	0.46
3:D:56:ARG:HE	3:D:148:LEU:HB3	1.79	0.46
3:D:156:ASP:O	3:D:158:GLU:N	2.48	0.46
6:A:74:MET:O	6:A:76:GLU:N	2.48	0.46
6:A:120:GLU:OE1	6:A:123:ARG:HD2	2.15	0.46
6:A:441:PRO:HA	6:A:458:HIS:O	2.15	0.46
7:B:1181:GLU:HA	7:B:1187:ASN:O	2.16	0.46
9:E:98:ILE:HA	9:E:101:GLN:NE2	2.31	0.46
13:J:23:ASN:HB3	13:J:27:GLU:OE2	2.15	0.46
17:0:681:LEU:HB3	17:0:686:PHE:CE2	2.50	0.46
20:1:260:PHE:HD1	20:1:266:VAL:HG13	1.80	0.46
20:1:517:UNK:O	20:1:519:UNK:N	2.49	0.46
21:7:660:THR:HA	21:7:661:SER:HA	1.75	0.46
28:T:145:DT:H1'	28:T:146:DA:C8	2.50	0.46
2:R:118:HIS:HB2	2:R:120:TYR:CZ	2.50	0.46
6:A:683:ILE:O	6:A:687:LYS:HG2	2.15	0.46
6:A:711:ARG:NH2	12:I:96:SER:O	2.46	0.46
6:A:1127:ASP:CG	6:A:1130:GLN:H	2.23	0.46
6:A:1218:GLN:HA	6:A:1221:LYS:HD3	1.98	0.46
6:A:1441:PHE:CZ	10:F:92:ARG:HB3	2.51	0.46
7:B:468:GLU:H	7:B:471:LYS:HB2	1.80	0.46
7:B:647:GLY:N	7:B:648:HIS:C	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:1177:HIS:O	7:B:1179:GLN:HG3	2.15	0.46
10:F:97:ARG:O	10:F:101:ILE:HG13	2.16	0.46
11:H:36:CYS:HA	11:H:126:GLU:O	2.16	0.46
14:K:5:ASP:O	14:K:8:GLU:HG2	2.14	0.46
17:0:13:PRO:HG3	17:0:89:LEU:HD11	1.96	0.46
17:0:252:LEU:HD12	17:0:435:MET:HG3	1.96	0.46
17:0:465:PRO:HD2	17:0:656:PHE:HD2	1.80	0.46
17:0:473:LEU:HB2	17:0:475:PHE:CE1	2.50	0.46
18:4:61:LEU:HD11	18:4:73:VAL:HB	1.96	0.46
18:4:288:ILE:HB	18:4:295:VAL:HG22	1.97	0.46
21:7:443:LYS:HD3	21:7:444:GLU:H	1.81	0.46
21:7:587:LYS:HG3	21:7:708:LEU:HD23	1.96	0.46
21:7:636:ARG:HH12	21:7:657:VAL:HG23	1.81	0.46
21:7:751:ALA:O	21:7:756:ARG:NH2	2.46	0.46
23:2:243:SER:O	23:2:247:ARG:N	2.31	0.46
23:2:503:ASP:HA	23:2:506:LYS:HG2	1.97	0.46
26:V:65:ASN:O	26:V:81:LYS:N	2.39	0.46
4:G:40:GLY:H	4:G:154:VAL:HA	1.81	0.46
6:A:84:ILE:HD11	6:A:270:LEU:HD12	1.98	0.46
6:A:998:LEU:HA	6:A:1011:GLN:NE2	2.28	0.46
7:B:890:TYR:OH	7:B:936:ASP:OD2	2.34	0.46
7:B:1114:LEU:HD12	7:B:1114:LEU:HA	1.61	0.46
7:B:1183:LYS:HB2	7:B:1183:LYS:HE3	1.71	0.46
11:H:145:ARG:NH1	11:H:146:ARG:CZ	2.79	0.46
13:J:58:GLU:O	13:J:61:LEU:N	2.48	0.46
21:7:552:VAL:HG11	21:7:731:TYR:CD2	2.50	0.46
21:7:668:THR:OG1	21:7:694:LYS:NZ	2.31	0.46
21:7:692:ARG:NE	21:7:692:ARG:HA	2.30	0.46
28:T:159:DT:H2'	28:T:160:DT:C6	2.51	0.46
29:O:202:ILE:HG13	29:O:222:GLU:O	2.16	0.46
30:W:136:ALA:HB1	30:W:147:PHE:CD2	2.51	0.46
31:P:9:G:C6	31:P:10:A:C6	3.04	0.46
1:Q:104:ARG:HD2	1:Q:104:ARG:HA	1.55	0.46
1:Q:365:TYR:CE2	1:Q:367:ALA:HB2	2.50	0.46
2:R:80:LYS:HB3	2:R:81:TRP:CD1	2.51	0.46
4:G:111:THR:HG22	4:G:112:LYS:H	1.79	0.46
6:A:872:GLY:O	6:A:1058:VAL:HG12	2.15	0.46
6:A:898:ARG:HB3	6:A:906:HIS:CD2	2.51	0.46
6:A:934:LYS:O	6:A:937:VAL:HG22	2.15	0.46
6:A:956:LEU:HD23	6:A:956:LEU:HA	1.63	0.46
7:B:794:ASN:C	7:B:795:ILE:HD12	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:E:39:LEU:O	9:E:42:PHE:HB3	2.15	0.46
11:H:57:VAL:O	11:H:58:THR:OG1	2.29	0.46
13:J:50:ILE:HA	13:J:50:ILE:HD13	1.60	0.46
13:J:61:LEU:HD23	13:J:61:LEU:HA	1.67	0.46
14:K:50:LEU:HD13	14:K:75:ILE:HD12	1.98	0.46
17:O:76:MET:HA	17:O:79:ILE:HB	1.97	0.46
19:6:164:ASN:ND2	19:6:305:VAL:O	2.49	0.46
21:7:342:ASP:OD1	21:7:342:ASP:N	2.46	0.46
21:7:438:PHE:HB2	21:7:455:SER:HB2	1.98	0.46
22:5:7:GLY:HA3	22:5:41:LEU:HD11	1.97	0.46
27:N:20:DT:C4	27:N:21:DA:N6	2.83	0.46
27:N:30:DA:C2	27:N:31:DT:C2	3.03	0.46
2:R:63:ARG:HG2	2:R:65:ASN:N	2.29	0.46
2:R:68:VAL:HG21	2:R:134:VAL:HG21	1.98	0.46
4:G:112:LYS:HA	4:G:112:LYS:HD2	1.74	0.46
5:M:276:THR:HA	5:M:279:VAL:HG12	1.98	0.46
6:A:882:SER:O	6:A:1025:ARG:NH2	2.40	0.46
6:A:1147:THR:HG23	12:I:48:LEU:HD11	1.98	0.46
6:A:1239:ARG:HH12	6:A:1241:ARG:NH1	2.13	0.46
7:B:185:THR:OG1	7:B:188:ASP:OD1	2.24	0.46
7:B:313:MET:HE3	7:B:313:MET:HB3	1.67	0.46
7:B:546:SER:OG	7:B:632:ARG:N	2.49	0.46
7:B:863:GLU:OE2	7:B:873:THR:HA	2.16	0.46
17:O:17:ILE:HG13	17:O:18:TYR:H	1.79	0.46
19:6:444:ILE:O	19:6:449:HIS:HA	2.16	0.46
21:7:578:MET:HA	21:7:581:TYR:CZ	2.50	0.46
22:5:58:LEU:HD23	23:2:450:ARG:HH11	1.80	0.46
27:N:17:DG:H22	28:T:149:DC:H42	1.63	0.46
27:N:22:DT:H1'	29:O:215:THR:OG1	2.16	0.46
29:O:67:LEU:HD11	29:O:220:ARG:HG3	1.98	0.46
29:O:161:VAL:HA	29:O:215:THR:HB	1.98	0.46
30:W:136:ALA:HB1	30:W:147:PHE:CG	2.51	0.46
2:R:73:LEU:HD12	2:R:74:PRO:CD	2.46	0.46
2:R:74:PRO:HB2	2:R:76:PHE:HD1	1.80	0.46
6:A:578:LEU:HA	6:A:578:LEU:HD12	1.56	0.46
6:A:1100:ARG:NH1	6:A:1103:GLU:OE1	2.37	0.46
6:A:1167:GLU:HA	6:A:1170:ILE:HG12	1.97	0.46
6:A:1208:THR:OG1	6:A:1211:GLN:HG3	2.16	0.46
6:A:1221:LYS:HE2	6:A:1221:LYS:HB2	1.58	0.46
6:A:1286:LYS:HG3	6:A:1304:TRP:CH2	2.51	0.46
7:B:744:HIS:O	7:B:747:MET:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:1099:VAL:O	7:B:1101:ASP:N	2.49	0.46
9:E:87:SER:N	9:E:114:ASN:HB2	2.31	0.46
11:H:38:LEU:HD12	11:H:39:THR:N	2.31	0.46
12:I:33:SER:O	12:I:35:VAL:HG23	2.16	0.46
18:4:175:ARG:HH12	18:4:252:MET:HB3	1.80	0.46
23:2:10:VAL:HA	23:2:13:TYR:HB3	1.98	0.46
2:R:62:GLU:HG2	2:R:63:ARG:N	2.31	0.46
5:M:37:ARG:HG3	6:A:416:ARG:NH2	2.28	0.46
5:M:276:THR:O	5:M:280:VAL:HG13	2.16	0.46
6:A:43:GLU:OE2	6:A:48:ALA:HB3	2.16	0.46
6:A:507:VAL:HG13	6:A:521:MET:HE1	1.96	0.46
6:A:557:ASP:OD1	6:A:559:VAL:N	2.48	0.46
6:A:809:THR:N	6:A:812:GLU:OE2	2.40	0.46
6:A:1035:TYR:N	6:A:1035:TYR:CD1	2.79	0.46
6:A:1266:THR:HG23	6:A:1270:ASN:OD1	2.16	0.46
7:B:365:THR:OG1	7:B:367:LEU:N	2.38	0.46
7:B:416:LEU:HD12	7:B:416:LEU:HA	1.69	0.46
7:B:796:LEU:HD12	7:B:796:LEU:HA	1.68	0.46
7:B:838:SER:HB2	7:B:839:MET:CG	2.46	0.46
7:B:900:ALA:HB3	15:L:61:THR:HB	1.98	0.46
7:B:906:SER:O	7:B:941:LEU:HD21	2.16	0.46
17:0:527:VAL:HG22	17:0:531:LYS:HE3	1.98	0.46
28:T:149:DC:H2"	28:T:150:DG:C8	2.51	0.46
5:M:275:ILE:H	5:M:275:ILE:HD12	1.81	0.45
6:A:658:LEU:HG	6:A:659:HIS:ND1	2.31	0.45
6:A:1217:LYS:O	6:A:1221:LYS:N	2.49	0.45
6:A:1359:ASP:CG	6:A:1361:SER:H	2.24	0.45
7:B:234:ILE:H	7:B:234:ILE:HG12	1.43	0.45
8:C:174:ALA:HB3	8:C:233:GLU:O	2.16	0.45
9:E:119:SER:O	9:E:123:LEU:HD22	2.16	0.45
17:0:106:LEU:HD12	17:0:199:MET:HG3	1.97	0.45
17:0:244:CYS:O	17:0:247:SER:OG	2.30	0.45
17:0:508:SER:HB2	17:0:546:TYR:CE1	2.51	0.45
19:6:188:ASN:ND2	19:6:191:ASP:OD2	2.49	0.45
21:7:132:LEU:O	21:7:202:LYS:N	2.44	0.45
21:7:241:ILE:O	21:7:245:LEU:N	2.39	0.45
21:7:604:LYS:O	21:7:669:CYS:N	2.50	0.45
1:Q:110:ASP:O	1:Q:114:MET:HB2	2.16	0.45
1:Q:372:SER:HG	2:R:73:LEU:N	2.14	0.45
2:R:295:PRO:O	2:R:299:ILE:N	2.31	0.45
3:D:154:PHE:HB3	3:D:160:VAL:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:37:ARG:NH1	6:A:417:TYR:OH	2.48	0.45
5:M:127:GLN:HA	5:M:130:PHE:HB2	1.98	0.45
6:A:220:THR:OG1	6:A:221:SER:N	2.50	0.45
6:A:382:PRO:HG3	6:A:428:TYR:CZ	2.50	0.45
6:A:399:HIS:HB3	6:A:400:PRO:HD3	1.97	0.45
7:B:128:LEU:HB2	7:B:167:ILE:O	2.16	0.45
7:B:519:TRP:CD1	7:B:519:TRP:C	2.94	0.45
9:E:37:LEU:HD23	9:E:38:PRO:HD2	1.98	0.45
9:E:157:SER:N	9:E:160:GLU:OE1	2.49	0.45
10:F:136:ARG:O	10:F:137:TYR:CG	2.70	0.45
17:0:63:TYR:O	17:0:67:ARG:NH2	2.49	0.45
17:0:257:LEU:HA	17:0:260:ALA:HB3	1.97	0.45
17:0:446:ILE:HD12	17:0:473:LEU:HD13	1.97	0.45
19:6:251:ILE:HG12	19:6:276:LEU:HD13	1.99	0.45
20:1:466:UNK:O	20:1:468:UNK:N	2.49	0.45
21:7:362:ILE:HD11	21:7:367:GLU:HB3	1.98	0.45
2:R:70:LEU:HD12	2:R:71:VAL:H	1.81	0.45
4:G:83:LYS:HE3	4:G:150:CYS:HB2	1.97	0.45
5:M:251:GLN:NE2	5:M:252:VAL:HG23	2.31	0.45
6:A:276:LEU:HD23	6:A:276:LEU:HA	1.56	0.45
6:A:288:ALA:HA	6:A:291:GLU:CD	2.41	0.45
6:A:559:VAL:HG13	11:H:78:SER:HA	1.98	0.45
6:A:904:THR:O	6:A:907:THR:HB	2.16	0.45
7:B:68:THR:HA	7:B:90:ILE:O	2.17	0.45
7:B:140:ILE:HA	7:B:141:ASP:HA	1.68	0.45
7:B:219:ALA:HB3	7:B:222:ILE:HD12	1.99	0.45
7:B:864:LYS:HA	7:B:872:GLU:CD	2.42	0.45
7:B:880:THR:OG1	7:B:934:LYS:NZ	2.33	0.45
7:B:1106:ARG:NH2	7:B:1109:GLY:O	2.49	0.45
9:E:4:GLU:N	9:E:4:GLU:OE1	2.49	0.45
9:E:94:LYS:HE3	9:E:123:LEU:HG	1.99	0.45
14:K:82:ASP:OD1	14:K:84:LYS:HG3	2.16	0.45
17:0:49:THR:HA	17:0:52:LEU:HB2	1.97	0.45
17:0:256:ALA:O	17:0:260:ALA:N	2.43	0.45
17:0:351:VAL:HB	17:0:421:GLU:HG2	1.97	0.45
17:0:487:LEU:HG	17:0:489:LYS:H	1.82	0.45
19:6:347:TYR:N	19:6:356:VAL:O	2.39	0.45
23:2:356:GLN:HE22	23:2:360:LEU:HD11	1.81	0.45
24:X:144:VAL:N	24:X:176:GLY:HA3	2.31	0.45
29:O:61:SER:OG	29:O:62:GLY:N	2.50	0.45
29:O:133:LYS:HB2	29:O:155:PHE:CZ	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:378:VAL:HB	2:R:68:VAL:HA	1.97	0.45
6:A:55:ASP:HA	6:A:58:LEU:HD23	1.97	0.45
6:A:220:THR:C	6:A:222:LEU:N	2.75	0.45
6:A:866:PHE:HE2	9:E:211:TYR:H	1.65	0.45
6:A:1312:ASN:OD1	6:A:1315:GLU:HG2	2.16	0.45
7:B:641:GLU:HB2	7:B:652:LYS:HG3	1.99	0.45
11:H:58:THR:H	11:H:143:LEU:HB2	1.80	0.45
15:L:31:CYS:HB2	15:L:48:CYS:HB2	1.57	0.45
17:O:217:LYS:HD3	17:O:308:GLU:HG3	1.98	0.45
18:4:146:ARG:HA	18:4:191:PHE:CZ	2.52	0.45
21:7:627:ILE:O	21:7:653:PHE:HB2	2.17	0.45
29:O:70:ILE:HG12	29:O:160:ILE:HG23	1.98	0.45
5:M:152:GLU:OE1	7:B:868:MET:HB2	2.17	0.45
5:M:210:MET:HE3	5:M:213:ILE:HB	1.99	0.45
6:A:23:SER:OG	6:A:23:SER:O	2.33	0.45
6:A:555:ASP:N	6:A:555:ASP:OD1	2.47	0.45
6:A:1038:THR:OG1	6:A:1040:GLN:N	2.50	0.45
6:A:1233:ASP:OD1	6:A:1233:ASP:N	2.44	0.45
7:B:793:ALA:HB3	7:B:856:PHE:HB2	1.98	0.45
10:F:86:THR:OG1	10:F:89:GLU:OE1	2.33	0.45
11:H:89:LEU:C	11:H:91:ASP:H	2.24	0.45
17:O:2:LYS:HA	17:O:10:VAL:O	2.17	0.45
17:O:90:MET:HB2	17:O:175:VAL:HG21	1.99	0.45
17:O:285:GLU:OE2	17:O:288:LYS:NZ	2.31	0.45
17:O:507:SER:OG	17:O:508:SER:N	2.49	0.45
19:6:129:THR:OG1	19:6:234:ILE:HA	2.17	0.45
19:6:153:ALA:HA	19:6:156:PHE:HB3	1.97	0.45
21:7:519:ARG:NE	21:7:521:ASP:HB2	2.32	0.45
21:7:590:ALA:HA	21:7:739:LEU:HD11	1.99	0.45
21:7:625:PRO:HD2	21:7:649:ILE:HG12	1.98	0.45
23:2:28:SER:O	23:2:31:THR:OG1	2.35	0.45
24:X:207:CYS:SG	24:X:241:PRO:HA	2.56	0.45
24:X:259:PHE:CE1	30:W:109:LEU:HD11	2.49	0.45
30:W:17:VAL:HG21	30:W:29:LEU:HD22	1.97	0.45
30:W:149:CYS:H	30:W:154:GLU:N	2.14	0.45
1:Q:102:PRO:O	1:Q:103:LEU:HD13	2.16	0.45
2:R:63:ARG:HB3	2:R:66:ARG:NH1	2.32	0.45
3:D:141:LEU:O	3:D:145:MET:HG2	2.16	0.45
4:G:5:LYS:O	4:G:76:ALA:N	2.31	0.45
4:G:142:ARG:O	4:G:170:ALA:HA	2.17	0.45
5:M:167:SER:C	5:M:169:GLU:H	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:326:ARG:HG2	6:A:1406:VAL:HG11	1.98	0.45
6:A:352:VAL:HG21	7:B:1099:VAL:HG12	1.99	0.45
6:A:863:VAL:HG11	6:A:866:PHE:CE1	2.51	0.45
6:A:1407:GLU:CD	6:A:1407:GLU:N	2.73	0.45
7:B:110:HIS:ND1	7:B:111:ALA:O	2.43	0.45
7:B:254:LEU:HD13	7:B:360:PHE:HE1	1.82	0.45
7:B:979:LYS:HD3	31:P:10:A:OP1	2.17	0.45
7:B:1159:ARG:HG2	7:B:1160:VAL:N	2.31	0.45
8:C:3:GLU:HG2	14:K:100:ALA:HB1	1.98	0.45
8:C:90:ASP:OD1	8:C:90:ASP:C	2.60	0.45
10:F:112:GLU:OE2	10:F:123:LYS:NZ	2.40	0.45
11:H:89:LEU:C	11:H:91:ASP:N	2.75	0.45
1:Q:378:VAL:HA	1:Q:384:PHE:CE1	2.52	0.45
2:R:80:LYS:C	2:R:81:TRP:HD1	2.24	0.45
4:G:14:HIS:HB3	4:G:17:PHE:CE1	2.52	0.45
4:G:132:SER:OG	4:G:133:SER:N	2.50	0.45
5:M:251:GLN:HA	5:M:254:THR:HG22	1.99	0.45
6:A:217:LYS:HE2	6:A:217:LYS:HB2	1.64	0.45
6:A:391:LEU:O	6:A:394:ASN:N	2.48	0.45
6:A:407:ARG:HA	6:A:430:TRP:CG	2.52	0.45
7:B:399:ASP:O	7:B:400:HIS:C	2.60	0.45
7:B:802:PRO:HG3	7:B:809:MET:HE1	1.99	0.45
10:F:128:LYS:NZ	10:F:148:VAL:O	2.49	0.45
11:H:99:GLY:HA3	11:H:118:PHE:CD2	2.52	0.45
17:O:343:LYS:HG2	17:O:347:LYS:NZ	2.31	0.45
19:6:239:LEU:HD11	19:6:268:ALA:HB1	1.99	0.45
20:1:193:LYS:O	20:1:196:GLN:HG3	2.17	0.45
20:1:633:TYR:O	20:1:637:TYR:N	2.36	0.45
21:7:393:THR:HG23	21:7:486:ILE:HG21	1.98	0.45
28:T:147:DT:H1'	29:O:207:PHE:CE1	2.51	0.45
29:O:172:LEU:HD21	29:O:206:ILE:HG22	1.99	0.45
29:O:214:LEU:HB3	29:O:223:ILE:HD12	1.97	0.45
30:W:134:LEU:O	30:W:138:GLN:HG2	2.17	0.45
2:R:110:GLU:HG2	2:R:117:PRO:N	2.32	0.45
3:D:26:THR:OG1	3:D:26:THR:O	2.25	0.45
5:M:310:LYS:HA	5:M:313:TYR:HB3	1.97	0.45
6:A:288:ALA:HA	6:A:291:GLU:OE1	2.16	0.45
6:A:830:LYS:HB2	6:A:1082:ASN:ND2	2.32	0.45
6:A:841:LEU:HA	6:A:841:LEU:HD23	1.59	0.45
6:A:1292:PRO:HA	6:A:1298:TYR:HA	1.97	0.45
6:A:1442:ASP:OD1	6:A:1442:ASP:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:872:GLU:HG2	7:B:916:THR:HG22	1.96	0.45
7:B:894:ASP:OD2	15:L:58:LYS:NZ	2.36	0.45
8:C:155:LEU:C	8:C:155:LEU:HD12	2.42	0.45
8:C:231:ASN:C	8:C:231:ASN:ND2	2.75	0.45
12:I:78:CYS:SG	12:I:80:SER:N	2.76	0.45
13:J:22:LEU:O	13:J:26:GLN:HG2	2.16	0.45
15:L:32:ALA:HB3	15:L:55:ILE:HG13	1.97	0.45
17:O:376:PHE:HB3	17:O:379:GLU:OE2	2.17	0.45
29:O:69:ASN:HA	29:O:126:ALA:O	2.17	0.45
29:O:164:CYS:O	29:O:211:LYS:HA	2.17	0.45
29:O:164:CYS:SG	29:O:212:ILE:HB	2.56	0.45
30:W:99:LYS:HA	30:W:186:LEU:HD13	1.98	0.45
5:M:171:ILE:HG13	5:M:172:MET:HE2	1.99	0.45
6:A:164:ARG:C	6:A:166:GLY:H	2.25	0.45
6:A:333:GLU:HA	6:A:338:GLY:HA3	1.97	0.45
6:A:598:LEU:O	6:A:599:SER:C	2.60	0.45
6:A:1034:GLU:C	6:A:1036:ARG:HG3	2.42	0.45
6:A:1192:LEU:HD11	6:A:1194:ARG:HB2	1.99	0.45
6:A:1199:ARG:HA	6:A:1236:LEU:HD11	1.98	0.45
6:A:1211:GLN:HG3	6:A:1211:GLN:H	1.45	0.45
7:B:333:PHE:O	7:B:333:PHE:HD1	2.00	0.45
7:B:712:PRO:HD2	7:B:733:HIS:HD2	1.81	0.45
7:B:785:TYR:CD2	7:B:786:ASN:N	2.85	0.45
7:B:957:ASN:CG	7:B:958:GLN:N	2.74	0.45
8:C:208:GLU:H	8:C:208:GLU:HG3	1.34	0.45
9:E:97:VAL:C	9:E:101:GLN:HE22	2.25	0.45
11:H:145:ARG:HD3	11:H:145:ARG:HA	1.51	0.45
12:I:68:LEU:HA	12:I:68:LEU:HD23	1.62	0.45
15:L:62:LYS:HB2	15:L:63:ARG:HH22	1.82	0.45
17:O:79:ILE:HD13	17:O:79:ILE:HA	1.85	0.45
18:4:29:ILE:O	18:4:178:VAL:HA	2.17	0.45
30:W:123:MET:CG	30:W:157:VAL:HB	2.47	0.45
1:Q:398:ARG:HE	1:Q:398:ARG:HB2	1.59	0.45
5:M:130:PHE:CG	5:M:151:LYS:HE2	2.52	0.45
5:M:215:ARG:HD3	5:M:215:ARG:HA	1.56	0.45
5:M:282:ILE:O	5:M:286:ILE:HG22	2.17	0.45
6:A:526:ASP:HB2	7:B:835:GLN:CD	2.41	0.45
6:A:544:ASP:OD1	6:A:545:GLN:N	2.47	0.45
7:B:70:ILE:HA	7:B:89:GLU:OE2	2.17	0.45
7:B:238:ALA:HB2	7:B:385:LEU:HB2	1.98	0.45
7:B:294:ASP:H	12:I:12:ASN:HD22	1.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:662:MET:HE3	7:B:662:MET:HB3	1.78	0.45
7:B:797:TYR:HB3	7:B:798:TYR:CD2	2.52	0.45
7:B:1095:LEU:HD23	7:B:1095:LEU:HA	1.63	0.45
8:C:262:LEU:HA	8:C:262:LEU:HD23	1.64	0.45
9:E:83:CYS:SG	9:E:85:GLU:N	2.90	0.45
17:0:656:PHE:HA	17:0:692:GLN:HG2	1.98	0.45
18:4:86:LEU:HA	18:4:128:GLU:HB3	1.98	0.45
19:6:154:ILE:HG23	19:6:193:ILE:HD12	2.00	0.45
20:1:588:ASP:O	20:1:592:LYS:N	2.35	0.45
23:2:25:LEU:HD21	23:2:226:PHE:CE2	2.51	0.45
23:2:56:GLU:OE1	23:2:99:ASN:HB3	2.17	0.45
27:N:13:DG:H2''	27:N:14:DC:O4'	2.16	0.45
28:T:22:DT:H2'	28:T:23:DC:H5'	1.99	0.45
31:P:6:G:C2	31:P:7:A:C8	3.05	0.45
1:Q:120:LYS:HE2	1:Q:394:LYS:NZ	2.32	0.44
2:R:99:LYS:HB2	2:R:103:LYS:CE	2.46	0.44
6:A:55:ASP:C	6:A:57:ARG:N	2.75	0.44
6:A:219:PHE:CD1	6:A:220:THR:N	2.79	0.44
6:A:635:ARG:HA	6:A:635:ARG:NH1	2.33	0.44
6:A:1025:ARG:HD3	6:A:1025:ARG:HA	1.69	0.44
6:A:1034:GLU:HB2	6:A:1035:TYR:CD1	2.51	0.44
6:A:1098:VAL:N	6:A:1099:PRO:HD2	2.32	0.44
6:A:1100:ARG:NH2	6:A:1351:GLU:OE1	2.42	0.44
6:A:1286:LYS:HG3	6:A:1304:TRP:CZ3	2.52	0.44
7:B:380:TYR:CZ	7:B:384:ARG:HD3	2.51	0.44
7:B:492:LEU:HD23	7:B:492:LEU:HA	1.68	0.44
7:B:820:GLY:N	7:B:1091:TYR:OH	2.50	0.44
9:E:197:LYS:HA	9:E:211:TYR:HD1	1.81	0.44
15:L:47:ARG:HH12	15:L:54:ARG:CZ	2.30	0.44
17:0:210:TYR:OH	17:0:235:ASP:O	2.33	0.44
17:0:223:SER:HB2	17:0:226:VAL:HG22	1.99	0.44
17:0:333:SER:HB2	17:0:337:ARG:NH2	2.32	0.44
17:0:490:LYS:NZ	17:0:700:GLY:HA2	2.32	0.44
17:0:493:LEU:HB3	17:0:495:MET:HE2	2.00	0.44
17:0:694:PRO:HB2	17:0:696:TRP:CD1	2.52	0.44
18:4:247:TYR:CZ	20:1:503:VAL:HG22	2.53	0.44
21:7:457:TYR:OH	21:7:488:ASP:N	2.50	0.44
21:7:524:ILE:H	21:7:524:ILE:HD12	1.82	0.44
27:N:22:DT:O2	29:O:215:THR:OG1	2.21	0.44
29:O:170:ILE:HD13	29:O:234:LEU:HD22	1.99	0.44
29:O:227:PHE:HA	29:O:230:ILE:HG22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:W:5:ILE:O	30:W:9:VAL:HG23	2.17	0.44
30:W:38:LEU:O	30:W:86:TYR:HA	2.17	0.44
3:D:138:ASN:O	3:D:141:LEU:HB3	2.17	0.44
3:D:154:PHE:CD2	3:D:160:VAL:HG13	2.52	0.44
5:M:123:ASP:N	5:M:123:ASP:OD1	2.48	0.44
6:A:29:ALA:HB1	7:B:1184:GLY:HA2	1.99	0.44
6:A:265:LYS:HD2	6:A:265:LYS:HA	1.74	0.44
6:A:664:THR:OG1	6:A:668:ASP:OD2	2.28	0.44
6:A:854:ASN:O	6:A:867:ILE:HA	2.16	0.44
6:A:993:LEU:HD23	6:A:1022:LEU:HD21	1.99	0.44
6:A:1277:GLU:OE1	6:A:1277:GLU:N	2.47	0.44
7:B:98:THR:OG1	7:B:99:LYS:O	2.31	0.44
8:C:62:PHE:CE1	8:C:66:ARG:HD2	2.51	0.44
11:H:62:SER:OG	11:H:63:LEU:HG	2.17	0.44
14:K:87:LEU:HD12	14:K:87:LEU:HA	1.78	0.44
15:L:48:CYS:O	15:L:48:CYS:SG	2.76	0.44
17:O:436:ARG:HE	17:O:634:ILE:CG2	2.30	0.44
20:1:235:UNK:HA	20:1:381:LEU:HD11	1.99	0.44
21:7:557:VAL:N	21:7:707:SER:O	2.49	0.44
22:5:13:ASP:OD1	22:5:15:SER:OG	2.30	0.44
25:U:249:ASP:OD1	26:V:119:LYS:NZ	2.47	0.44
1:Q:117:HIS:HE1	1:Q:390:ASP:OD2	2.00	0.44
3:D:56:ARG:CB	3:D:148:LEU:HD22	2.46	0.44
4:G:116:PRO:HD3	4:G:164:LYS:HA	1.99	0.44
5:M:38:PHE:HD1	5:M:56:LEU:HD23	1.82	0.44
6:A:67:CYS:O	6:A:71:GLN:N	2.50	0.44
6:A:83:HIS:HD2	6:A:238:CYS:SG	2.41	0.44
6:A:426:LEU:H	6:A:426:LEU:HG	1.54	0.44
6:A:1223:ASP:HB2	6:A:1224:LEU:HD12	1.99	0.44
7:B:95:ILE:HD12	7:B:129:PHE:O	2.17	0.44
7:B:1060:ARG:HD2	7:B:1060:ARG:HA	1.55	0.44
8:C:50:GLU:OE2	15:L:66:GLN:HA	2.17	0.44
9:E:118:PRO:O	9:E:121:MET:HB2	2.17	0.44
13:J:51:LEU:HD23	13:J:51:LEU:C	2.43	0.44
14:K:49:GLU:HG2	14:K:94:ILE:HG13	2.00	0.44
17:O:37:ASN:ND2	17:O:475:PHE:HD2	2.16	0.44
17:O:107:GLY:HA2	17:O:207:ILE:HB	1.99	0.44
17:O:714:ILE:HA	17:O:717:THR:HG22	1.99	0.44
17:O:734:GLU:O	17:O:738:VAL:N	2.51	0.44
19:6:244:PRO:HB3	20:1:230:PRO:HB3	2.00	0.44
19:6:441:ASP:HA	19:6:444:ILE:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1:280:GLU:HA	20:1:284:TRP:CD1	2.52	0.44
21:7:622:MET:H	21:7:622:MET:HG3	1.67	0.44
29:O:185:TYR:CD2	29:O:187:PRO:HD3	2.53	0.44
2:R:75:MET:CE	2:R:75:MET:H	2.30	0.44
2:R:119:GLU:HB3	2:R:233:TYR:N	2.32	0.44
3:D:168:LYS:HD3	3:D:168:LYS:HA	1.84	0.44
4:G:35:GLU:OE1	4:G:47:CYS:HA	2.17	0.44
4:G:114:LEU:HD21	4:G:160:ILE:HG23	2.00	0.44
5:M:198:VAL:C	5:M:200:THR:H	2.25	0.44
6:A:332:LYS:HG3	6:A:333:GLU:OE1	2.17	0.44
6:A:473:SER:OG	6:A:650:GLN:NE2	2.50	0.44
6:A:965:GLN:HG2	6:A:965:GLN:H	1.47	0.44
6:A:1059:HIS:ND1	10:F:87:LYS:HG2	2.33	0.44
6:A:1197:LEU:C	6:A:1236:LEU:HD12	2.43	0.44
6:A:1336:MET:HE3	6:A:1336:MET:HB3	1.77	0.44
7:B:240:ILE:O	7:B:240:ILE:HG13	2.17	0.44
7:B:860:MET:SD	7:B:861:ASP:N	2.90	0.44
8:C:127:ARG:O	8:C:129:ILE:N	2.51	0.44
10:F:140:ASP:CG	10:F:142:SER:HG	2.26	0.44
15:L:30:ILE:HG22	15:L:31:CYS:O	2.18	0.44
23:2:431:GLN:NE2	23:2:435:PRO:HD2	2.31	0.44
1:Q:135:LEU:HD23	1:Q:136:PRO:HA	1.99	0.44
1:Q:343:ARG:HH21	1:Q:346:GLU:CD	2.19	0.44
3:D:76:LYS:HA	3:D:76:LYS:HD2	1.68	0.44
3:D:208:GLU:C	3:D:212:LYS:HZ3	2.24	0.44
6:A:70:CYS:C	6:A:72:GLU:HG3	2.43	0.44
6:A:74:MET:C	6:A:76:GLU:H	2.25	0.44
6:A:332:LYS:HD2	6:A:332:LYS:HA	1.59	0.44
6:A:344:ARG:HH21	7:B:1119:VAL:C	2.25	0.44
6:A:1227:ILE:O	6:A:1239:ARG:N	2.30	0.44
6:A:1404:GLU:O	6:A:1408:ILE:HG12	2.18	0.44
6:A:1443:VAL:HG12	6:A:1443:VAL:O	2.16	0.44
7:B:901:PRO:O	15:L:61:THR:HG22	2.17	0.44
7:B:911:ILE:HG12	7:B:939:THR:O	2.18	0.44
7:B:1155:SER:OG	7:B:1156:ASP:OD1	2.34	0.44
8:C:195:GLN:N	8:C:200:GLU:OE2	2.38	0.44
9:E:69:ILE:HA	9:E:72:PHE:O	2.17	0.44
13:J:6:ARG:O	13:J:7:CYS:C	2.59	0.44
14:K:49:GLU:O	14:K:52:ASN:HB2	2.16	0.44
14:K:57:LEU:N	14:K:76:GLN:O	2.44	0.44
17:O:666:LEU:HD11	17:O:681:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:7:606:ILE:HD13	21:7:665:PRO:HG2	1.99	0.44
23:2:90:ASN:ND2	23:2:99:ASN:OD1	2.51	0.44
25:U:258:TRP:NE1	26:V:66:LEU:HD23	2.32	0.44
1:Q:141:ARG:HB3	1:Q:348:TYR:CB	2.47	0.44
4:G:153:GLN:HE21	4:G:153:GLN:HB2	1.48	0.44
5:M:268:GLU:HB3	5:M:315:ILE:HD11	2.00	0.44
7:B:103:ASN:HB2	7:B:169:ARG:HH22	1.82	0.44
7:B:260:GLY:O	7:B:267:ARG:HD3	2.18	0.44
8:C:59:ALA:O	8:C:62:PHE:HB3	2.18	0.44
11:H:101:ALA:HB2	11:H:116:TYR:CE2	2.52	0.44
12:I:101:PHE:N	12:I:110:PHE:O	2.42	0.44
18:4:90:SER:HB3	19:6:407:GLN:NE2	2.32	0.44
20:1:264:PRO:O	20:1:268:LYS:HG2	2.18	0.44
21:7:599:GLU:HA	21:7:650:ASN:HD22	1.83	0.44
21:7:604:LYS:HD3	21:7:694:LYS:NZ	2.33	0.44
21:7:612:VAL:HG13	21:7:629:GLY:HA3	2.00	0.44
23:2:109:ARG:NH1	23:2:109:ARG:HA	2.33	0.44
24:X:201:THR:HA	30:W:34:PHE:CB	2.48	0.44
27:N:20:DT:H4'	29:O:194:ILE:HD11	1.99	0.44
29:O:200:PRO:HG2	29:O:226:ALA:HB2	1.99	0.44
29:O:220:ARG:HG2	29:O:224:TYR:CE2	2.53	0.44
30:W:122:TYR:CZ	30:W:147:PHE:HE2	2.35	0.44
1:Q:106:ILE:HG23	1:Q:107:PRO:O	2.18	0.44
5:M:132:LYS:O	5:M:135:MET:HG2	2.18	0.44
6:A:206:GLU:HG3	6:A:207:ILE:H	1.82	0.44
6:A:526:ASP:OD1	7:B:1013:ASN:ND2	2.41	0.44
6:A:878:ILE:HG22	6:A:879:GLU:N	2.33	0.44
6:A:1207:LEU:HA	6:A:1207:LEU:HD23	1.68	0.44
7:B:215:GLN:NE2	7:B:479:VAL:HG12	2.32	0.44
7:B:838:SER:HB2	7:B:839:MET:HG2	1.99	0.44
7:B:1110:PRO:O	7:B:1119:VAL:HG13	2.16	0.44
12:I:42:LEU:HD12	12:I:43:VAL:N	2.33	0.44
17:0:342:LEU:HA	17:0:345:ARG:HB2	1.99	0.44
17:0:701:LEU:HD12	17:0:705:ASP:HB3	2.00	0.44
17:0:709:SER:O	17:0:713:ALA:N	2.42	0.44
18:4:136:GLU:HA	18:4:140:ILE:CG1	2.44	0.44
19:6:164:ASN:O	19:6:167:SER:OG	2.31	0.44
19:6:349:CYS:SG	19:6:368:LEU:HD11	2.58	0.44
20:1:260:PHE:CG	20:1:267:LYS:HD3	2.53	0.44
24:X:219:GLU:O	24:X:223:GLN:HG2	2.18	0.44
27:N:31:DT:C2	27:N:32:DG:C8	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:74:VAL:HG11	29:O:152:PHE:CE1	2.53	0.44
30:W:28:VAL:HG11	30:W:58:ILE:HD13	1.98	0.44
1:Q:104:ARG:HA	2:R:92:LEU:HB3	2.00	0.44
1:Q:350:TRP:H	1:Q:350:TRP:CD1	2.36	0.44
2:R:94:LYS:NZ	2:R:94:LYS:H	2.15	0.44
3:D:67:ARG:HB3	3:D:67:ARG:CZ	2.48	0.44
4:G:98:GLY:O	4:G:130:TYR:OH	2.36	0.44
4:G:148:GLU:HG3	4:G:162:SER:HB3	1.99	0.44
5:M:186:ALA:HB2	5:M:237:THR:OG1	2.17	0.44
5:M:186:ALA:HB1	5:M:238:TYR:CG	2.53	0.44
6:A:108:MET:HE3	6:A:172:PRO:HD2	1.99	0.44
6:A:333:GLU:N	6:A:333:GLU:OE2	2.50	0.44
6:A:497:THR:HG21	7:B:1149:GLU:CD	2.43	0.44
6:A:598:LEU:HD23	6:A:598:LEU:HA	1.77	0.44
6:A:811:GLN:O	6:A:814:PHE:N	2.51	0.44
7:B:370:PHE:HD1	7:B:373:ARG:HE	1.61	0.44
7:B:461:LEU:HD23	7:B:461:LEU:HA	1.70	0.44
7:B:953:LEU:HD23	7:B:953:LEU:C	2.43	0.44
7:B:1152:MET:HE3	7:B:1152:MET:HB3	1.70	0.44
12:I:108:HIS:CE1	12:I:110:PHE:HB3	2.53	0.44
17:O:276:LYS:HE2	17:O:276:LYS:HB2	1.89	0.44
21:7:695:ARG:HD3	21:7:695:ARG:HA	1.80	0.44
25:U:258:TRP:HB2	25:U:283:ALA:H	1.82	0.44
30:W:192:SER:HB3	30:W:194:ILE:HG13	1.99	0.44
4:G:50:ASP:OD2	4:G:53:ASN:HB2	2.18	0.44
6:A:69:THR:HA	6:A:71:GLN:NE2	2.32	0.44
6:A:95:PHE:HB3	6:A:234:MET:HE3	1.99	0.44
6:A:276:LEU:HD11	6:A:293:GLU:HA	2.00	0.44
6:A:372:LYS:HD3	6:A:397:ASN:O	2.18	0.44
6:A:567:LYS:HG2	6:A:568:PRO:HD2	2.00	0.44
6:A:964:ILE:HD13	6:A:964:ILE:HA	1.69	0.44
6:A:1084:PHE:CD2	6:A:1086:PHE:HB2	2.53	0.44
6:A:1377:THR:O	6:A:1379:GLY:N	2.51	0.44
6:A:1381:LEU:HA	6:A:1381:LEU:HD23	1.77	0.44
7:B:68:THR:HG22	7:B:91:SER:HA	1.99	0.44
7:B:1084:GLN:NE2	8:C:191:TYR:HA	2.32	0.44
8:C:220:ASP:OD1	8:C:222:LYS:N	2.51	0.44
10:F:107:VAL:HG12	10:F:109:VAL:H	1.83	0.44
11:H:13:SER:N	11:H:27:GLU:O	2.50	0.44
11:H:82:PRO:CA	11:H:87:ARG:HD2	2.48	0.44
11:H:123:MET:HE3	11:H:123:MET:HB3	1.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:123:MET:HE2	11:H:142:LEU:HD13	1.99	0.44
13:J:25:LEU:HA	13:J:25:LEU:HD23	1.67	0.44
18:4:210:ILE:HD13	18:4:227:THR:HG21	1.99	0.44
24:X:268:LEU:HD21	30:W:101:LYS:HE3	1.99	0.44
27:N:21:DA:N3	29:O:205:LEU:HD11	2.32	0.44
30:W:9:VAL:HG22	30:W:189:ILE:HD13	1.99	0.44
6:A:141:LEU:HD23	6:A:141:LEU:HA	1.79	0.43
6:A:1230:GLU:O	6:A:1233:ASP:N	2.43	0.43
7:B:129:PHE:CD1	7:B:166:PHE:HA	2.52	0.43
7:B:408:LEU:HA	7:B:408:LEU:HD23	1.56	0.43
11:H:111:LEU:HD23	11:H:111:LEU:HA	1.60	0.43
12:I:58:VAL:HG11	12:I:109:ILE:HD11	1.99	0.43
12:I:59:VAL:C	12:I:61:ASP:H	2.26	0.43
12:I:99:LEU:HA	12:I:99:LEU:HD23	1.74	0.43
12:I:104:LEU:HA	12:I:104:LEU:HD13	1.55	0.43
19:6:134:GLU:N	19:6:206:GLY:O	2.45	0.43
21:7:409:VAL:HA	21:7:486:ILE:HB	2.00	0.43
23:2:146:ILE:HD12	23:2:146:ILE:HA	1.89	0.43
24:X:157:ASP:O	24:X:161:GLU:N	2.45	0.43
3:D:66:ARG:HG2	3:D:133:THR:HG22	2.00	0.43
4:G:59:GLY:O	10:F:133:VAL:HG11	2.18	0.43
6:A:445:ASN:HA	6:A:454:SER:O	2.18	0.43
6:A:732:LEU:HA	6:A:732:LEU:HD23	1.69	0.43
6:A:781:ASP:HB3	6:A:790:ASP:OD1	2.18	0.43
6:A:785:PRO:HG2	6:A:786:HIS:CD2	2.53	0.43
6:A:1161:THR:HG22	6:A:1163:ILE:H	1.81	0.43
7:B:766:ARG:HD3	7:B:766:ARG:HA	1.62	0.43
7:B:1037:LEU:HD23	7:B:1037:LEU:HA	1.67	0.43
8:C:69:LEU:O	13:J:6:ARG:HD2	2.18	0.43
9:E:30:ILE:HG23	9:E:34:GLU:OE1	2.18	0.43
17:0:110:SER:OG	17:0:111:ARG:N	2.51	0.43
17:0:195:ILE:O	17:0:199:MET:HG2	2.18	0.43
17:0:224:ASN:HD21	17:0:228:LYS:NZ	2.15	0.43
17:0:327:ARG:HB3	17:0:330:HIS:HB3	2.00	0.43
18:4:86:LEU:HD11	18:4:132:LEU:HD13	1.99	0.43
20:1:346:ASP:HB2	20:1:347:PRO:HD3	1.99	0.43
5:M:174:ALA:O	5:M:178:ILE:HG12	2.17	0.43
6:A:43:GLU:C	6:A:45:GLN:H	2.26	0.43
6:A:71:GLN:C	6:A:73:GLY:N	2.76	0.43
6:A:315:LEU:HA	6:A:321:PRO:HA	2.00	0.43
6:A:427:GLN:O	6:A:428:TYR:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:746:MET:CE	7:B:1015:HIS:HA	2.48	0.43
6:A:901:LEU:HD22	6:A:919:ILE:HG22	2.00	0.43
6:A:1208:THR:N	6:A:1211:GLN:OE1	2.40	0.43
6:A:1433:MET:HB2	6:A:1433:MET:HE3	1.60	0.43
7:B:230:ALA:N	7:B:231:PRO:HD2	2.33	0.43
7:B:1084:GLN:HE22	8:C:191:TYR:HA	1.82	0.43
9:E:164:LEU:O	9:E:165:LEU:C	2.60	0.43
14:K:14:GLU:N	14:K:16:GLU:OE1	2.52	0.43
14:K:29:ASN:HD22	14:K:79:GLU:HA	1.83	0.43
15:L:47:ARG:N	15:L:53:HIS:O	2.45	0.43
17:0:171:LEU:HD11	17:0:195:ILE:HG21	2.00	0.43
17:0:465:PRO:HD2	17:0:656:PHE:CD2	2.54	0.43
17:0:720:PHE:CZ	17:0:724:MET:HG3	2.53	0.43
18:4:119:ARG:HH22	18:4:123:GLU:HG2	1.82	0.43
21:7:341:TYR:CD2	21:7:343:PHE:HD1	2.35	0.43
21:7:421:ARG:NH1	21:7:437:VAL:HG11	2.33	0.43
2:R:73:LEU:HA	2:R:224:VAL:HB	2.00	0.43
5:M:248:LEU:HA	5:M:249:PRO:HD3	1.86	0.43
6:A:107:CYS:HB3	6:A:111:GLY:N	2.34	0.43
6:A:657:LEU:HA	6:A:657:LEU:HD12	1.68	0.43
6:A:673:GLY:O	6:A:676:MET:N	2.51	0.43
6:A:903:ASN:O	6:A:907:THR:OG1	2.36	0.43
7:B:59:LEU:HD12	7:B:59:LEU:HA	1.50	0.43
7:B:70:ILE:HA	7:B:89:GLU:CD	2.42	0.43
7:B:96:TYR:N	7:B:129:PHE:O	2.36	0.43
7:B:710:LEU:HA	7:B:710:LEU:HD13	1.55	0.43
7:B:792:MET:HE2	7:B:792:MET:HB2	1.64	0.43
7:B:806:THR:OG1	7:B:809:MET:HG3	2.18	0.43
7:B:884:ARG:HB2	7:B:936:ASP:H	1.83	0.43
7:B:1174:LYS:N	7:B:1179:GLN:O	2.51	0.43
8:C:22:LEU:HD12	8:C:22:LEU:HA	1.52	0.43
8:C:67:LEU:HD23	8:C:67:LEU:HA	1.64	0.43
9:E:28:TYR:HA	9:E:64:PRO:HA	1.99	0.43
9:E:46:TYR:O	9:E:54:GLN:N	2.48	0.43
11:H:93:TYR:CG	11:H:143:LEU:HD22	2.53	0.43
17:0:116:LEU:HD23	17:0:158:TYR:CE2	2.53	0.43
17:0:460:SER:HB2	17:0:463:ILE:HG13	1.99	0.43
18:4:258:LEU:CB	18:4:260:PRO:HD3	2.49	0.43
27:N:17:DG:H2''	27:N:18:DT:O4'	2.18	0.43
27:N:17:DG:H2'	27:N:18:DT:C6	2.53	0.43
28:T:150:DG:C4	28:T:151:DC:N3	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:4:ILE:HG23	4:G:49:LEU:HD11	2.01	0.43
5:M:154:TYR:CD1	5:M:172:MET:HE1	2.53	0.43
5:M:156:LEU:HD23	5:M:156:LEU:HA	1.76	0.43
6:A:944:ARG:NH1	6:A:1296:GLY:O	2.49	0.43
6:A:1203:ASN:C	6:A:1206:ASP:H	2.26	0.43
7:B:605:ARG:NH2	7:B:691:GLU:OE2	2.50	0.43
7:B:1096:ARG:O	7:B:1097:HIS:CG	2.72	0.43
8:C:10:ILE:HG13	14:K:108:GLU:HG2	2.01	0.43
10:F:146:TRP:CD1	10:F:146:TRP:N	2.87	0.43
11:H:83:GLN:O	11:H:85:GLY:N	2.50	0.43
13:J:63:TYR:C	13:J:65:PRO:HD2	2.43	0.43
18:4:78:ALA:HB2	18:4:152:ALA:CB	2.49	0.43
19:6:126:LEU:HB3	19:6:160:PHE:CZ	2.54	0.43
19:6:237:GLY:HA2	19:6:266:LEU:HB2	2.01	0.43
23:2:378:ILE:HD12	23:2:382:SER:HB2	2.00	0.43
28:T:152:DG:C5	28:T:153:DC:C4	3.06	0.43
1:Q:399:ASN:OD1	1:Q:402:ALA:HA	2.19	0.43
5:M:26:GLU:OE2	6:A:407:ARG:NH1	2.52	0.43
5:M:40:GLU:N	5:M:40:GLU:OE2	2.52	0.43
6:A:56:PRO:C	6:A:57:ARG:HH11	2.26	0.43
6:A:359:LEU:HA	6:A:359:LEU:HD12	1.60	0.43
6:A:450:LEU:O	6:A:451:HIS:CD2	2.72	0.43
6:A:507:VAL:O	6:A:508:PRO:C	2.62	0.43
6:A:1046:LEU:HD12	6:A:1046:LEU:HA	1.70	0.43
6:A:1333:ILE:HA	6:A:1333:ILE:HD13	1.83	0.43
7:B:173:MET:HE3	7:B:173:MET:HB2	1.70	0.43
9:E:153:HIS:O	9:E:154:ILE:HD13	2.19	0.43
10:F:143:PHE:CD1	10:F:143:PHE:C	2.97	0.43
11:H:100:THR:OG1	11:H:138:GLU:HG2	2.18	0.43
12:I:19:ASP:CB	12:I:24:ARG:H	2.19	0.43
17:O:350:HIS:ND1	30:W:184:ASP:OD2	2.52	0.43
19:6:124:ARG:HA	19:6:229:THR:N	2.33	0.43
19:6:129:THR:HA	19:6:172:ILE:HB	2.00	0.43
19:6:143:PRO:HD3	19:6:148:MET:HE3	2.00	0.43
21:7:233:PHE:C	21:7:315:SER:HB2	2.44	0.43
21:7:546:LYS:HA	21:7:546:LYS:HD2	1.84	0.43
28:T:137:DA:C2	28:T:138:DG:C4	3.07	0.43
29:O:205:LEU:O	29:O:213:VAL:N	2.41	0.43
4:G:97:HIS:H	4:G:97:HIS:CD2	2.36	0.43
4:G:131:GLN:N	4:G:131:GLN:OE1	2.51	0.43
6:A:360:GLU:HB2	6:A:363:GLN:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1191:TRP:HD1	6:A:1256:GLU:OE1	2.01	0.43
7:B:355:ILE:HD13	7:B:355:ILE:HA	1.79	0.43
7:B:706:GLN:H	7:B:710:LEU:CD2	2.27	0.43
7:B:739:THR:C	7:B:740:HIS:ND1	2.77	0.43
7:B:848:ARG:HB3	13:J:8:PHE:HD1	1.83	0.43
7:B:861:ASP:CG	7:B:914:LYS:HZ3	2.19	0.43
7:B:1099:VAL:C	7:B:1101:ASP:N	2.74	0.43
8:C:3:GLU:CD	14:K:104:ASN:HB2	2.43	0.43
11:H:84:ALA:N	14:K:54:ARG:HH12	2.17	0.43
15:L:33:GLU:HB2	15:L:53:HIS:NE2	2.34	0.43
17:O:659:MET:HA	17:O:662:ALA:HB3	1.99	0.43
25:U:262:LEU:O	25:U:279:ALA:N	2.49	0.43
28:T:137:DA:C4	28:T:138:DG:C8	3.07	0.43
1:Q:342:LEU:O	1:Q:346:GLU:HG3	2.18	0.43
3:D:215:SER:HA	3:D:218:GLU:HG2	2.01	0.43
5:M:185:VAL:HA	7:B:106:ASP:CG	2.44	0.43
6:A:305:ASP:C	6:A:305:ASP:OD1	2.62	0.43
6:A:935:GLN:NE2	6:A:935:GLN:O	2.51	0.43
6:A:1047:SER:OG	6:A:1048:ASN:N	2.52	0.43
6:A:1285:MET:HB3	6:A:1285:MET:HE3	1.73	0.43
6:A:1333:ILE:HD13	6:A:1381:LEU:HD12	2.00	0.43
8:C:136:ASP:OD2	8:C:140:ASN:N	2.52	0.43
11:H:61:SER:O	11:H:139:ASN:ND2	2.48	0.43
12:I:37:GLU:CD	12:I:37:GLU:C	2.87	0.43
13:J:22:LEU:HA	13:J:22:LEU:HD23	1.70	0.43
17:O:492:PHE:HB2	17:O:679:MET:HE1	2.00	0.43
18:4:28:VAL:HG13	18:4:57:LEU:HD21	2.00	0.43
19:6:231:GLU:HA	19:6:260:ARG:O	2.19	0.43
21:7:387:PRO:HB3	21:7:540:TRP:CH2	2.54	0.43
21:7:443:LYS:HD3	21:7:444:GLU:N	2.34	0.43
21:7:584:ASN:HB3	21:7:587:LYS:HB3	2.01	0.43
23:2:25:LEU:O	23:2:31:THR:OG1	2.31	0.43
23:2:428:GLU:OE1	23:2:428:GLU:N	2.52	0.43
28:T:21:DC:H2'	28:T:22:DT:H6	1.81	0.43
28:T:147:DT:H5'	29:O:211:LYS:HE2	2.00	0.43
29:O:102:VAL:N	29:O:115:ILE:O	2.37	0.43
30:W:179:ILE:HG23	30:W:183:ILE:HG23	2.00	0.43
1:Q:353:GLU:OE1	1:Q:353:GLU:N	2.52	0.43
1:Q:376:LEU:HD12	2:R:69:TRP:HB3	2.00	0.43
2:R:79:GLU:N	2:R:79:GLU:OE1	2.52	0.43
3:D:142:LYS:HA	3:D:142:LYS:HD3	1.74	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:177:LEU:HD11	5:M:181:ARG:HH21	1.83	0.43
6:A:573:SER:OG	6:A:574:GLY:N	2.51	0.43
6:A:849:MET:HE3	6:A:1063:MET:SD	2.59	0.43
6:A:913:LEU:HD11	6:A:981:LEU:O	2.18	0.43
7:B:102:VAL:CG1	7:B:112:LEU:HD22	2.48	0.43
7:B:232:SER:C	7:B:261:ARG:HH22	2.26	0.43
8:C:143:LEU:HG	13:J:2:ILE:HD11	2.00	0.43
9:E:89:GLY:O	9:E:92:THR:OG1	2.22	0.43
11:H:24:CYS:HB2	11:H:44:VAL:HG11	2.01	0.43
15:L:29:TYR:O	15:L:30:ILE:HD13	2.18	0.43
17:0:428:ALA:O	17:0:430:VAL:HG13	2.19	0.43
17:0:486:THR:O	17:0:737:SER:OG	2.29	0.43
18:4:25:LEU:HB3	18:4:174:SER:HB3	2.00	0.43
18:4:236:LEU:HD22	18:4:238:VAL:HG12	2.00	0.43
21:7:385:VAL:HG23	21:7:538:ALA:N	2.34	0.43
21:7:548:HIS:HB3	21:7:693:ALA:HA	2.00	0.43
21:7:586:THR:O	21:7:590:ALA:N	2.37	0.43
24:X:260:VAL:HG22	30:W:20:PHE:HA	2.01	0.43
1:Q:141:ARG:HB3	1:Q:348:TYR:HB2	2.00	0.43
1:Q:362:VAL:O	1:Q:395:PHE:HA	2.19	0.43
3:D:123:LEU:HD22	3:D:149:THR:HB	2.00	0.43
3:D:188:ALA:O	3:D:192:LYS:HG3	2.18	0.43
4:G:38:CYS:O	4:G:155:SER:HA	2.18	0.43
6:A:116:ASP:HA	6:A:117:GLU:HA	1.61	0.43
6:A:933:TYR:O	6:A:937:VAL:HG13	2.18	0.43
6:A:981:LEU:HD21	6:A:1039:LYS:HA	2.01	0.43
6:A:1032:LEU:O	6:A:1036:ARG:HG2	2.18	0.43
6:A:1032:LEU:HD23	6:A:1032:LEU:HA	1.77	0.43
9:E:40:GLU:H	9:E:40:GLU:CD	2.19	0.43
9:E:180:ARG:HH12	9:E:192:ARG:HB2	1.83	0.43
14:K:108:GLU:HA	14:K:111:LEU:HD22	2.00	0.43
17:0:154:GLU:CD	17:0:154:GLU:H	2.27	0.43
17:0:524:SER:HA	17:0:527:VAL:HG12	2.01	0.43
18:4:28:VAL:HG22	18:4:57:LEU:HD11	2.01	0.43
18:4:117:ARG:HA	18:4:120:ASN:ND2	2.33	0.43
19:6:173:ILE:HG13	19:6:180:GLN:HB2	2.01	0.43
20:1:258:ASN:O	20:1:261:GLU:HG3	2.18	0.43
29:O:132:SER:O	29:O:136:SER:OG	2.37	0.43
1:Q:108:LYS:HE2	1:Q:108:LYS:HB2	1.76	0.42
1:Q:127:ILE:HG12	1:Q:129:PRO:HD3	2.01	0.42
3:D:44:GLU:HG2	3:D:45:GLU:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:70:CYS:O	6:A:72:GLU:N	2.47	0.42
6:A:1224:LEU:O	6:A:1226:VAL:HG23	2.19	0.42
6:A:1436:ILE:HA	6:A:1436:ILE:HD13	1.76	0.42
7:B:234:ILE:HG21	7:B:257:LYS:HB3	2.01	0.42
7:B:847:ASP:HB3	8:C:167:HIS:CE1	2.54	0.42
7:B:1010:LEU:HD12	7:B:1010:LEU:HA	1.64	0.42
8:C:4:GLU:OE1	8:C:4:GLU:N	2.51	0.42
8:C:179:GLU:HG2	8:C:180:TYR:N	2.34	0.42
8:C:190:ASP:OD1	8:C:191:TYR:N	2.52	0.42
8:C:230:MET:HE2	8:C:230:MET:HB3	1.94	0.42
9:E:81:GLU:HG2	9:E:96:PHE:CD1	2.54	0.42
10:F:99:LEU:O	10:F:103:MET:HG3	2.18	0.42
10:F:118:LEU:HD22	10:F:122:MET:HE2	2.01	0.42
14:K:40:HIS:O	14:K:41:THR:C	2.62	0.42
21:7:230:ASN:O	21:7:345:ASN:HB3	2.19	0.42
21:7:449:GLU:HG3	21:7:453:VAL:HG22	2.00	0.42
23:2:481:LEU:HD21	23:2:491:PHE:CG	2.54	0.42
29:O:113:ALA:HB2	29:O:139:TYR:CE2	2.54	0.42
29:O:123:VAL:HG21	29:O:136:SER:OG	2.19	0.42
5:M:215:ARG:O	5:M:218:SER:OG	2.35	0.42
6:A:214:ILE:HG22	6:A:218:ASP:OD1	2.18	0.42
6:A:332:LYS:C	6:A:333:GLU:CD	2.87	0.42
6:A:457:ALA:O	6:A:507:VAL:HG23	2.19	0.42
6:A:609:ASP:C	6:A:611:GLN:N	2.77	0.42
6:A:860:LEU:HB2	6:A:862:ASN:OD1	2.19	0.42
6:A:874:ASP:OD1	6:A:874:ASP:C	2.62	0.42
6:A:1022:LEU:HA	6:A:1022:LEU:HD12	1.72	0.42
6:A:1104:ILE:HG22	6:A:1105:LEU:HD23	2.01	0.42
6:A:1263:ILE:O	6:A:1267:MET:HG2	2.19	0.42
6:A:1442:ASP:HA	10:F:134:ILE:O	2.19	0.42
7:B:555:ILE:HA	7:B:558:LEU:HD12	2.01	0.42
7:B:617:ARG:NH2	12:I:61:ASP:OD1	2.42	0.42
7:B:773:MET:HB2	7:B:773:MET:HE3	1.81	0.42
18:4:33:ALA:O	18:4:37:TRP:N	2.30	0.42
19:6:133:SER:HB2	19:6:207:ASN:HA	2.01	0.42
20:1:613:THR:O	20:1:617:LYS:N	2.52	0.42
21:7:397:ILE:HD12	21:7:430:LEU:HD22	1.99	0.42
21:7:403:ILE:HD11	21:7:407:VAL:HG22	2.01	0.42
23:2:481:LEU:HD13	23:2:484:LYS:HB3	2.02	0.42
24:X:193:LEU:O	24:X:197:ARG:HG3	2.19	0.42
30:W:8:ILE:O	30:W:12:LEU:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:W:123:MET:HE3	30:W:123:MET:HB3	1.72	0.42
1:Q:121:PHE:HD1	1:Q:361:TRP:CD2	2.37	0.42
2:R:118:HIS:CG	2:R:120:TYR:HH	2.37	0.42
5:M:157:CYS:HB2	5:M:163:LEU:HD11	2.01	0.42
6:A:436:ILE:HD12	6:A:436:ILE:HG23	1.71	0.42
6:A:1155:ASP:CG	6:A:1162:VAL:HG23	2.44	0.42
7:B:40:GLU:CD	7:B:681:TRP:HB3	2.44	0.42
7:B:310:MET:HE3	7:B:310:MET:HB2	1.73	0.42
7:B:334:ILE:H	7:B:334:ILE:HG12	1.65	0.42
7:B:563:MET:HA	7:B:589:VAL:O	2.18	0.42
7:B:1072:MET:HE2	7:B:1072:MET:HB3	1.66	0.42
10:F:96:THR:O	10:F:100:GLN:HG3	2.19	0.42
11:H:42:ILE:HG23	11:H:95:TYR:CE2	2.55	0.42
11:H:54:SER:HB3	11:H:146:ARG:HD3	2.01	0.42
13:J:23:ASN:O	13:J:24:LEU:C	2.62	0.42
15:L:31:CYS:SG	15:L:34:CYS:SG	3.17	0.42
17:O:52:LEU:HD22	17:O:233:ILE:HD13	2.02	0.42
17:O:236:GLU:HB3	17:O:238:HIS:HE1	1.84	0.42
17:O:338:LEU:HD23	17:O:342:LEU:HD23	2.01	0.42
19:6:233:LEU:HA	19:6:262:LYS:O	2.20	0.42
19:6:233:LEU:HD21	19:6:264:LEU:HD22	2.01	0.42
21:7:659:ASP:HA	21:7:660:THR:HA	1.58	0.42
22:5:27:MET:HE1	22:5:49:PHE:HB3	2.01	0.42
23:2:110:ASN:O	23:2:115:GLY:N	2.52	0.42
29:O:175:LEU:HA	29:O:237:PHE:CE2	2.54	0.42
2:R:126:LYS:HG2	2:R:128:VAL:O	2.19	0.42
3:D:204:ASP:O	3:D:207:LEU:HB2	2.19	0.42
4:G:146:LYS:O	4:G:161:GLY:HA2	2.20	0.42
5:M:118:VAL:O	5:M:124:ASN:HB3	2.19	0.42
6:A:367:PRO:HG3	6:A:466:SER:O	2.19	0.42
6:A:501:LEU:HD23	6:A:501:LEU:HA	1.65	0.42
6:A:549:MET:O	6:A:550:LEU:C	2.63	0.42
6:A:562:THR:HA	11:H:79:TRP:HB2	2.02	0.42
6:A:663:SER:OG	7:B:827:ILE:O	2.29	0.42
6:A:1209:MET:HE2	6:A:1236:LEU:HD22	2.01	0.42
7:B:933:SER:OG	7:B:934:LYS:N	2.52	0.42
7:B:1207:LEU:HD23	7:B:1207:LEU:HA	1.57	0.42
17:O:173:LYS:HD2	17:O:173:LYS:HA	1.86	0.42
17:O:349:LEU:HB3	30:W:180:GLN:HG2	2.01	0.42
17:O:372:LYS:HB2	17:O:373:PRO:HD3	2.01	0.42
19:6:352:CYS:SG	19:6:354:SER:OG	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:7:606:ILE:HG12	21:7:652:ILE:HD11	2.01	0.42
23:2:410:ARG:HA	23:2:413:GLU:HB2	2.01	0.42
25:U:252:THR:OG1	25:U:259:LYS:HB2	2.20	0.42
27:N:31:DT:O2	28:T:135:DA:H2	2.03	0.42
28:T:141:DT:H2''	29:O:99:PHE:CG	2.54	0.42
28:T:146:DA:C6	28:T:147:DT:C4	3.07	0.42
4:G:57:GLN:HG2	4:G:58:ARG:N	2.34	0.42
6:A:92:HIS:O	6:A:93:VAL:C	2.63	0.42
6:A:123:ARG:NH1	6:A:123:ARG:HB2	2.33	0.42
6:A:135:PHE:HB2	6:A:222:LEU:O	2.20	0.42
6:A:351:THR:O	6:A:486:GLU:HB3	2.20	0.42
6:A:711:ARG:HH12	12:I:95:THR:C	2.26	0.42
6:A:1001:ARG:NH1	10:F:82:THR:HA	2.33	0.42
6:A:1209:MET:H	6:A:1231:ASP:CG	2.21	0.42
6:A:1211:GLN:HA	6:A:1214:GLU:HG2	2.00	0.42
6:A:1389:PHE:CG	6:A:1390:ASN:N	2.87	0.42
6:A:1390:ASN:O	6:A:1399:ARG:HD2	2.20	0.42
7:B:757:PRO:CG	7:B:983:ARG:HH21	2.32	0.42
8:C:241:ASP:OD2	14:K:109:TRP:NE1	2.53	0.42
9:E:186:LEU:O	9:E:189:GLY:N	2.52	0.42
10:F:71:GLU:HA	10:F:72:LYS:HA	1.74	0.42
11:H:135:LEU:HA	11:H:135:LEU:HD23	1.66	0.42
12:I:5:ARG:HB3	12:I:5:ARG:CZ	2.48	0.42
12:I:24:ARG:H	12:I:24:ARG:HG3	1.72	0.42
12:I:34:TYR:HH	12:I:36:GLU:CD	2.27	0.42
12:I:77:LYS:HE2	12:I:77:LYS:HB3	1.69	0.42
16:3:140:ASN:O	16:3:144:ILE:N	2.47	0.42
17:0:57:ILE:HG22	17:0:93:ARG:HH21	1.84	0.42
17:0:525:MET:O	17:0:529:PHE:HD2	2.02	0.42
17:0:685:ARG:HB3	17:0:689:LYS:NZ	2.35	0.42
18:4:279:THR:HG21	18:4:281:ARG:HE	1.85	0.42
19:6:123:ILE:C	19:6:228:CYS:HA	2.44	0.42
19:6:136:MET:O	19:6:145:ARG:HB2	2.19	0.42
21:7:352:LEU:O	21:7:404:LYS:NZ	2.53	0.42
21:7:408:ILE:HG13	21:7:485:ILE:HG13	2.02	0.42
28:T:147:DT:H5'	29:O:211:LYS:HG3	2.01	0.42
30:W:122:TYR:HD2	30:W:156:LEU:HB2	1.83	0.42
1:Q:114:MET:HA	2:R:137:GLU:O	2.19	0.42
1:Q:119:LEU:HB2	2:R:133:TYR:H	1.85	0.42
3:D:166:LEU:O	3:D:170:THR:HG23	2.18	0.42
4:G:119:LEU:HA	4:G:132:SER:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:200:THR:HA	5:M:203:PHE:HB3	2.00	0.42
6:A:329:LEU:HD22	6:A:335:ARG:HB2	2.02	0.42
6:A:662:PHE:HD2	7:B:829:CYS:SG	2.43	0.42
6:A:709:THR:HB	6:A:712:GLU:HG3	2.01	0.42
6:A:881:GLN:CD	6:A:959:ASN:HA	2.45	0.42
6:A:1140:HIS:NE2	6:A:1272:THR:OG1	2.35	0.42
6:A:1359:ASP:OD1	6:A:1360:GLY:N	2.52	0.42
7:B:1074:ASN:OD1	7:B:1076:HIS:N	2.53	0.42
7:B:1096:ARG:C	7:B:1097:HIS:CG	2.98	0.42
7:B:1133:MET:HB2	7:B:1133:MET:HE3	1.76	0.42
10:F:116:ASP:HB3	10:F:119:ARG:CG	2.49	0.42
10:F:140:ASP:OD1	10:F:142:SER:N	2.35	0.42
14:K:36:GLU:HB3	14:K:37:LYS:HE2	2.01	0.42
18:4:52:LYS:NZ	18:4:240:SER:O	2.47	0.42
18:4:67:PHE:CD1	18:4:253:PHE:HZ	2.37	0.42
21:7:350:PRO:HG2	21:7:480:ARG:HH22	1.85	0.42
21:7:594:LEU:HD22	21:7:598:HIS:HE1	1.85	0.42
24:X:206:SER:OG	24:X:207:CYS:N	2.52	0.42
29:O:160:ILE:O	29:O:215:THR:HA	2.20	0.42
29:O:163:SER:HB3	29:O:213:VAL:HG13	2.01	0.42
4:G:26:LEU:HA	4:G:26:LEU:HD23	1.64	0.42
6:A:149:GLU:O	6:A:164:ARG:NH1	2.52	0.42
7:B:192:LEU:HD23	7:B:192:LEU:HA	1.73	0.42
8:C:80:LEU:HD12	8:C:80:LEU:HA	1.78	0.42
8:C:101:LEU:HD12	8:C:101:LEU:HA	1.79	0.42
8:C:137:LYS:HE3	8:C:137:LYS:HB3	1.57	0.42
8:C:171:GLY:C	8:C:173:ALA:H	2.28	0.42
11:H:108:SER:OG	11:H:109:LYS:N	2.51	0.42
12:I:59:VAL:HG23	12:I:61:ASP:N	2.34	0.42
14:K:16:GLU:OE1	14:K:16:GLU:N	2.52	0.42
21:7:626:PHE:O	21:7:628:TYR:HD1	2.03	0.42
1:Q:342:LEU:HB3	1:Q:343:ARG:HH22	1.85	0.42
2:R:92:LEU:HD12	2:R:93:GLY:O	2.19	0.42
3:D:37:GLN:HG2	3:D:47:LEU:HA	2.00	0.42
4:G:117:GLN:H	4:G:117:GLN:CD	2.28	0.42
6:A:912:LEU:O	6:A:979:SER:HB3	2.20	0.42
6:A:1148:ILE:HG23	12:I:49:ILE:HG13	2.02	0.42
6:A:1172:LEU:O	6:A:1174:PHE:N	2.53	0.42
7:B:125:SER:HA	7:B:171:PRO:HA	2.01	0.42
7:B:590:HIS:CD2	7:B:591:ARG:O	2.73	0.42
7:B:1132:GLU:H	7:B:1132:GLU:HG2	1.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:214:ASN:HB3	8:C:217:ASP:OD2	2.19	0.42
9:E:79:TRP:CD1	9:E:96:PHE:HE1	2.36	0.42
11:H:26:ILE:HD13	11:H:26:ILE:HA	1.56	0.42
11:H:110:ASP:O	11:H:111:LEU:HD23	2.19	0.42
15:L:31:CYS:SG	15:L:34:CYS:CA	3.06	0.42
15:L:34:CYS:SG	15:L:36:SER:CB	3.08	0.42
19:6:142:ARG:NH1	19:6:294:GLU:OE2	2.52	0.42
21:7:431:GLN:N	21:7:431:GLN:OE1	2.53	0.42
21:7:477:LEU:HA	21:7:482:TRP:NE1	2.34	0.42
23:2:19:GLN:HG3	23:2:85:HIS:CG	2.55	0.42
29:O:63:ILE:HB	29:O:227:PHE:CZ	2.54	0.42
30:W:5:ILE:HG13	30:W:192:SER:OG	2.20	0.42
3:D:174:PRO:O	3:D:177:VAL:HG22	2.19	0.42
4:G:3:PHE:O	4:G:77:VAL:HA	2.20	0.42
5:M:166:LYS:HA	5:M:166:LYS:HD3	1.83	0.42
6:A:10:PRO:HD2	7:B:1191:ILE:O	2.20	0.42
6:A:21:LEU:HD11	6:A:1414:ALA:HA	2.01	0.42
6:A:46:THR:C	6:A:48:ALA:N	2.77	0.42
6:A:279:LEU:HB3	6:A:289:ILE:CD1	2.50	0.42
6:A:374:LEU:HA	6:A:374:LEU:HD23	1.79	0.42
6:A:451:HIS:HB3	6:A:453:MET:N	2.35	0.42
7:B:319:GLU:HG2	12:I:15:TYR:OH	2.20	0.42
13:J:23:ASN:O	13:J:27:GLU:HG2	2.20	0.42
14:K:19:LEU:HA	14:K:19:LEU:HD23	1.74	0.42
17:O:360:LEU:O	17:O:364:LYS:N	2.46	0.42
19:6:451:CYS:HB3	19:6:454:CYS:HB2	2.02	0.42
21:7:581:TYR:CE1	21:7:714:GLN:HB3	2.55	0.42
27:N:23:DA:N1	28:T:144:DA:N6	2.68	0.42
28:T:157:DT:C4	28:T:158:DT:C4	3.07	0.42
3:D:40:HIS:CE1	4:G:6:ASP:HB3	2.54	0.42
4:G:64:THR:OG1	4:G:65:ASP:N	2.53	0.42
5:M:54:ASP:OD1	5:M:55:LYS:N	2.53	0.42
5:M:283:TYR:HA	5:M:286:ILE:HG22	2.01	0.42
6:A:507:VAL:O	6:A:510:GLN:N	2.37	0.42
6:A:587:HIS:O	6:A:588:LEU:C	2.63	0.42
6:A:1121:GLU:C	6:A:1123:GLY:H	2.27	0.42
6:A:1153:TYR:CD1	6:A:1163:ILE:HD11	2.55	0.42
6:A:1409:LEU:HA	6:A:1409:LEU:HD23	1.62	0.42
6:A:1442:ASP:HB2	10:F:136:ARG:CA	2.50	0.42
7:B:852:ARG:HH11	7:B:852:ARG:HD3	1.69	0.42
7:B:879:ARG:NH2	7:B:885:MET:HE2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:5:GLY:HA3	8:C:6:PRO:HD3	1.87	0.42
9:E:88:VAL:HG21	9:E:110:PHE:HE1	1.83	0.42
11:H:79:TRP:CH2	11:H:81:PRO:HA	2.54	0.42
12:I:82:GLU:N	12:I:82:GLU:CD	2.78	0.42
17:O:428:ALA:O	30:W:11:ASN:HB3	2.20	0.42
17:O:726:GLN:NE2	19:6:290:ILE:HG13	2.35	0.42
21:7:410:LEU:O	21:7:488:ASP:N	2.53	0.42
23:2:422:LEU:HA	23:2:425:ASN:OD1	2.20	0.42
23:2:446:LEU:O	23:2:450:ARG:N	2.42	0.42
27:N:29:DT:C2	28:T:138:DG:C2	3.08	0.42
28:T:146:DA:H2	29:O:207:PHE:HZ	1.68	0.42
29:O:179:HIS:CD2	29:O:237:PHE:HE2	2.38	0.42
2:R:99:LYS:HD2	2:R:99:LYS:HA	1.89	0.41
3:D:176:GLU:H	3:D:176:GLU:HG3	1.59	0.41
6:A:129:LYS:HB2	6:A:129:LYS:HE2	1.84	0.41
6:A:968:GLN:O	6:A:972:HIS:N	2.53	0.41
7:B:45:SER:OG	7:B:46:GLN:N	2.53	0.41
7:B:68:THR:O	7:B:69:LEU:HD23	2.20	0.41
7:B:420:LEU:HD11	7:B:456:GLY:HA3	2.01	0.41
7:B:468:GLU:O	7:B:471:LYS:N	2.53	0.41
7:B:471:LYS:HB3	7:B:471:LYS:HE2	1.75	0.41
7:B:910:VAL:HA	7:B:940:PRO:HA	2.02	0.41
11:H:58:THR:O	11:H:143:LEU:N	2.51	0.41
11:H:61:SER:HB2	11:H:139:ASN:HD21	1.85	0.41
12:I:17:ARG:HD3	12:I:28:GLU:OE2	2.20	0.41
14:K:47:ARG:HE	14:K:47:ARG:HB3	1.61	0.41
17:O:140:GLN:O	17:O:144:LYS:NZ	2.53	0.41
17:O:584:GLU:HG3	17:O:585:THR:N	2.35	0.41
17:O:590:CYS:SG	17:O:596:ALA:HB3	2.60	0.41
18:4:299:ILE:N	18:4:300:PRO:HD2	2.34	0.41
21:7:420:TRP:O	21:7:423:GLN:HG2	2.20	0.41
23:2:365:HIS:ND1	23:2:365:HIS:O	2.53	0.41
23:2:503:ASP:OD1	23:2:507:ARG:NH1	2.53	0.41
29:O:106:ILE:HD11	29:O:135:ALA:HA	2.02	0.41
1:Q:337:GLU:OE2	1:Q:339:ALA:HB3	2.20	0.41
3:D:40:HIS:CE1	4:G:74:TYR:H	2.37	0.41
3:D:167:LEU:HA	3:D:170:THR:CG2	2.50	0.41
3:D:188:ALA:HB1	3:D:207:LEU:HD12	2.02	0.41
5:M:188:THR:HB	5:M:191:GLU:CD	2.45	0.41
6:A:57:ARG:HB2	6:A:68:GLN:CB	2.50	0.41
6:A:102:VAL:O	6:A:105:CYS:N	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:177:ASP:O	6:A:178:GLY:C	2.61	0.41
6:A:239:LEU:HD12	6:A:239:LEU:HA	1.76	0.41
6:A:595:THR:H	6:A:595:THR:HG23	1.55	0.41
6:A:596:THR:C	6:A:598:LEU:N	2.74	0.41
6:A:1150:SER:O	12:I:45:ARG:HA	2.20	0.41
6:A:1225:PHE:CZ	6:A:1227:ILE:HD11	2.56	0.41
7:B:48:LEU:HA	7:B:48:LEU:HD23	1.69	0.41
7:B:555:ILE:H	7:B:555:ILE:HG13	1.42	0.41
7:B:710:LEU:O	7:B:733:HIS:HB3	2.20	0.41
7:B:755:ILE:HD12	7:B:755:ILE:HG23	1.82	0.41
7:B:881:ASN:C	7:B:883:LEU:HG	2.46	0.41
7:B:882:THR:O	7:B:884:ARG:N	2.53	0.41
9:E:43:LYS:O	9:E:47:CYS:HB2	2.20	0.41
9:E:48:ASP:N	9:E:52:ARG:O	2.37	0.41
9:E:136:ASN:OD1	9:E:136:ASN:C	2.63	0.41
10:F:97:ARG:HD2	10:F:97:ARG:HA	1.71	0.41
12:I:68:LEU:HB3	12:I:84:VAL:HG13	2.02	0.41
16:3:128:LYS:O	16:3:132:LYS:N	2.47	0.41
17:0:60:GLN:CD	17:0:69:ILE:HD11	2.45	0.41
17:0:184:TYR:CE1	17:0:188:LYS:HG3	2.54	0.41
17:0:357:LYS:HB2	17:0:413:GLU:OE1	2.20	0.41
17:0:581:LEU:HA	17:0:584:GLU:HG2	2.00	0.41
19:6:120:ARG:HE	19:6:307:PRO:HB2	1.85	0.41
27:N:17:DG:N3	28:T:150:DG:N2	2.67	0.41
28:T:140:DT:H2'	28:T:141:DT:H71	2.02	0.41
30:W:144:ARG:NH2	30:W:146:GLU:H	2.17	0.41
31:P:6:G:C6	31:P:7:A:H1'	2.55	0.41
1:Q:106:ILE:HB	1:Q:385:THR:HG21	2.02	0.41
3:D:157:GLN:CD	3:D:157:GLN:H	2.28	0.41
5:M:272:LYS:H	29:O:208:VAL:HG11	1.85	0.41
6:A:49:LYS:HE3	6:A:49:LYS:HB3	1.86	0.41
6:A:49:LYS:HD3	6:A:55:ASP:O	2.20	0.41
6:A:167:CYS:O	6:A:168:GLY:C	2.63	0.41
6:A:664:THR:HG22	7:B:1014:PRO:HB3	2.02	0.41
6:A:982:THR:HG23	6:A:985:ASP:OD2	2.20	0.41
7:B:135:ARG:NH1	7:B:137:TYR:O	2.53	0.41
7:B:782:LEU:HD23	7:B:782:LEU:HA	1.67	0.41
7:B:842:ASN:HB3	7:B:845:SER:HB3	2.02	0.41
7:B:1187:ASN:HD21	7:B:1190:ASP:CB	2.26	0.41
8:C:54:ASN:OD1	8:C:55:THR:N	2.53	0.41
11:H:13:SER:OG	11:H:27:GLU:O	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:40:LEU:HD12	11:H:41:ASP:H	1.85	0.41
12:I:74:GLU:HB2	12:I:81:ARG:CZ	2.50	0.41
15:L:48:CYS:HG	15:L:51:CYS:H	1.68	0.41
17:O:69:ILE:HB	17:O:205:ILE:HG13	2.02	0.41
18:4:55:GLU:O	18:4:59:VAL:HG23	2.21	0.41
18:4:114:UNK:C	18:4:116:ARG:N	2.83	0.41
21:7:712:ASP:H	21:7:716:MET:HE3	1.85	0.41
30:W:65:ARG:HG2	30:W:93:HIS:HB3	2.03	0.41
5:M:318:GLU:OE1	5:M:319:HIS:ND1	2.53	0.41
6:A:72:GLU:OE2	6:A:80:HIS:NE2	2.52	0.41
6:A:1142:THR:OG1	6:A:1143:LEU:N	2.52	0.41
6:A:1263:ILE:HD12	6:A:1263:ILE:HA	1.84	0.41
6:A:1377:THR:C	6:A:1379:GLY:H	2.28	0.41
7:B:89:GLU:O	7:B:135:ARG:N	2.48	0.41
7:B:120:ARG:HE	7:B:120:ARG:HB3	1.67	0.41
7:B:269:ILE:H	7:B:317:CYS:HG	1.65	0.41
7:B:585:VAL:HB	7:B:587:HIS:HE1	1.84	0.41
7:B:838:SER:HB3	7:B:988:GLY:HA3	2.02	0.41
7:B:976:ILE:CD1	7:B:992:ILE:HA	2.51	0.41
7:B:979:LYS:HZ3	31:P:10:A:P	2.43	0.41
7:B:997:GLU:HG2	7:B:998:ASP:N	2.35	0.41
17:O:19:PRO:HG3	17:O:739:TRP:CE2	2.56	0.41
17:O:413:GLU:O	17:O:414:GLU:HG3	2.20	0.41
17:O:495:MET:HA	17:O:705:ASP:OD2	2.19	0.41
18:4:34:PRO:HD2	18:4:80:SER:CB	2.50	0.41
18:4:175:ARG:NE	18:4:256:PRO:HG3	2.26	0.41
20:1:256:ILE:HG13	20:1:257:LEU:N	2.34	0.41
21:7:564:GLU:OE1	21:7:757:ARG:HB2	2.21	0.41
22:5:8:ALA:HB2	22:5:44:PRO:HG3	2.02	0.41
23:2:394:ASP:OD1	23:2:395:GLN:N	2.54	0.41
30:W:44:LYS:NZ	30:W:51:LYS:HG2	2.34	0.41
1:Q:333:LYS:H	7:B:70:ILE:HG12	1.84	0.41
1:Q:352:MET:HG2	1:Q:361:TRP:HB2	2.02	0.41
2:R:96:ARG:O	2:R:104:ILE:HG23	2.20	0.41
3:D:183:LEU:HD12	3:D:195:ILE:HD11	2.03	0.41
4:G:110:VAL:HA	4:G:161:GLY:O	2.20	0.41
6:A:414:ASP:OD1	6:A:415:LEU:N	2.53	0.41
6:A:495:GLU:O	6:A:498:ARG:HG3	2.21	0.41
6:A:618:GLU:OE1	6:A:620:LYS:N	2.44	0.41
6:A:752:LYS:HD3	6:A:752:LYS:HA	1.86	0.41
6:A:765:VAL:HG23	6:A:802:ASN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:843:LYS:HD2	6:A:843:LYS:HA	1.71	0.41
6:A:1235:LYS:HB2	6:A:1237:ILE:HD11	2.03	0.41
6:A:1293:SER:OG	6:A:1297:GLU:O	2.30	0.41
7:B:20:ASP:OD2	7:B:21:GLU:N	2.52	0.41
7:B:1035:ALA:O	7:B:1039:GLY:N	2.53	0.41
8:C:29:MET:HE3	8:C:29:MET:HB2	1.81	0.41
8:C:201:TRP:HA	8:C:202:PRO:HD3	1.96	0.41
9:E:93:MET:HE3	9:E:93:MET:HB3	1.67	0.41
10:F:147:SER:O	10:F:149:GLU:N	2.54	0.41
12:I:52:ILE:HA	12:I:120:GLN:O	2.20	0.41
14:K:7:PHE:HA	14:K:10:PHE:CZ	2.55	0.41
17:0:108:LEU:HD22	17:0:200:ILE:HD11	2.02	0.41
17:0:132:LYS:HE3	17:0:132:LYS:HB2	1.89	0.41
17:0:267:LEU:HD22	17:0:399:LEU:HD13	2.00	0.41
17:0:527:VAL:O	17:0:531:LYS:HG3	2.20	0.41
17:0:575:ASP:OD1	17:0:575:ASP:N	2.54	0.41
17:0:632:SER:OG	17:0:633:ARG:N	2.53	0.41
18:4:67:PHE:HE1	23:2:44:LYS:HB3	1.85	0.41
18:4:180:THR:HG23	18:4:214:LYS:HA	2.01	0.41
23:2:100:LEU:HA	23:2:100:LEU:HD23	1.79	0.41
24:X:193:LEU:HD21	24:X:228:SER:HA	2.02	0.41
27:N:18:DT:C4	28:T:148:DA:N1	2.88	0.41
1:Q:104:ARG:O	1:Q:385:THR:HG23	2.21	0.41
1:Q:134:HIS:HB3	1:Q:354:ASP:OD1	2.20	0.41
2:R:124:LEU:HD22	2:R:220:HIS:NE2	2.36	0.41
6:A:139:TRP:O	6:A:143:LYS:HB3	2.19	0.41
6:A:217:LYS:HG3	6:A:218:ASP:H	1.85	0.41
6:A:595:THR:HG21	6:A:604:GLY:HA3	2.02	0.41
6:A:726:ARG:HE	6:A:726:ARG:HB3	1.60	0.41
6:A:878:ILE:C	6:A:879:GLU:HG2	2.46	0.41
6:A:903:ASN:CG	6:A:904:THR:N	2.79	0.41
6:A:1155:ASP:HB3	6:A:1241:ARG:HH21	1.86	0.41
7:B:301:ILE:HD13	7:B:382:ILE:HG21	2.02	0.41
7:B:523:CYS:HB2	7:B:750:GLY:HA3	2.02	0.41
7:B:1175:LEU:C	7:B:1177:HIS:N	2.78	0.41
10:F:138:LEU:HA	10:F:138:LEU:HD13	1.56	0.41
10:F:147:SER:O	10:F:150:GLU:HG2	2.20	0.41
11:H:95:TYR:HA	11:H:95:TYR:HD1	1.73	0.41
11:H:136:LYS:HE2	11:H:136:LYS:HB2	1.80	0.41
17:0:709:SER:HB3	17:0:712:MET:HB3	2.02	0.41
18:4:228:THR:H	18:4:228:THR:HG22	1.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1:194:VAL:HA	20:1:197:GLU:HG2	2.01	0.41
23:2:337:GLY:O	23:2:406:PRO:HB2	2.21	0.41
23:2:419:LYS:NZ	23:2:426:CYS:O	2.35	0.41
23:2:435:PRO:O	23:2:439:ASP:N	2.40	0.41
2:R:66:ARG:O	2:R:217:THR:N	2.54	0.41
2:R:74:PRO:HB2	2:R:76:PHE:CE1	2.56	0.41
4:G:31:LEU:HD11	4:G:51:TYR:CE1	2.55	0.41
4:G:97:HIS:NE2	30:W:145:THR:O	2.52	0.41
6:A:404:TYR:CD1	6:A:414:ASP:HA	2.56	0.41
6:A:1435:PRO:O	6:A:1436:ILE:HD13	2.21	0.41
7:B:356:LEU:HD23	7:B:356:LEU:N	2.36	0.41
7:B:693:ILE:HA	7:B:693:ILE:HD13	1.75	0.41
7:B:706:GLN:O	7:B:707:PRO:C	2.61	0.41
7:B:1151:LEU:HD12	7:B:1151:LEU:HA	1.74	0.41
19:6:243:ASP:O	20:1:389:LEU:HD22	2.20	0.41
21:7:562:THR:OG1	21:7:563:ALA:N	2.52	0.41
24:X:258:GLU:O	24:X:262:MET:N	2.51	0.41
25:U:267:VAL:HG12	25:U:269:ILE:HG13	2.03	0.41
26:V:69:TYR:HB2	26:V:76:TRP:HZ3	1.83	0.41
27:N:37:DG:C2	27:N:38:DT:C2	3.08	0.41
28:T:18:DA:N3	28:T:18:DA:H3'	2.36	0.41
1:Q:97:GLU:OE2	1:Q:99:ASN:N	2.54	0.41
1:Q:125:LYS:O	1:Q:127:ILE:N	2.54	0.41
1:Q:141:ARG:NE	1:Q:348:TYR:O	2.53	0.41
1:Q:333:LYS:N	7:B:70:ILE:HG12	2.36	0.41
6:A:43:GLU:H	6:A:43:GLU:CD	2.26	0.41
6:A:226:GLU:C	6:A:226:GLU:CD	2.88	0.41
6:A:369:SER:N	14:K:2:ASN:OD1	2.40	0.41
6:A:839:ARG:O	6:A:843:LYS:HG2	2.20	0.41
6:A:1067:LEU:HD12	6:A:1067:LEU:HA	1.83	0.41
6:A:1134:ILE:O	6:A:1135:ARG:C	2.63	0.41
6:A:1193:LEU:HD12	6:A:1194:ARG:N	2.35	0.41
6:A:1341:ILE:HD12	6:A:1341:ILE:HA	1.85	0.41
6:A:1425:SER:O	6:A:1429:ILE:HG13	2.21	0.41
6:A:1441:PHE:HZ	10:F:92:ARG:CB	2.33	0.41
7:B:239:GLU:HG2	7:B:240:ILE:N	2.36	0.41
7:B:423:LYS:NZ	7:B:468:GLU:OE2	2.29	0.41
7:B:1079:LYS:HG2	7:B:1080:LYS:N	2.36	0.41
7:B:1156:ASP:N	7:B:1156:ASP:OD1	2.50	0.41
7:B:1173:ALA:O	7:B:1175:LEU:N	2.53	0.41
9:E:65:THR:O	9:E:68:SER:OG	2.25	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:30:LEU:HD12	13:J:30:LEU:HA	1.52	0.41
17:0:120:VAL:HG21	34:0:801:SF4:S4	2.61	0.41
17:0:636:LYS:O	17:0:640:GLU:HG2	2.21	0.41
19:6:137:LEU:HD23	19:6:137:LEU:HA	1.85	0.41
20:1:562:LYS:HD2	20:1:562:LYS:HA	1.94	0.41
21:7:583:MET:HB3	21:7:763:VAL:HG21	2.02	0.41
21:7:633:GLN:O	21:7:637:MET:HG2	2.21	0.41
23:2:273:LYS:HG3	23:2:276:LEU:HD23	2.03	0.41
24:X:224:LEU:O	24:X:229:LYS:N	2.53	0.41
27:N:19:DA:N6	28:T:146:DA:H61	2.19	0.41
28:T:144:DA:H1'	29:O:69:ASN:ND2	2.36	0.41
29:O:74:VAL:HA	29:O:154:ASP:O	2.20	0.41
29:O:194:ILE:HD12	29:O:205:LEU:HD22	2.03	0.41
1:Q:106:ILE:HD12	1:Q:106:ILE:HA	1.87	0.41
1:Q:376:LEU:O	1:Q:378:VAL:N	2.53	0.41
2:R:69:TRP:CH2	2:R:220:HIS:HD2	2.39	0.41
5:M:266:ILE:O	5:M:266:ILE:HG23	2.21	0.41
6:A:42:ASP:C	6:A:44:THR:H	2.29	0.41
6:A:147:VAL:HG23	6:A:148:CYS:N	2.36	0.41
6:A:217:LYS:NZ	6:A:218:ASP:HA	2.36	0.41
6:A:340:LEU:HD13	6:A:1429:ILE:HG23	2.02	0.41
6:A:420:ARG:HB3	6:A:423:ASP:CB	2.50	0.41
6:A:780:VAL:H	7:B:699:GLU:CD	2.28	0.41
6:A:834:THR:HB	6:A:1077:THR:HG22	2.01	0.41
6:A:849:MET:HE2	6:A:1061:GLY:HA2	2.03	0.41
6:A:857:ARG:CZ	10:F:139:PRO:HG2	2.51	0.41
6:A:878:ILE:CG2	6:A:955:PRO:HB2	2.51	0.41
6:A:899:VAL:HG13	6:A:1029:ARG:HH11	1.85	0.41
6:A:1189:SER:HB3	6:A:1242:VAL:O	2.21	0.41
6:A:1267:MET:N	6:A:1267:MET:HE2	2.36	0.41
6:A:1444:MET:C	10:F:132:LEU:O	2.64	0.41
7:B:69:LEU:HD23	7:B:69:LEU:HA	1.70	0.41
7:B:193:LYS:HZ1	13:J:65:PRO:HD3	1.86	0.41
7:B:386:LEU:HD22	7:B:386:LEU:HA	1.85	0.41
7:B:637:LEU:HD23	7:B:637:LEU:HA	1.63	0.41
7:B:644:GLU:HG2	7:B:648:HIS:NE2	2.36	0.41
7:B:745:PRO:C	7:B:747:MET:H	2.28	0.41
7:B:815:ARG:HE	7:B:815:ARG:HB3	1.39	0.41
8:C:51:VAL:HG13	15:L:65:VAL:HG13	2.03	0.41
8:C:58:LEU:HD23	8:C:58:LEU:HA	1.79	0.41
8:C:106:GLU:H	8:C:106:GLU:HG2	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:E:71:LYS:HE2	9:E:71:LYS:HB3	1.82	0.41
9:E:99:HIS:CD2	9:E:103:LYS:HZ1	2.39	0.41
9:E:180:ARG:NH1	9:E:192:ARG:HB2	2.36	0.41
10:F:122:MET:HB2	10:F:122:MET:HE3	1.74	0.41
11:H:104:PHE:HE1	11:H:136:LYS:HD3	1.86	0.41
15:L:31:CYS:SG	15:L:34:CYS:CB	3.08	0.41
17:0:48:LYS:O	17:0:52:LEU:HB2	2.21	0.41
19:6:365:CYS:O	20:1:559:GLU:HA	2.20	0.41
21:7:355:ASP:OD2	21:7:357:LYS:NZ	2.49	0.41
21:7:361:GLN:H	21:7:361:GLN:HG2	1.68	0.41
21:7:528:ASN:O	21:7:532:GLY:N	2.53	0.41
21:7:671:ILE:HG13	21:7:706:TYR:HB2	2.02	0.41
23:2:143:TRP:O	23:2:146:ILE:HG22	2.21	0.41
27:N:21:DA:H5''	29:O:196:ARG:HH22	1.86	0.41
28:T:130:DG:C2	28:T:131:DT:C2	3.08	0.41
29:O:94:TYR:HB2	29:O:102:VAL:HA	2.02	0.41
29:O:182:PHE:O	29:O:195:TYR:HA	2.21	0.41
29:O:204:LEU:HD22	29:O:230:ILE:HG21	2.02	0.41
29:O:206:ILE:HG23	29:O:212:ILE:CD1	2.49	0.41
30:W:113:LEU:HG	30:W:165:ASN:OD1	2.21	0.41
1:Q:123:SER:H	1:Q:361:TRP:HH2	1.69	0.41
2:R:64:SER:HA	2:R:214:ILE:HG22	2.02	0.41
2:R:105:THR:OG1	2:R:120:TYR:O	2.38	0.41
5:M:51:VAL:HG12	6:A:412:ARG:O	2.21	0.41
5:M:132:LYS:HE3	5:M:132:LYS:HB2	1.89	0.41
6:A:84:ILE:O	6:A:239:LEU:N	2.50	0.41
6:A:151:ASP:HB3	6:A:162:VAL:O	2.21	0.41
6:A:340:LEU:HD23	6:A:340:LEU:HA	1.73	0.41
6:A:901:LEU:HA	6:A:901:LEU:HD23	1.87	0.41
7:B:387:LEU:HD12	7:B:387:LEU:HA	1.64	0.41
11:H:102:TYR:CE1	11:H:115:TYR:HB3	2.56	0.41
17:0:293:LEU:HD22	17:0:319:GLU:HG3	2.03	0.41
17:0:611:ASP:OD1	17:0:612:PHE:N	2.54	0.41
19:6:346:GLY:HA2	19:6:358:SER:N	2.36	0.41
21:7:370:LEU:HD22	21:7:374:PHE:CZ	2.56	0.41
21:7:409:VAL:O	21:7:455:SER:N	2.40	0.41
21:7:417:VAL:HG13	21:7:454:VAL:HG22	2.02	0.41
27:N:23:DA:H4'	29:O:158:GLN:O	2.21	0.41
30:W:44:LYS:HZ3	30:W:51:LYS:HG2	1.86	0.41
3:D:63:LEU:HB3	3:D:130:LEU:HD13	2.04	0.40
3:D:151:PHE:C	3:D:153:ARG:HD3	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:108:MET:HE2	6:A:171:GLN:OE1	2.21	0.40
6:A:114:LEU:HB3	6:A:145:LYS:HG2	2.03	0.40
6:A:407:ARG:HA	6:A:430:TRP:CD1	2.56	0.40
6:A:497:THR:HG22	7:B:1146:PHE:HA	2.03	0.40
6:A:1077:THR:H	6:A:1077:THR:HG23	1.64	0.40
6:A:1092:LYS:C	6:A:1094:VAL:HG13	2.46	0.40
6:A:1109:LYS:HE2	6:A:1109:LYS:HB2	1.69	0.40
6:A:1224:LEU:HA	6:A:1241:ARG:O	2.22	0.40
6:A:1443:VAL:HG13	10:F:148:VAL:HG13	2.03	0.40
7:B:65:GLU:OE2	7:B:247:GLY:HA2	2.21	0.40
7:B:731:VAL:O	7:B:732:SER:OG	2.31	0.40
7:B:806:THR:HG22	7:B:1045:SER:HA	2.02	0.40
7:B:901:PRO:HA	7:B:949:VAL:HG12	2.04	0.40
8:C:153:LEU:HD11	8:C:155:LEU:HD23	2.01	0.40
11:H:4:THR:HG21	11:H:7:ASP:HB2	2.02	0.40
11:H:55:LEU:O	11:H:146:ARG:CZ	2.69	0.40
15:L:40:LEU:HD12	15:L:40:LEU:HA	1.81	0.40
17:O:285:GLU:HA	17:O:288:LYS:HD2	2.03	0.40
17:O:523:GLY:HA3	17:O:559:ILE:HG12	2.03	0.40
17:O:732:ASP:OD1	17:O:733:GLN:N	2.54	0.40
20:1:253:ARG:HA	20:1:256:ILE:HG12	2.03	0.40
20:1:273:ASN:HB3	20:1:277:ASN:O	2.20	0.40
20:1:278:PHE:O	20:1:283:PHE:HB2	2.21	0.40
23:2:382:SER:HA	23:2:385:ARG:HH11	1.86	0.40
27:N:21:DA:H5'	29:O:196:ARG:NH2	2.37	0.40
29:O:172:LEU:O	29:O:176:ALA:N	2.54	0.40
29:O:185:TYR:CZ	29:O:187:PRO:HB3	2.56	0.40
31:P:6:G:H3'	31:P:6:G:N3	2.36	0.40
2:R:94:LYS:HZ3	2:R:94:LYS:C	2.25	0.40
5:M:142:LEU:HD12	5:M:142:LEU:HA	1.73	0.40
6:A:209:ASN:O	6:A:210:ILE:C	2.64	0.40
6:A:409:SER:OG	6:A:411:ASP:OD1	2.38	0.40
6:A:489:LEU:HD23	6:A:489:LEU:C	2.46	0.40
6:A:849:MET:HB2	6:A:1063:MET:SD	2.61	0.40
6:A:909:ASP:CG	6:A:911:SER:H	2.29	0.40
6:A:1017:LEU:HA	6:A:1017:LEU:HD12	1.88	0.40
6:A:1242:VAL:HG12	6:A:1243:VAL:H	1.86	0.40
7:B:232:SER:O	7:B:261:ARG:CZ	2.69	0.40
7:B:483:LEU:HA	7:B:483:LEU:HD12	1.63	0.40
7:B:552:MET:HA	7:B:555:ILE:CD1	2.51	0.40
7:B:1030:LEU:HA	7:B:1030:LEU:HD12	1.78	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:22:LEU:O	8:C:228:PHE:N	2.48	0.40
8:C:183:TRP:CZ2	8:C:207:CYS:HB3	2.56	0.40
9:E:52:ARG:HE	9:E:52:ARG:HB2	1.70	0.40
9:E:58:MET:O	9:E:59:SER:C	2.64	0.40
11:H:24:CYS:SG	11:H:44:VAL:HG11	2.61	0.40
11:H:83:GLN:C	11:H:85:GLY:H	2.29	0.40
12:I:19:ASP:HB2	12:I:24:ARG:NH1	2.36	0.40
17:O:506:ILE:O	17:O:683:ASP:HA	2.21	0.40
18:4:138:LYS:O	18:4:142:GLN:N	2.55	0.40
19:6:144:ASN:HD21	19:6:146:HIS:HB3	1.85	0.40
19:6:169:MET:O	19:6:192:HIS:NE2	2.54	0.40
19:6:181:LEU:HD11	19:6:184:GLN:HA	2.02	0.40
21:7:409:VAL:HB	21:7:454:VAL:HA	2.02	0.40
21:7:460:VAL:HG13	21:7:474:MET:SD	2.62	0.40
23:2:58:PRO:HB3	23:2:95:THR:HG21	2.02	0.40
25:U:250:LYS:O	25:U:261:SER:N	2.45	0.40
28:T:25:DC:H6	28:T:25:DC:H5"	1.86	0.40
29:O:120:LYS:HA	29:O:120:LYS:HD3	1.86	0.40
29:O:138:LYS:O	29:O:142:ILE:HG13	2.21	0.40
2:R:99:LYS:C	2:R:103:LYS:N	2.79	0.40
6:A:525:GLN:NE2	7:B:836:GLU:HG2	2.36	0.40
6:A:927:VAL:HA	6:A:930:ASP:OD2	2.22	0.40
6:A:1063:MET:SD	6:A:1436:ILE:HG23	2.61	0.40
6:A:1084:PHE:HD2	6:A:1086:PHE:HB2	1.86	0.40
6:A:1153:TYR:HB2	6:A:1192:LEU:HD23	2.03	0.40
7:B:262:GLU:C	7:B:264:SER:H	2.30	0.40
7:B:282:ILE:HG13	7:B:283:VAL:N	2.36	0.40
7:B:532:ALA:O	7:B:533:CYS:C	2.64	0.40
7:B:1032:SER:HB2	7:B:1089:PRO:HG2	2.04	0.40
9:E:31:THR:OG1	9:E:34:GLU:N	2.41	0.40
9:E:140:LEU:HA	9:E:140:LEU:HD23	1.81	0.40
11:H:142:LEU:C	11:H:143:LEU:HG	2.46	0.40
15:L:25:ALA:HB3	15:L:37:LYS:NZ	2.37	0.40
17:O:19:PRO:HG3	17:O:739:TRP:CD2	2.57	0.40
17:O:332:VAL:O	17:O:336:LYS:HG3	2.21	0.40
17:O:375:ARG:HG3	17:O:410:SER:OG	2.22	0.40
19:6:127:ILE:HG21	19:6:220:LEU:HD23	2.02	0.40
19:6:128:LEU:HD12	19:6:233:LEU:HD13	2.03	0.40
19:6:174:MET:HG2	19:6:209:SER:H	1.87	0.40
19:6:298:LYS:HA	19:6:298:LYS:HD2	1.82	0.40
21:7:585:PRO:HB3	21:7:750:TYR:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:5:3:ARG:HH11	23:2:460:SER:HB2	1.86	0.40
24:X:207:CYS:HB3	24:X:242:ARG:H	1.86	0.40
26:V:84:GLN:HB3	26:V:105:VAL:HG12	2.02	0.40
2:R:76:PHE:CZ	2:R:120:TYR:HE2	2.38	0.40
2:R:135:PHE:HA	2:R:215:VAL:H	1.86	0.40
3:D:68:ARG:HG2	3:D:72:ARG:NH2	2.36	0.40
4:G:61:ILE:HG12	10:F:133:VAL:HG12	2.03	0.40
4:G:151:ILE:HA	4:G:151:ILE:HD13	1.80	0.40
5:M:37:ARG:HD2	5:M:37:ARG:HA	1.53	0.40
5:M:283:TYR:O	5:M:287:LEU:HG	2.21	0.40
6:A:107:CYS:HB2	6:A:148:CYS:SG	2.61	0.40
6:A:968:GLN:HA	6:A:973:ILE:CD1	2.51	0.40
6:A:1005:GLU:N	6:A:1005:GLU:CD	2.79	0.40
6:A:1143:LEU:O	6:A:1146:VAL:HG12	2.21	0.40
6:A:1335:ILE:HA	6:A:1335:ILE:HD13	1.77	0.40
7:B:258:LEU:HD13	7:B:269:ILE:HG12	2.02	0.40
7:B:778:MET:HE2	7:B:794:ASN:CG	2.47	0.40
7:B:1223:ASP:N	7:B:1223:ASP:OD1	2.54	0.40
8:C:66:ARG:HH11	8:C:66:ARG:HD3	1.67	0.40
8:C:94:LYS:HE3	8:C:94:LYS:HB2	1.89	0.40
8:C:118:LEU:HA	8:C:118:LEU:HD23	1.56	0.40
8:C:176:ILE:HG12	8:C:232:VAL:HG22	2.03	0.40
8:C:243:VAL:HG12	8:C:244:VAL:N	2.37	0.40
9:E:77:SER:O	9:E:106:GLN:HB3	2.20	0.40
9:E:178:ILE:HG23	9:E:214:CYS:HA	2.03	0.40
10:F:140:ASP:OD1	10:F:142:SER:OG	2.35	0.40
11:H:10:PHE:HB3	11:H:28:ALA:HB1	2.03	0.40
11:H:57:VAL:O	11:H:93:TYR:CZ	2.74	0.40
14:K:42:LEU:HA	14:K:42:LEU:HD12	1.78	0.40
15:L:34:CYS:SG	15:L:36:SER:HB3	2.62	0.40
15:L:48:CYS:O	15:L:49:LYS:C	2.65	0.40
15:L:61:THR:HG1	15:L:63:ARG:HG2	1.87	0.40
17:0:37:ASN:HD22	17:0:475:PHE:HD2	1.69	0.40
17:0:614:HIS:HB3	17:0:618:ARG:NH2	2.36	0.40
18:4:159:TYR:HE1	19:6:407:GLN:HB2	1.86	0.40
25:U:286:VAL:OXT	29:O:110:LYS:HD2	2.21	0.40
29:O:75:THR:HG22	29:O:77:GLY:H	1.86	0.40
1:Q:118:LEU:HB2	1:Q:392:VAL:HA	2.04	0.40
1:Q:139:LEU:HA	1:Q:351:VAL:O	2.22	0.40
3:D:206:GLU:HA	3:D:209:ARG:NE	2.37	0.40
6:A:325:ILE:O	6:A:328:ARG:N	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:336:ILE:HG23	6:A:336:ILE:HD12	1.82	0.40
6:A:563:PRO:HB3	6:A:572:TRP:CE2	2.57	0.40
6:A:1348:LEU:HA	6:A:1348:LEU:HD12	1.72	0.40
7:B:126:SER:O	7:B:170:LEU:N	2.41	0.40
7:B:313:MET:HG3	7:B:390:LEU:HD21	2.02	0.40
7:B:1059:LEU:HD12	7:B:1059:LEU:HA	1.80	0.40
8:C:62:PHE:HE1	8:C:66:ARG:HD2	1.87	0.40
10:F:94:LEU:HD23	10:F:94:LEU:HA	1.87	0.40
10:F:135:ARG:HD2	10:F:143:PHE:CE2	2.57	0.40
15:L:26:THR:HA	15:L:62:LYS:NZ	2.36	0.40
17:O:57:ILE:HD11	17:O:86:LEU:HD11	2.03	0.40
17:O:156:CYS:C	17:O:158:TYR:H	2.29	0.40
17:O:565:LYS:HE3	17:O:565:LYS:HB2	1.86	0.40
17:O:620:VAL:O	17:O:680:VAL:HG22	2.22	0.40
17:O:731:LYS:HA	17:O:734:GLU:CD	2.47	0.40
21:7:392:LYS:HE2	21:7:392:LYS:HB3	1.83	0.40
21:7:641:GLN:O	21:7:645:TYR:HB3	2.22	0.40
27:N:19:DA:N3	29:O:190:PHE:HD1	2.18	0.40
28:T:148:DA:H2'	28:T:148:DA:H5'	1.89	0.40
29:O:136:SER:HB2	29:O:152:PHE:CE1	2.47	0.40
30:W:49:ILE:HD11	30:W:54:LEU:HD12	2.02	0.40
30:W:102:VAL:HG13	30:W:179:ILE:HG12	2.04	0.40
30:W:131:TYR:HA	30:W:135:GLU:OE1	2.21	0.40
30:W:176:MET:HE3	30:W:180:GLN:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	140/735 (19%)	119 (85%)	21 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	R	142/398 (36%)	126 (89%)	16 (11%)	0	100	100
3	D	153/221 (69%)	140 (92%)	13 (8%)	0	100	100
4	G	169/171 (99%)	156 (92%)	13 (8%)	0	100	100
5	M	228/345 (66%)	196 (86%)	29 (13%)	3 (1%)	9	35
6	A	1395/1733 (80%)	1227 (88%)	161 (12%)	7 (0%)	24	57
7	B	1096/1224 (90%)	942 (86%)	149 (14%)	5 (0%)	24	57
8	C	264/318 (83%)	241 (91%)	22 (8%)	1 (0%)	30	61
9	E	212/215 (99%)	199 (94%)	13 (6%)	0	100	100
10	F	83/155 (54%)	73 (88%)	10 (12%)	0	100	100
11	H	129/146 (88%)	97 (75%)	31 (24%)	1 (1%)	16	47
12	I	117/122 (96%)	95 (81%)	22 (19%)	0	100	100
13	J	63/70 (90%)	52 (82%)	11 (18%)	0	100	100
14	K	112/120 (93%)	101 (90%)	11 (10%)	0	100	100
15	L	44/70 (63%)	30 (68%)	14 (32%)	0	100	100
16	3	70/321 (22%)	65 (93%)	5 (7%)	0	100	100
17	0	752/778 (97%)	701 (93%)	51 (7%)	0	100	100
18	4	279/338 (82%)	246 (88%)	33 (12%)	0	100	100
19	6	336/461 (73%)	295 (88%)	39 (12%)	2 (1%)	21	52
20	1	256/543 (47%)	237 (93%)	17 (7%)	2 (1%)	16	47
21	7	630/843 (75%)	578 (92%)	52 (8%)	0	100	100
22	5	64/72 (89%)	59 (92%)	5 (8%)	0	100	100
23	2	456/513 (89%)	412 (90%)	44 (10%)	0	100	100
24	X	145/328 (44%)	126 (87%)	19 (13%)	0	100	100
25	U	44/286 (15%)	39 (89%)	5 (11%)	0	100	100
26	V	45/122 (37%)	45 (100%)	0	0	100	100
29	O	178/240 (74%)	165 (93%)	13 (7%)	0	100	100
30	W	189/482 (39%)	179 (95%)	10 (5%)	0	100	100
All	All	7791/11370 (68%)	6941 (89%)	829 (11%)	21 (0%)	37	67

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	M	269	ILE

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Mol	Chain	Res	Type
5	M	270	ALA
6	A	68	GLN
6	A	72	GLU
6	A	609	ASP
7	B	837	ASP
7	B	838	SER
19	6	411	PRO
6	A	466	SER
11	H	58	THR
7	B	1046	PRO
5	M	158	HIS
6	A	47	ARG
8	C	175	ALA
6	A	958	VAL
7	B	991	GLY
19	6	112	LYS
20	1	229	GLY
6	A	957	PRO
7	B	712	PRO
20	1	351	GLY

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 PDB entries followed by that with respect to all EM entries.

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	
1	Q	108/641 (17%)	86 (80%)	22 (20%)	1	5
2	R	78/362 (22%)	60 (77%)	18 (23%)	1	4
3	D	139/200 (70%)	125 (90%)	14 (10%)	7	28
4	G	152/152 (100%)	131 (86%)	21 (14%)	3	15
5	M	202/299 (68%)	166 (82%)	36 (18%)	2	9
6	A	1224/1520 (80%)	1004 (82%)	220 (18%)	2	8
7	B	967/1061 (91%)	817 (84%)	150 (16%)	2	12
8	C	234/274 (85%)	191 (82%)	43 (18%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	E	196/197 (100%)	166 (85%)	30 (15%)	3	12
10	F	75/137 (55%)	63 (84%)	12 (16%)	2	12
11	H	117/128 (91%)	95 (81%)	22 (19%)	1	7
12	I	113/116 (97%)	82 (73%)	31 (27%)	0	1
13	J	60/65 (92%)	49 (82%)	11 (18%)	2	8
14	K	99/102 (97%)	88 (89%)	11 (11%)	6	24
15	L	40/57 (70%)	27 (68%)	13 (32%)	0	0
16	3	1/303 (0%)	1 (100%)	0	100	100
17	0	686/707 (97%)	656 (96%)	30 (4%)	25	56
18	4	198/298 (66%)	180 (91%)	18 (9%)	9	32
19	6	247/406 (61%)	234 (95%)	13 (5%)	20	51
20	1	169/396 (43%)	163 (96%)	6 (4%)	31	62
21	7	414/737 (56%)	393 (95%)	21 (5%)	21	52
22	5	53/66 (80%)	53 (100%)	0	100	100
23	2	258/468 (55%)	247 (96%)	11 (4%)	26	57
24	X	54/295 (18%)	54 (100%)	0	100	100
25	U	42/260 (16%)	40 (95%)	2 (5%)	23	54
26	V	46/108 (43%)	45 (98%)	1 (2%)	45	71
29	O	152/205 (74%)	139 (91%)	13 (9%)	10	34
30	W	155/429 (36%)	142 (92%)	13 (8%)	10	35
All	All	6279/9989 (63%)	5497 (88%)	782 (12%)	7	19

All (782) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Q	98	TYR
1	Q	100	GLU
1	Q	104	ARG
1	Q	106	ILE
1	Q	110	ASP
1	Q	111	LEU
1	Q	112	GLU
1	Q	114	MET
1	Q	118	LEU
1	Q	122	GLN

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Mol	Chain	Res	Type
1	Q	130	VAL
1	Q	132	ASP
1	Q	135	LEU
1	Q	331	GLN
1	Q	336	ASP
1	Q	350	TRP
1	Q	352	MET
1	Q	359	ASN
1	Q	380	ASP
1	Q	392	VAL
1	Q	396	THR
1	Q	403	THR
2	R	68	VAL
2	R	71	VAL
2	R	79	GLU
2	R	83	ASP
2	R	94	LYS
2	R	95	ILE
2	R	104	ILE
2	R	108	LEU
2	R	121	ASP
2	R	125	THR
2	R	126	LYS
2	R	127	LYS
2	R	128	VAL
2	R	129	VAL
2	R	130	GLU
2	R	136	THR
2	R	138	GLN
2	R	217	THR
3	D	26	THR
3	D	50	LEU
3	D	54	GLU
3	D	61	GLU
3	D	140	ASP
3	D	144	THR
3	D	156	ASP
3	D	157	GLN
3	D	160	VAL
3	D	169	SER
3	D	177	VAL
3	D	187	THR

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Mol	Chain	Res	Type
3	D	203	SER
3	D	208	GLU
4	G	13	LEU
4	G	21	ARG
4	G	39	THR
4	G	45	ILE
4	G	49	LEU
4	G	57	GLN
4	G	58	ARG
4	G	64	THR
4	G	65	ASP
4	G	72	VAL
4	G	83	LYS
4	G	91	VAL
4	G	97	HIS
4	G	101	VAL
4	G	111	THR
4	G	145	VAL
4	G	151	ILE
4	G	153	GLN
4	G	154	VAL
4	G	155	SER
4	G	163	ILE
5	M	22	LEU
5	M	40	GLU
5	M	47	LEU
5	M	51	VAL
5	M	56	LEU
5	M	58	ASP
5	M	123	ASP
5	M	125	GLU
5	M	133	ILE
5	M	134	THR
5	M	142	LEU
5	M	144	LYS
5	M	158	HIS
5	M	160	GLU
5	M	162	THR
5	M	170	SER
5	M	175	SER
5	M	176	ILE
5	M	177	LEU

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Mol	Chain	Res	Type
5	M	184	GLU
5	M	187	ARG
5	M	195	LEU
5	M	196	ILE
5	M	197	HIS
5	M	198	VAL
5	M	215	ARG
5	M	244	SER
5	M	250	MET
5	M	257	GLU
5	M	267	LYS
5	M	284	LEU
5	M	286	ILE
5	M	291	ILE
5	M	298	VAL
5	M	305	THR
5	M	311	SER
6	A	8	SER
6	A	13	THR
6	A	14	VAL
6	A	22	PHE
6	A	23	SER
6	A	30	ILE
6	A	37	PHE
6	A	45	GLN
6	A	47	ARG
6	A	50	ILE
6	A	57	ARG
6	A	58	LEU
6	A	61	ILE
6	A	63	ARG
6	A	64	ASN
6	A	68	GLN
6	A	71	GLN
6	A	72	GLU
6	A	84	ILE
6	A	93	VAL
6	A	96	ILE
6	A	99	ILE
6	A	102	VAL
6	A	106	VAL
6	A	115	LEU

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Mol	Chain	Res	Type
6	A	116	ASP
6	A	117	GLU
6	A	140	THR
6	A	144	THR
6	A	145	LYS
6	A	147	VAL
6	A	152	VAL
6	A	162	VAL
6	A	174	ILE
6	A	179	LEU
6	A	201	VAL
6	A	203	SER
6	A	206	GLU
6	A	217	LYS
6	A	219	PHE
6	A	220	THR
6	A	221	SER
6	A	225	ASN
6	A	227	VAL
6	A	235	ILE
6	A	236	LEU
6	A	237	THR
6	A	252	PHE
6	A	253	ASN
6	A	254	GLU
6	A	257	ARG
6	A	266	LEU
6	A	269	ILE
6	A	275	SER
6	A	278	THR
6	A	280	GLU
6	A	286	HIS
6	A	289	ILE
6	A	299	HIS
6	A	318	SER
6	A	345	VAL
6	A	352	VAL
6	A	354	SER
6	A	359	LEU
6	A	366	VAL
6	A	379	VAL
6	A	381	THR

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Mol	Chain	Res	Type
6	A	385	ILE
6	A	388	LEU
6	A	389	THR
6	A	398	GLU
6	A	408	ASP
6	A	411	ASP
6	A	419	LYS
6	A	438	ASP
6	A	447	GLN
6	A	449	SER
6	A	450	LEU
6	A	455	MET
6	A	460	VAL
6	A	469	ARG
6	A	470	LEU
6	A	472	LEU
6	A	476	SER
6	A	486	GLU
6	A	488	ASN
6	A	497	THR
6	A	502	SER
6	A	512	VAL
6	A	524	VAL
6	A	525	GLN
6	A	534	LEU
6	A	538	ASP
6	A	546	VAL
6	A	562	THR
6	A	566	ILE
6	A	567	LYS
6	A	571	LEU
6	A	573	SER
6	A	579	SER
6	A	589	GLN
6	A	612	ILE
6	A	616	VAL
6	A	621	THR
6	A	624	SER
6	A	634	THR
6	A	635	ARG
6	A	669	THR
6	A	672	ASP

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Mol	Chain	Res	Type
6	A	678	GLU
6	A	681	GLU
6	A	685	GLU
6	A	690	VAL
6	A	693	VAL
6	A	716	ASP
6	A	735	VAL
6	A	739	ASP
6	A	740	LEU
6	A	754	SER
6	A	783	THR
6	A	786	HIS
6	A	788	SER
6	A	790	ASP
6	A	803	SER
6	A	808	LEU
6	A	827	THR
6	A	829	VAL
6	A	837	ILE
6	A	845	LEU
6	A	849	MET
6	A	853	ASP
6	A	862	ASN
6	A	867	ILE
6	A	879	GLU
6	A	884	ASP
6	A	886	ILE
6	A	889	SER
6	A	899	VAL
6	A	903	ASN
6	A	905	ASP
6	A	907	THR
6	A	909	ASP
6	A	912	LEU
6	A	914	GLU
6	A	915	SER
6	A	927	VAL
6	A	948	VAL
6	A	963	ILE
6	A	965	GLN
6	A	972	HIS
6	A	977	LYS

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Mol	Chain	Res	Type
6	A	979	SER
6	A	982	THR
6	A	985	ASP
6	A	990	VAL
6	A	998	LEU
6	A	1000	LEU
6	A	1006	ILE
6	A	1015	VAL
6	A	1028	THR
6	A	1037	LEU
6	A	1038	THR
6	A	1043	ASP
6	A	1046	LEU
6	A	1049	ILE
6	A	1056	SER
6	A	1057	VAL
6	A	1062	GLU
6	A	1078	GLN
6	A	1089	VAL
6	A	1106	ASN
6	A	1107	VAL
6	A	1117	THR
6	A	1135	ARG
6	A	1138	ILE
6	A	1142	THR
6	A	1160	SER
6	A	1172	LEU
6	A	1174	PHE
6	A	1192	LEU
6	A	1196	GLU
6	A	1197	LEU
6	A	1198	ASP
6	A	1204	ASP
6	A	1208	THR
6	A	1211	GLN
6	A	1212	VAL
6	A	1219	THR
6	A	1223	ASP
6	A	1232	ASN
6	A	1233	ASP
6	A	1237	ILE
6	A	1240	CYS

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Mol	Chain	Res	Type
6	A	1242	VAL
6	A	1257	ASP
6	A	1261	LYS
6	A	1263	ILE
6	A	1265	ASN
6	A	1278	ASN
6	A	1290	LYS
6	A	1291	VAL
6	A	1299	VAL
6	A	1327	ILE
6	A	1329	THR
6	A	1334	ASP
6	A	1358	SER
6	A	1362	TYR
6	A	1368	MET
6	A	1372	VAL
6	A	1382	THR
6	A	1383	SER
6	A	1386	ARG
6	A	1392	SER
6	A	1400	CYS
6	A	1406	VAL
6	A	1407	GLU
6	A	1411	GLU
6	A	1425	SER
6	A	1430	LEU
6	A	1441	PHE
7	B	26	THR
7	B	30	SER
7	B	46	GLN
7	B	50	SER
7	B	55	VAL
7	B	62	ILE
7	B	68	THR
7	B	70	ILE
7	B	98	THR
7	B	134	LYS
7	B	137	TYR
7	B	138	GLU
7	B	167	ILE
7	B	183	GLU
7	B	188	ASP

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Mol	Chain	Res	Type
7	B	195	CYS
7	B	199	MET
7	B	208	SER
7	B	209	GLU
7	B	211	VAL
7	B	222	ILE
7	B	223	VAL
7	B	234	ILE
7	B	235	SER
7	B	240	ILE
7	B	253	THR
7	B	254	LEU
7	B	272	THR
7	B	283	VAL
7	B	294	ASP
7	B	304	ASP
7	B	305	VAL
7	B	312	GLU
7	B	334	ILE
7	B	345	LYS
7	B	347	LYS
7	B	349	ILE
7	B	355	ILE
7	B	357	GLN
7	B	364	ILE
7	B	365	THR
7	B	385	LEU
7	B	386	LEU
7	B	387	LEU
7	B	393	LYS
7	B	396	ASP
7	B	420	LEU
7	B	428	ILE
7	B	435	THR
7	B	446	LEU
7	B	448	ILE
7	B	453	ILE
7	B	455	SER
7	B	457	LEU
7	B	466	TRP
7	B	481	GLN
7	B	482	VAL

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Mol	Chain	Res	Type
7	B	487	THR
7	B	513	GLN
7	B	516	ASN
7	B	527	THR
7	B	531	GLN
7	B	547	VAL
7	B	555	ILE
7	B	568	ASP
7	B	574	SER
7	B	583	ASN
7	B	589	VAL
7	B	614	SER
7	B	624	LEU
7	B	625	LYS
7	B	628	THR
7	B	633	VAL
7	B	641	GLU
7	B	642	ASP
7	B	649	LYS
7	B	668	ASP
7	B	683	SER
7	B	685	LEU
7	B	690	VAL
7	B	698	GLU
7	B	708	GLU
7	B	710	LEU
7	B	722	ASP
7	B	731	VAL
7	B	733	HIS
7	B	736	THR
7	B	737	THR
7	B	764	SER
7	B	771	SER
7	B	783	THR
7	B	786	ASN
7	B	789	MET
7	B	812	LEU
7	B	815	ARG
7	B	825	VAL
7	B	836	GLU
7	B	837	ASP
7	B	845	SER

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Mol	Chain	Res	Type
7	B	864	LYS
7	B	868	MET
7	B	875	GLU
7	B	879	ARG
7	B	882	THR
7	B	887	HIS
7	B	891	ASP
7	B	893	LEU
7	B	894	ASP
7	B	896	ASP
7	B	899	ILE
7	B	908	GLU
7	B	909	ASP
7	B	944	THR
7	B	948	ILE
7	B	951	GLN
7	B	955	THR
7	B	958	GLN
7	B	962	LYS
7	B	963	PHE
7	B	971	THR
7	B	976	ILE
7	B	982	SER
7	B	989	THR
7	B	995	ARG
7	B	996	ARG
7	B	1002	THR
7	B	1007	VAL
7	B	1009	ASP
7	B	1022	THR
7	B	1023	VAL
7	B	1032	SER
7	B	1048	THR
7	B	1051	THR
7	B	1052	VAL
7	B	1061	GLU
7	B	1101	ASP
7	B	1111	MET
7	B	1113	VAL
7	B	1115	THR
7	B	1123	SER
7	B	1129	ARG

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Mol	Chain	Res	Type
7	B	1136	ASP
7	B	1151	LEU
7	B	1162	ILE
7	B	1165	ILE
7	B	1183	LYS
7	B	1191	ILE
7	B	1218	THR
7	B	1222	ARG
7	B	1224	PHE
8	C	3	GLU
8	C	14	SER
8	C	18	VAL
8	C	21	ILE
8	C	25	VAL
8	C	26	ASP
8	C	35	ARG
8	C	38	ILE
8	C	41	ILE
8	C	51	VAL
8	C	52	GLU
8	C	54	ASN
8	C	60	ASP
8	C	76	ASP
8	C	90	ASP
8	C	107	SER
8	C	111	THR
8	C	115	SER
8	C	119	VAL
8	C	123	ASN
8	C	125	MET
8	C	136	ASP
8	C	137	LYS
8	C	138	GLU
8	C	140	ASN
8	C	156	THR
8	C	163	ILE
8	C	166	GLU
8	C	176	ILE
8	C	186	LEU
8	C	195	GLN
8	C	196	ASP
8	C	197	SER

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Mol	Chain	Res	Type
8	C	208	GLU
8	C	211	ASP
8	C	215	GLU
8	C	217	ASP
8	C	231	ASN
8	C	235	VAL
8	C	240	VAL
8	C	243	VAL
8	C	244	VAL
8	C	258	ILE
9	E	2	ASP
9	E	4	GLU
9	E	5	ASN
9	E	19	VAL
9	E	30	ILE
9	E	31	THR
9	E	35	VAL
9	E	37	LEU
9	E	41	ASP
9	E	61	GLN
9	E	66	GLU
9	E	67	GLU
9	E	68	SER
9	E	84	ASP
9	E	85	GLU
9	E	92	THR
9	E	98	ILE
9	E	101	GLN
9	E	107	THR
9	E	123	LEU
9	E	131	THR
9	E	134	THR
9	E	142	VAL
9	E	149	LEU
9	E	155	ARG
9	E	178	ILE
9	E	199	ILE
9	E	202	SER
9	E	205	SER
9	E	215	MET
10	F	74	ILE
10	F	93	ILE

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Mol	Chain	Res	Type
10	F	96	THR
10	F	111	LEU
10	F	112	GLU
10	F	122	MET
10	F	128	LYS
10	F	132	LEU
10	F	133	VAL
10	F	134	ILE
10	F	142	SER
10	F	155	LEU
11	H	9	ILE
11	H	15	VAL
11	H	16	ASP
11	H	26	ILE
11	H	27	GLU
11	H	30	SER
11	H	32	THR
11	H	44	VAL
11	H	46	LEU
11	H	55	LEU
11	H	58	THR
11	H	88	SER
11	H	92	ASP
11	H	94	ASP
11	H	105	GLU
11	H	108	SER
11	H	112	ILE
11	H	130	ARG
11	H	142	LEU
11	H	143	LEU
11	H	144	ILE
11	H	145	ARG
12	I	3	THR
12	I	5	ARG
12	I	9	ASP
12	I	10	CYS
12	I	17	ARG
12	I	19	ASP
12	I	22	ASN
12	I	24	ARG
12	I	25	LEU
12	I	28	GLU

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Mol	Chain	Res	Type
12	I	32	CYS
12	I	37	GLU
12	I	40	SER
12	I	42	LEU
12	I	48	LEU
12	I	49	ILE
12	I	51	ASN
12	I	60	GLN
12	I	67	THR
12	I	70	ARG
12	I	71	SER
12	I	77	LYS
12	I	78	CYS
12	I	80	SER
12	I	83	ASN
12	I	88	SER
12	I	104	LEU
12	I	111	THR
12	I	118	ARG
12	I	119	THR
12	I	120	GLN
13	J	3	VAL
13	J	5	VAL
13	J	7	CYS
13	J	9	SER
13	J	20	SER
13	J	24	LEU
13	J	27	GLU
13	J	38	ARG
13	J	50	ILE
13	J	54	VAL
13	J	64	ASN
14	K	14	GLU
14	K	20	LYS
14	K	47	ARG
14	K	54	ARG
14	K	77	THR
14	K	82	ASP
14	K	93	SER
14	K	101	LEU
14	K	104	ASN
14	K	106	GLU

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Mol	Chain	Res	Type
14	K	114	LEU
15	L	26	THR
15	L	27	LEU
15	L	31	CYS
15	L	34	CYS
15	L	35	SER
15	L	43	THR
15	L	44	ASP
15	L	46	VAL
15	L	48	CYS
15	L	50	ASP
15	L	53	HIS
15	L	55	ILE
15	L	65	VAL
17	0	5	ILE
17	0	49	THR
17	0	79	ILE
17	0	109	THR
17	0	115	CYS
17	0	162	LEU
17	0	175	VAL
17	0	190	LEU
17	0	241	ASP
17	0	248	LEU
17	0	253	THR
17	0	287	GLU
17	0	315	ASP
17	0	325	ILE
17	0	344	THR
17	0	346	MET
17	0	349	LEU
17	0	351	VAL
17	0	388	LEU
17	0	393	VAL
17	0	395	ASP
17	0	404	THR
17	0	419	ILE
17	0	511	GLU
17	0	512	ILE
17	0	532	ILE
17	0	572	GLU
17	0	584	GLU

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Mol	Chain	Res	Type
17	0	585	THR
17	0	656	PHE
18	4	32	ILE
18	4	54	LEU
18	4	86	LEU
18	4	123	GLU
18	4	125	LEU
18	4	128	GLU
18	4	132	LEU
18	4	149	LEU
18	4	180	THR
18	4	210	ILE
18	4	212	VAL
18	4	228	THR
18	4	234	VAL
18	4	239	GLU
18	4	252	MET
18	4	263	VAL
18	4	276	CYS
18	4	287	PHE
19	6	118	TYR
19	6	123	ILE
19	6	166	ILE
19	6	176	ASN
19	6	181	LEU
19	6	185	VAL
19	6	270	VAL
19	6	291	LEU
19	6	310	VAL
19	6	368	LEU
19	6	372	LEU
19	6	440	CYS
19	6	448	LEU
20	1	282	GLU
20	1	331	HIS
20	1	339	LEU
20	1	348	VAL
20	1	381	LEU
20	1	504	ILE
21	7	311	ASP
21	7	313	VAL
21	7	318	ILE

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Mol	Chain	Res	Type
21	7	323	VAL
21	7	326	VAL
21	7	351	ASP
21	7	393	THR
21	7	408	ILE
21	7	431	GLN
21	7	435	CYS
21	7	437	VAL
21	7	447	GLN
21	7	453	VAL
21	7	478	THR
21	7	490	VAL
21	7	514	THR
21	7	573	THR
21	7	605	ILE
21	7	610	ASP
21	7	620	LEU
21	7	664	LEU
23	2	17	ILE
23	2	21	VAL
23	2	51	VAL
23	2	60	LEU
23	2	66	VAL
23	2	84	LEU
23	2	92	SER
23	2	112	LEU
23	2	222	LEU
23	2	379	THR
23	2	413	GLU
25	U	241	GLU
25	U	264	ASP
26	V	57	GLN
29	O	67	LEU
29	O	70	ILE
29	O	91	ASN
29	O	136	SER
29	O	161	VAL
29	O	181	THR
29	O	182	PHE
29	O	183	SER
29	O	205	LEU
29	O	213	VAL

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Mol	Chain	Res	Type
29	O	218	LYS
29	O	221	GLU
29	O	230	ILE
30	W	15	PHE
30	W	37	VAL
30	W	58	ILE
30	W	112	ASP
30	W	113	LEU
30	W	123	MET
30	W	126	ILE
30	W	133	GLN
30	W	147	PHE
30	W	149	CYS
30	W	151	LEU
30	W	156	LEU
30	W	179	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
1	Q	122	GLN
1	Q	128	ASN
2	R	138	GLN
3	D	28	GLN
3	D	40	HIS
4	G	96	GLN
4	G	97	HIS
4	G	131	GLN
4	G	153	GLN
4	G	158	HIS
5	M	124	ASN
5	M	212	ASN
6	A	68	GLN
6	A	80	HIS
6	A	83	HIS
6	A	109	HIS
6	A	282	ASN
6	A	316	GLN
6	A	339	ASN
6	A	390	GLN
6	A	576	GLN
6	A	700	ASN

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Mol	Chain	Res	Type
6	A	736	ASN
6	A	741	ASN
6	A	865	GLN
6	A	935	GLN
6	A	1173	HIS
6	A	1188	GLN
6	A	1218	GLN
6	A	1232	ASN
6	A	1278	ASN
7	B	300	HIS
7	B	481	GLN
7	B	686	ASN
7	B	770	GLN
7	B	794	ASN
7	B	1161	HIS
7	B	1177	HIS
7	B	1179	GLN
8	C	231	ASN
8	C	252	GLN
8	C	267	GLN
11	H	11	GLN
11	H	33	GLN
11	H	128	ASN
12	I	12	ASN
12	I	108	HIS
17	0	224	ASN
17	0	283	GLN
17	0	365	GLN
17	0	521	ASN
17	0	726	GLN
18	4	225	GLN
19	6	119	GLN
19	6	445	HIS
20	1	513	GLN
20	1	563	HIS
20	1	621	ASN
21	7	331	GLN
21	7	431	GLN
21	7	611	ASN
21	7	616	GLN
21	7	650	ASN
23	2	19	GLN

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Mol	Chain	Res	Type
23	2	90	ASN
23	2	99	ASN
23	2	344	ASN
23	2	352	ASN
23	2	356	GLN
23	2	469	ASN
23	2	498	ASN
24	X	265	ASN
24	X	270	GLN
26	V	65	ASN
26	V	82	ASN
29	O	68	GLN
29	O	158	GLN
30	W	138	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	P	4/5 (80%)	1 (25%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	P	8	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 16 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
34	SF4	0	801	17	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	SF4	0	801	17	-	-	0/6/5/5

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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	0	801	SF4	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	1	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	355:UNK	C	368:UNK	N	14.81
1	1	519:UNK	C	537:GLU	N	11.86

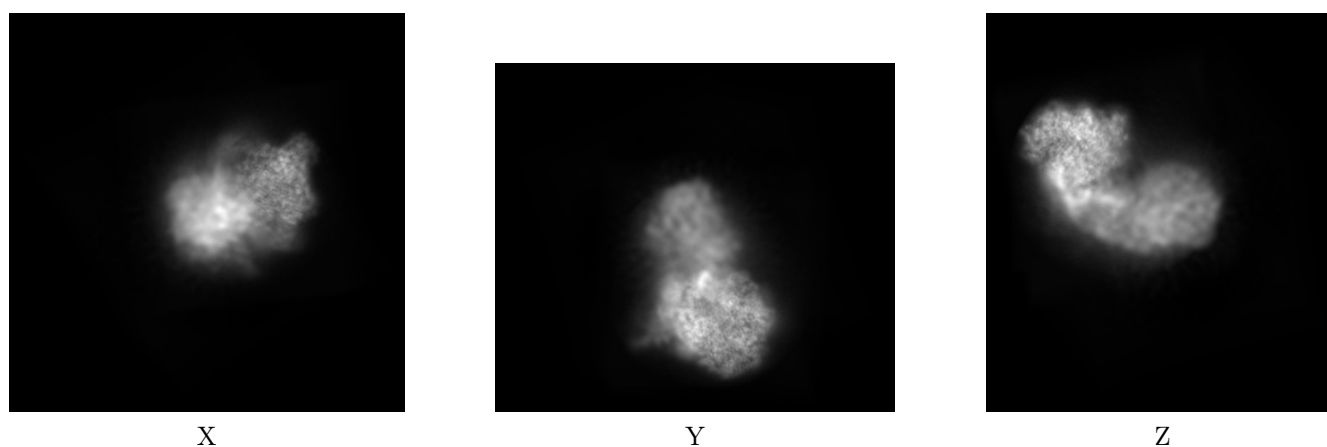
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23908. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

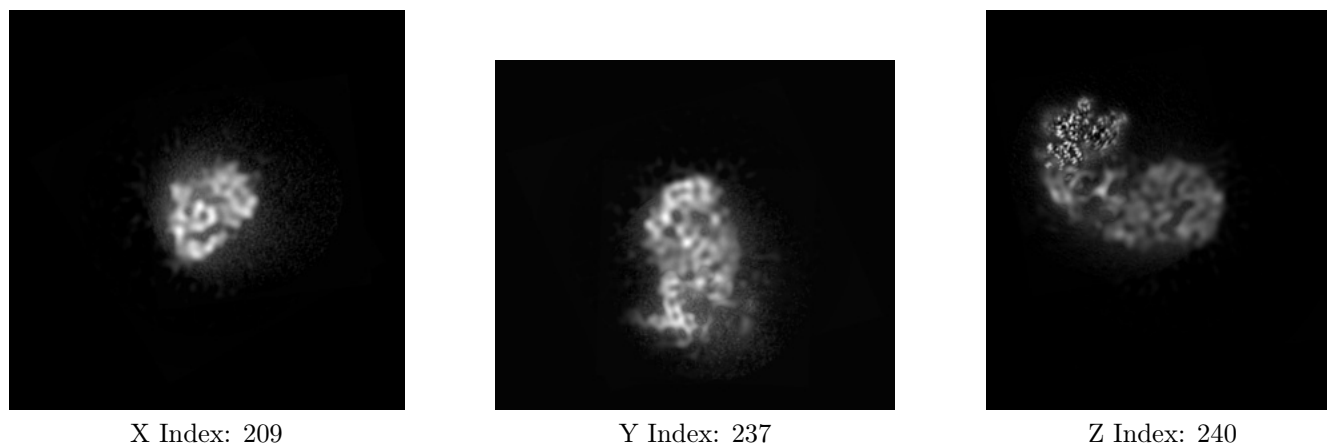
6.1.1 Primary map



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

6.2 Central slices [i](#)

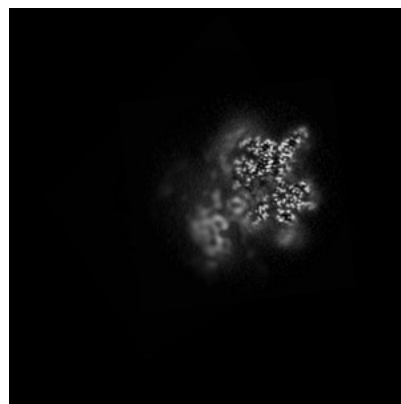
6.2.1 Primary map



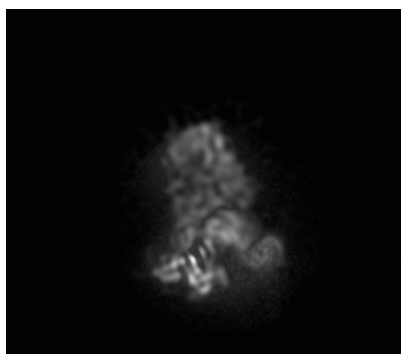
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

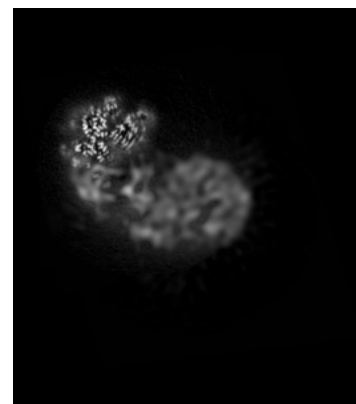
6.3.1 Primary map



X Index: 109



Y Index: 253

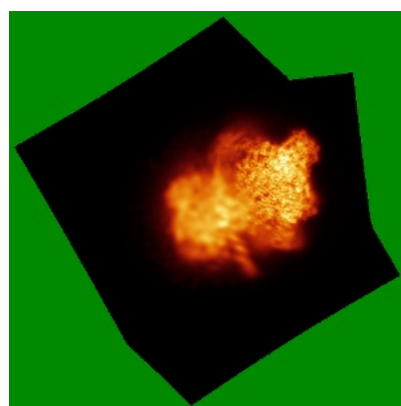


Z Index: 242

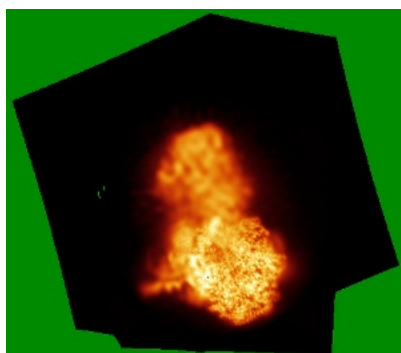
The images above show the largest variance slices of the map in three orthogonal directions.

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

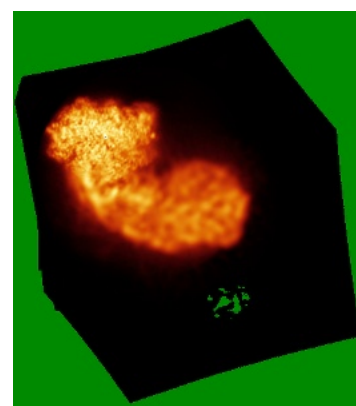
6.4.1 Primary map



X



Y

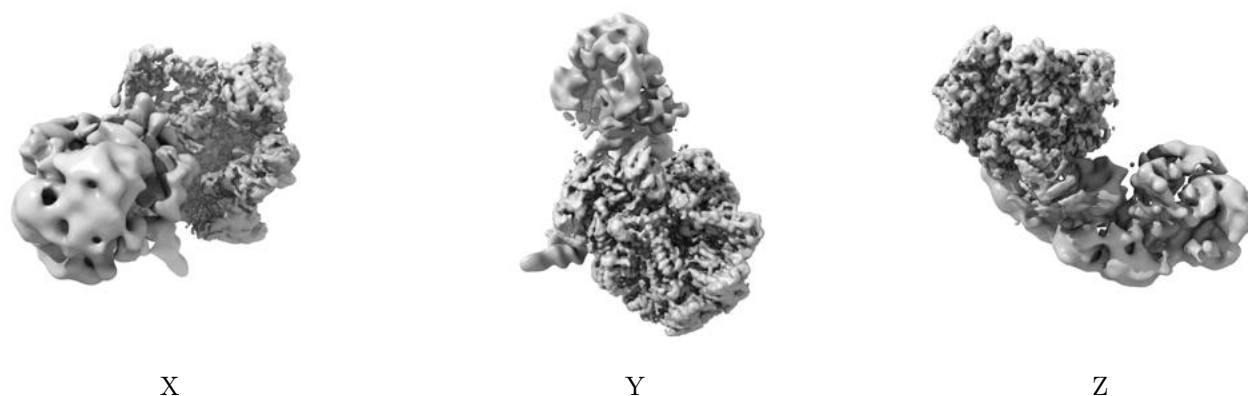


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

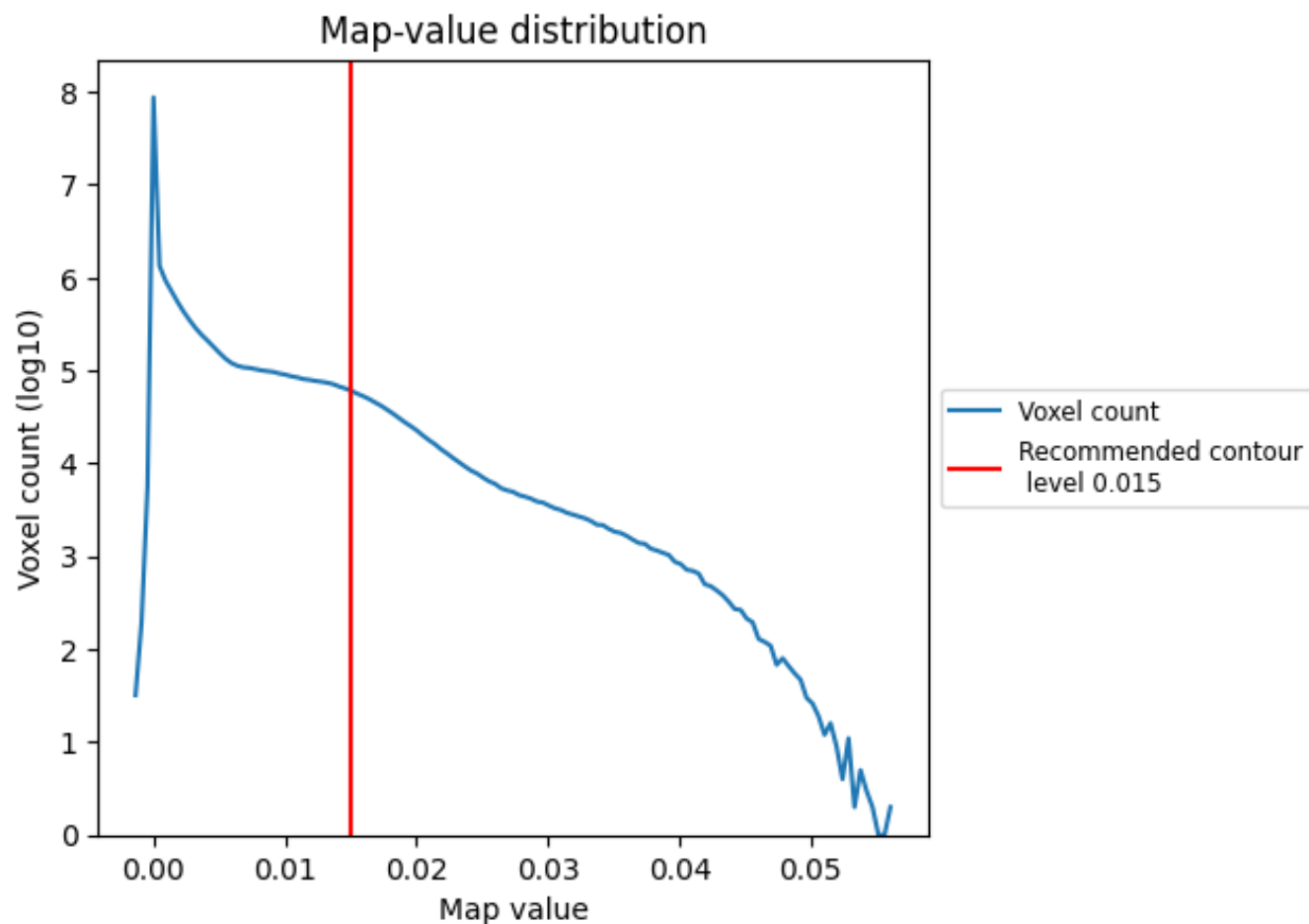
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

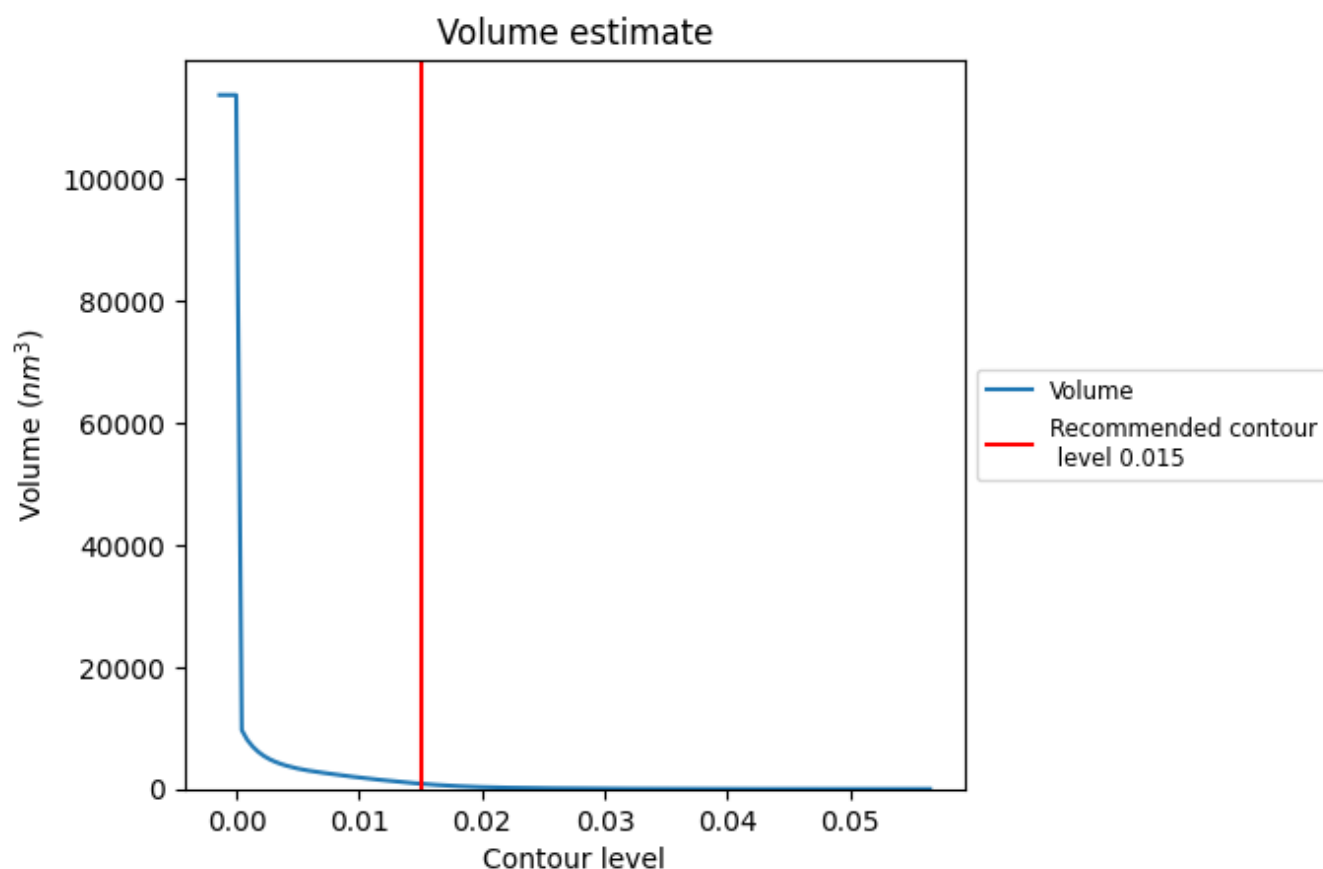
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 863 nm³; this corresponds to an approximate mass of 779 kDa.

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

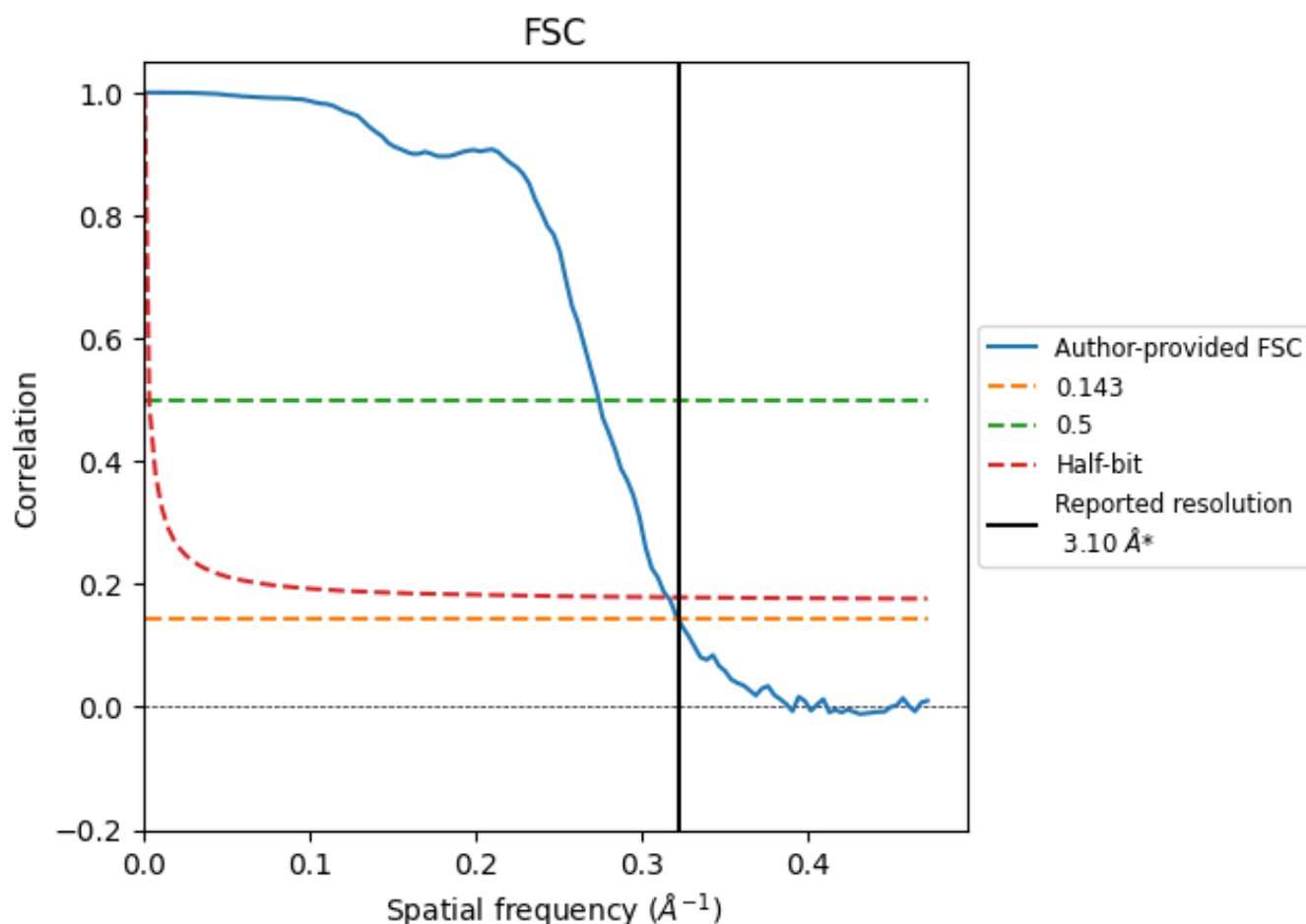
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

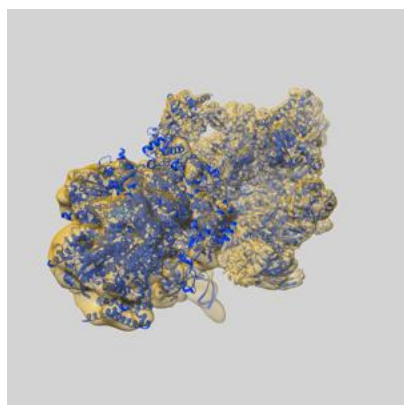
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.11	3.65	3.17
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

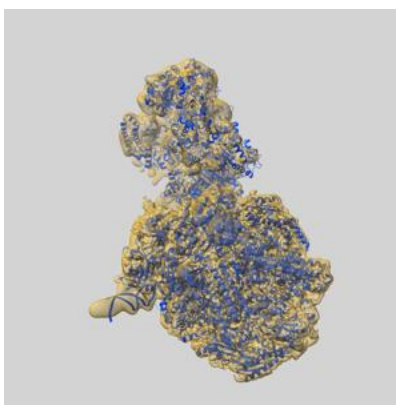
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23908 and PDB model 7ML4. Per-residue inclusion information can be found in section 3 on page 12.

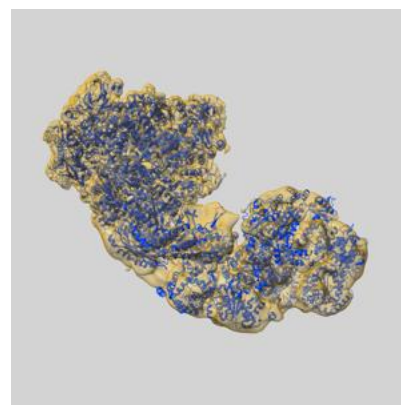
9.1 Map-model overlay [i](#)



X



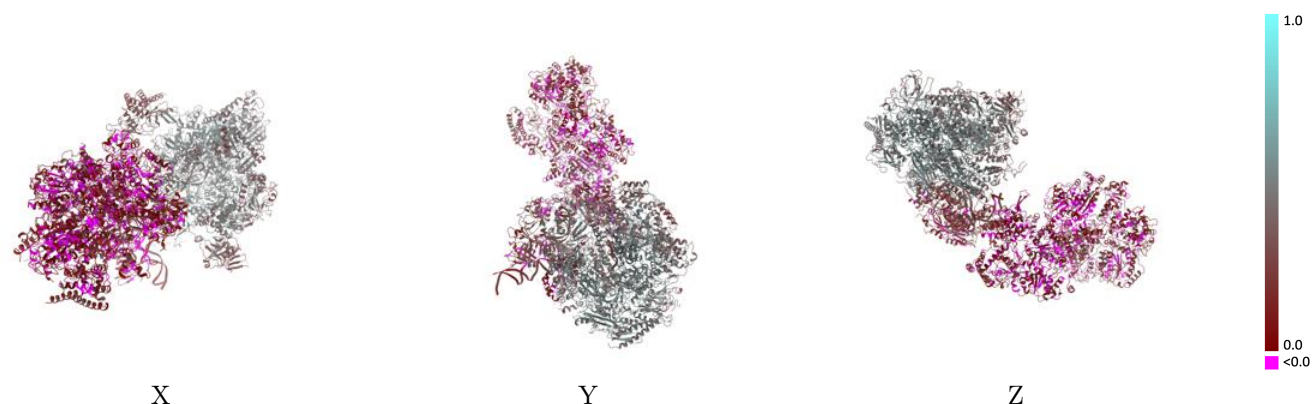
Y



Z

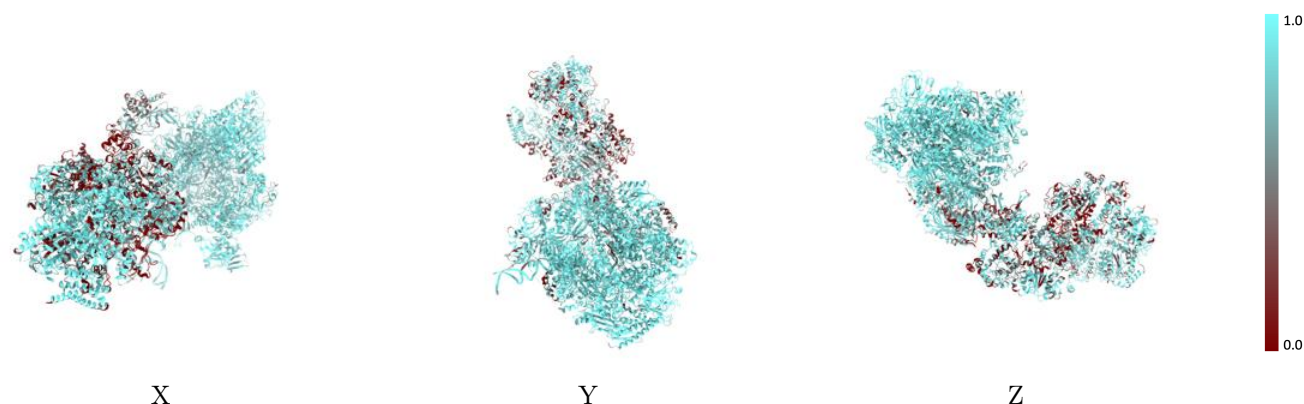
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



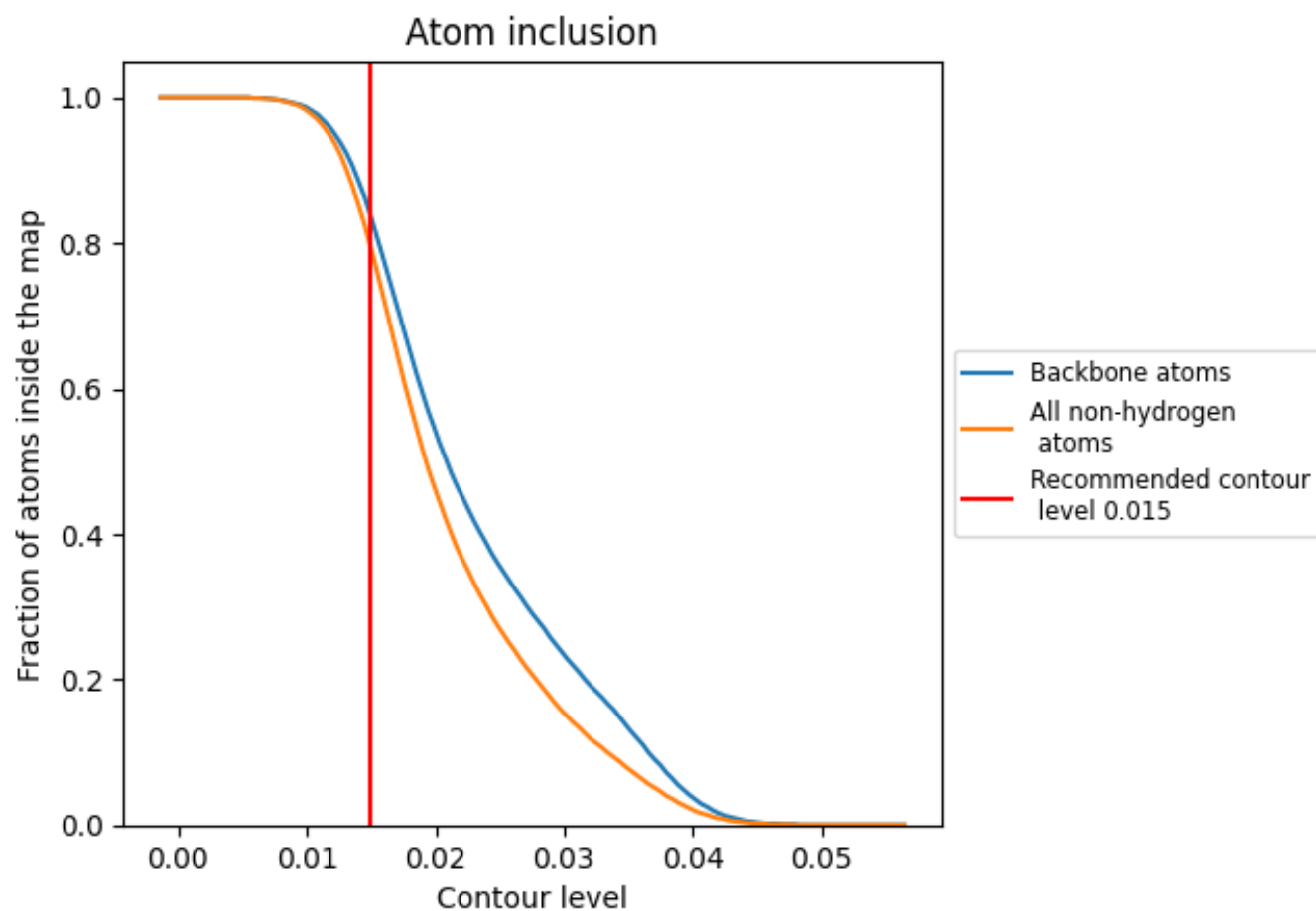
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7930	 0.2810
0	 0.6660	 0.0610
1	 0.5790	 0.0820
2	 0.6950	 0.0880
3	 0.4380	 0.1210
4	 0.7980	 0.0710
5	 0.4680	 0.0950
6	 0.7830	 0.0790
7	 0.4380	 0.0470
A	 0.9260	 0.4730
B	 0.9410	 0.4960
C	 0.9570	 0.4930
D	 0.4630	 0.2750
E	 0.9250	 0.4610
F	 0.9540	 0.5000
G	 0.6800	 0.3600
H	 0.9410	 0.4440
I	 0.8650	 0.4200
J	 0.9790	 0.5080
K	 0.8770	 0.4750
L	 0.9600	 0.4430
M	 0.7540	 0.1890
N	 0.9170	 0.1710
O	 0.8960	 0.0690
P	 0.6540	 0.2610
Q	 0.8950	 0.3570
R	 0.8490	 0.2590
T	 0.8460	 0.1830
U	 0.6490	 0.0900
V	 0.7880	 0.1090
W	 0.6690	 0.1000
X	 0.7940	 0.0640

