



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 07:39 AM UTC

PDB ID : 7YCX / pdb_00007ycx
EMDB ID : EMD-33741
Title : The structure of INTAC-PEC complex
Authors : Zheng, H.; Jin, Q.; Wang, X.; Qi, Y.; Liu, W.; Ren, Y.; Zhao, D.; Chen, F.X.;
Cheng, J.; Chen, X.; Xu, Y.
Deposited on : 2022-07-02
Resolution : 4.18 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

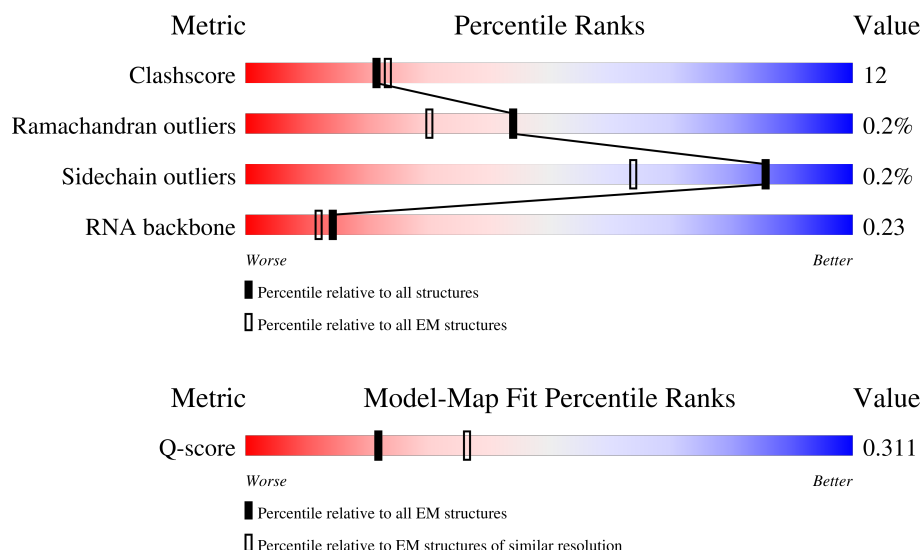
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.18 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	5389 (3.68 - 4.68)

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

Mol	Chain	Length	Quality of chain
1	A	2190	
2	B	1204	
3	D	963	

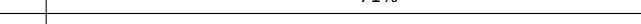
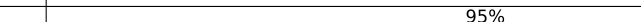
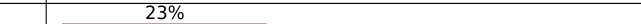
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Mol	Chain	Length	Quality of chain
4	E	1019	
5	F	887	
6	G	962	
7	H	995	
8	I	658	
9	K	600	
10	M	17	
11	P	589	
12	Q	309	
13	U	27	
14	1	1970	
15	2	1174	
16	3	271	
17	4	210	
18	5	127	
19	6	150	
20	7	125	
21	8	67	
22	9	117	
23	a	58	
24	b	48	
25	c	23	
26	d	48	
27	e	528	
28	f	580	

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Mol	Chain	Length	Quality of chain
29	g	590	
30	h	380	
31	i	121	
32	j	1087	
33	k	172	
34	l	142	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 113089 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 Integrator complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1779	Total	C	N	O	S	0	0
			13054	8226	2322	2432	74		

- Molecule 2 is a protein called Integrator complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1061	Total	C	N	O	S	0	0
			8328	5322	1412	1530	64		

- Molecule 3 is a protein called Integrator complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	828	Total	C	N	O	S	0	0
			6205	3931	1085	1158	31		

- Molecule 4 is a protein called Integrator complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	798	Total	C	N	O	S	0	0
			5244	3284	988	958	14		

- Molecule 5 is a protein called Integrator complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	560	Total	C	N	O	S	0	0
			4395	2809	750	813	23		

- Molecule 6 is a protein called Integrator complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	910	Total	C	N	O	S	0	0
			6928	4382	1212	1293	41		

- Molecule 7 is a protein called Integrator complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	937	Total	C	N	O	S	0	0
			7440	4761	1274	1361	44		

- Molecule 8 is a protein called Integrator complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	633	Total	C	N	O	S	0	0
			4985	3210	815	926	34		

- Molecule 9 is a protein called Integrator complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	590	Total	C	N	O	S	0	0
			4646	2964	806	841	35		

- Molecule 10 is a protein called Unknown2.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	M	17	Total	C	N	O	0	0
			85	51	17	17		

- Molecule 11 is a protein called Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	581	Total	C	N	O	S	0	0
			4527	2877	763	860	27		

- Molecule 12 is a protein called Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	293	Total	C	N	O	S	0	0
			2366	1497	405	449	15		

- Molecule 13 is a protein called Unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	U	27	Total	C	N	O	0	0
			135	81	27	27		

- Molecule 14 is a protein called DNA-directed RNA polymerase II subunit RPB1,DNA-directed RNA polymerase II subunit RPB1, CTD1, CTD2, CTD3, CTD4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1	1451	Total	C	N	O	S	0	0
			11345	7135	2033	2109	68		

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2	1113	Total	C	N	O	S	0	0
			8649	5489	1515	1581	64		

- Molecule 16 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3	259	Total	C	N	O	S	0	0
			2048	1289	354	399	6		

- Molecule 17 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	4	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 18 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	81	Total	C	N	O	S	0	0
			649	413	111	120	5		

- Molecule 19 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	6	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 20 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	7	117	Total	C	N	O	S	0	0
			950	587	169	183	11		

- Molecule 21 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	8	67	Total	C	N	O	S	0	0
			533	345	90	92	6		

- Molecule 22 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	9	117	Total	C	N	O	S	0	0
			937	604	154	177	2		

- Molecule 23 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	46	Total	C	N	O	S	0	0
			389	241	75	67	6		

- Molecule 24 is a DNA chain called non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	36	Total	C	N	O	P	0	0
			752	351	153	212	36		

- Molecule 25 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	23	Total	C	N	O	P	0	0
			406	179	56	148	23		

- Molecule 26 is a DNA chain called template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	45	Total	C	N	O	P	0	0
			909	431	157	276	45		

- Molecule 27 is a protein called Negative elongation factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	183	Total	C	N	O	S	0	0
			1410	895	239	269	7		

- Molecule 28 is a protein called Negative elongation factor B.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	f	480	Total	C	N	O	0	0
			1920	960	480	480		

- Molecule 29 is a protein called Negative elongation factor C/D.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	534	Total	C	N	O	S	0	0
			3764	2382	653	710	19		

- Molecule 30 is a protein called Negative elongation factor E.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	h	22	Total	C	N	O	0	0
			109	65	22	22		

- Molecule 31 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	i	116	Total	C	N	O	S	0	0
			911	570	159	173	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
i	-3	GLY	-	expression tag	UNP P63272
i	-2	PRO	-	expression tag	UNP P63272
i	-1	GLY	-	expression tag	UNP P63272
i	0	SER	-	expression tag	UNP P63272

- Molecule 32 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	j	482	Total	C	N	O	S	0	0
			3854	2448	681	708	17		

- Molecule 33 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	k	171	Total	C	N	O	S	0	0
			1299	849	205	238	7		

- Molecule 34 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	1	128	Total	C	N	O	S	0	0
			997	629	169	195	4		

- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

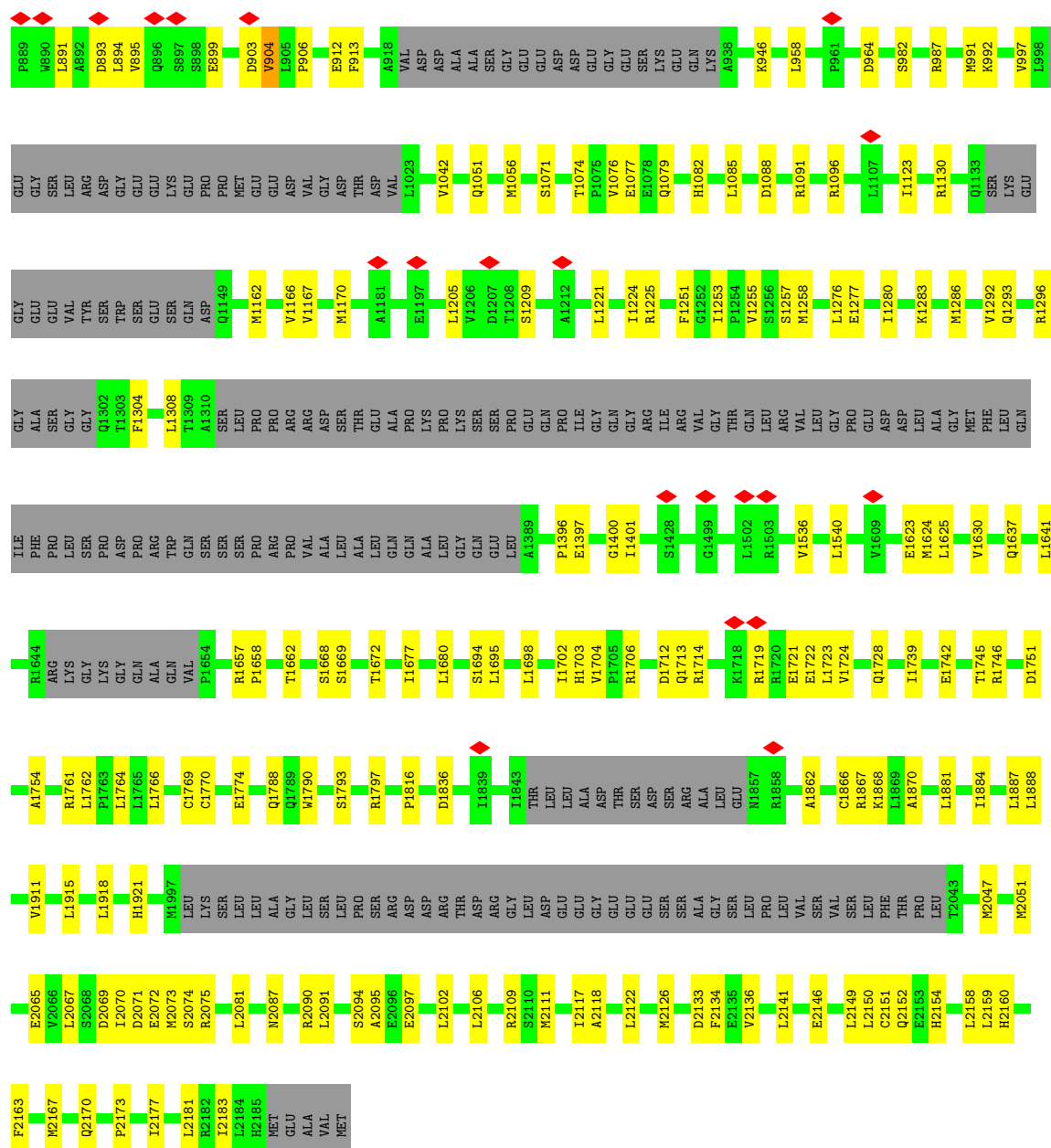
Mol	Chain	Residues	Atoms		AltConf
35	K	2	Total	Zn	0
			2	2	
35	1	2	Total	Zn	0
			2	2	
35	2	1	Total	Zn	0
			1	1	
35	3	1	Total	Zn	0
			1	1	
35	7	2	Total	Zn	0
			2	2	
35	8	1	Total	Zn	0
			1	1	
35	a	1	Total	Zn	0
			1	1	

- Molecule 36 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		AltConf
36	Q	2	Total	Mn	0
			2	2	

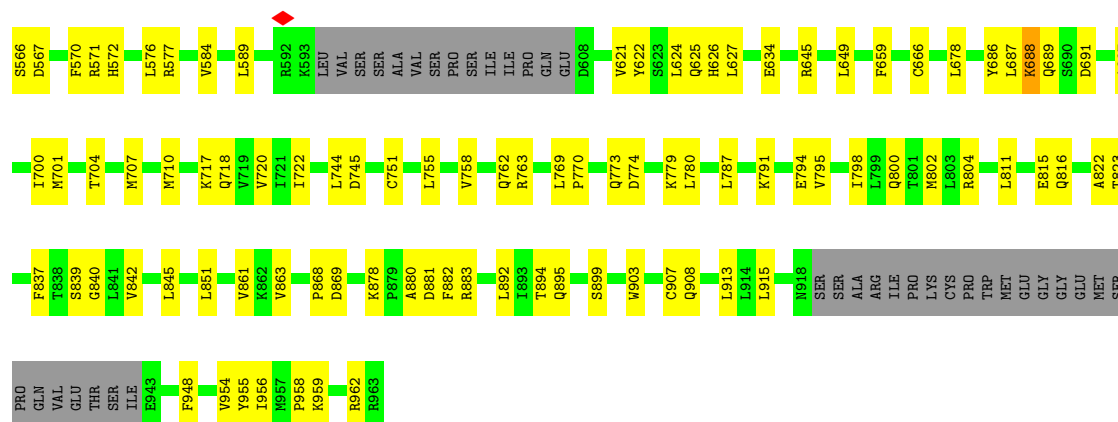
- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	1	1	Total	Mg	0
			1	1	

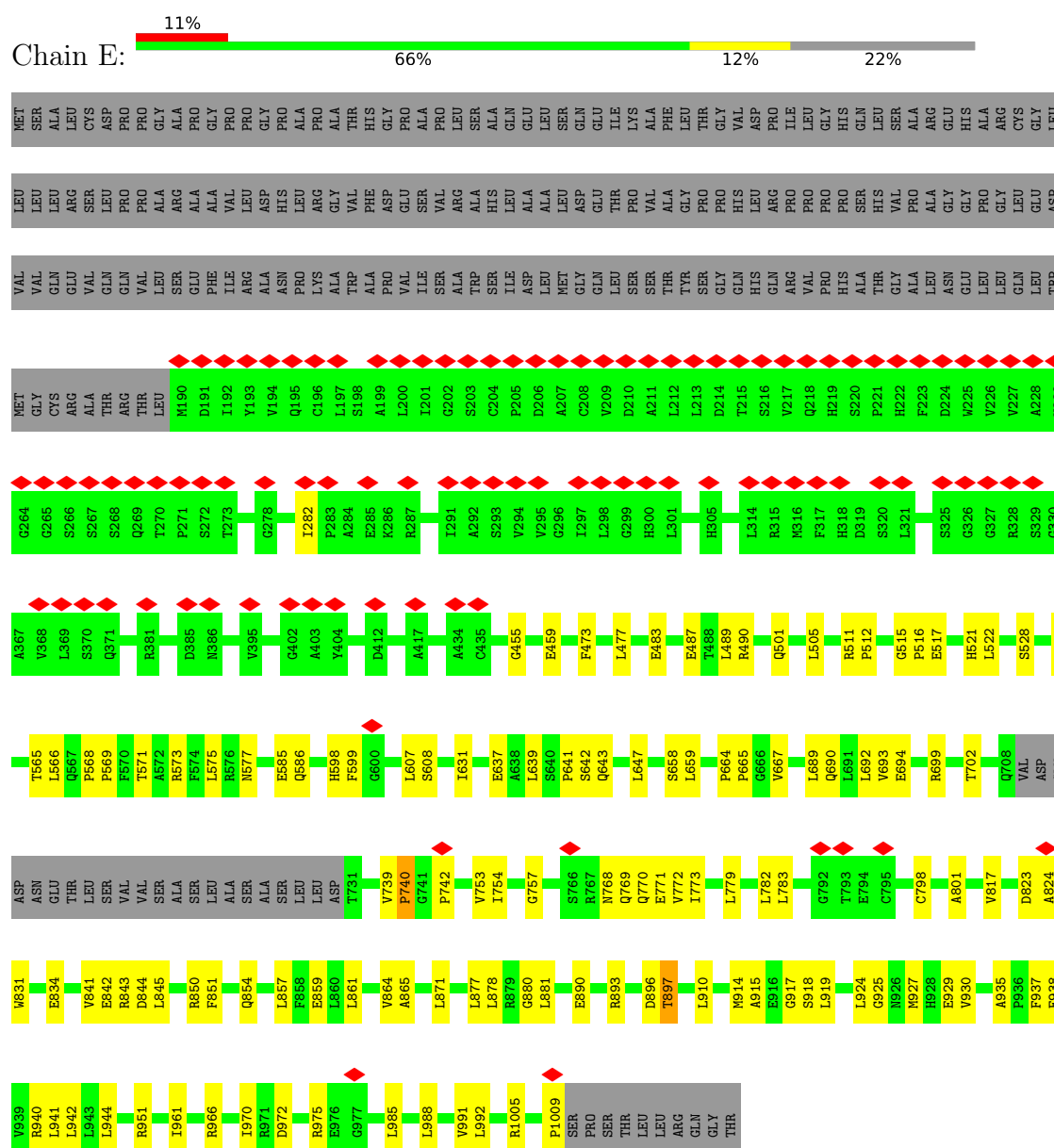


• Molecule 2: Integrator complex subunit 2

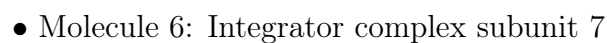


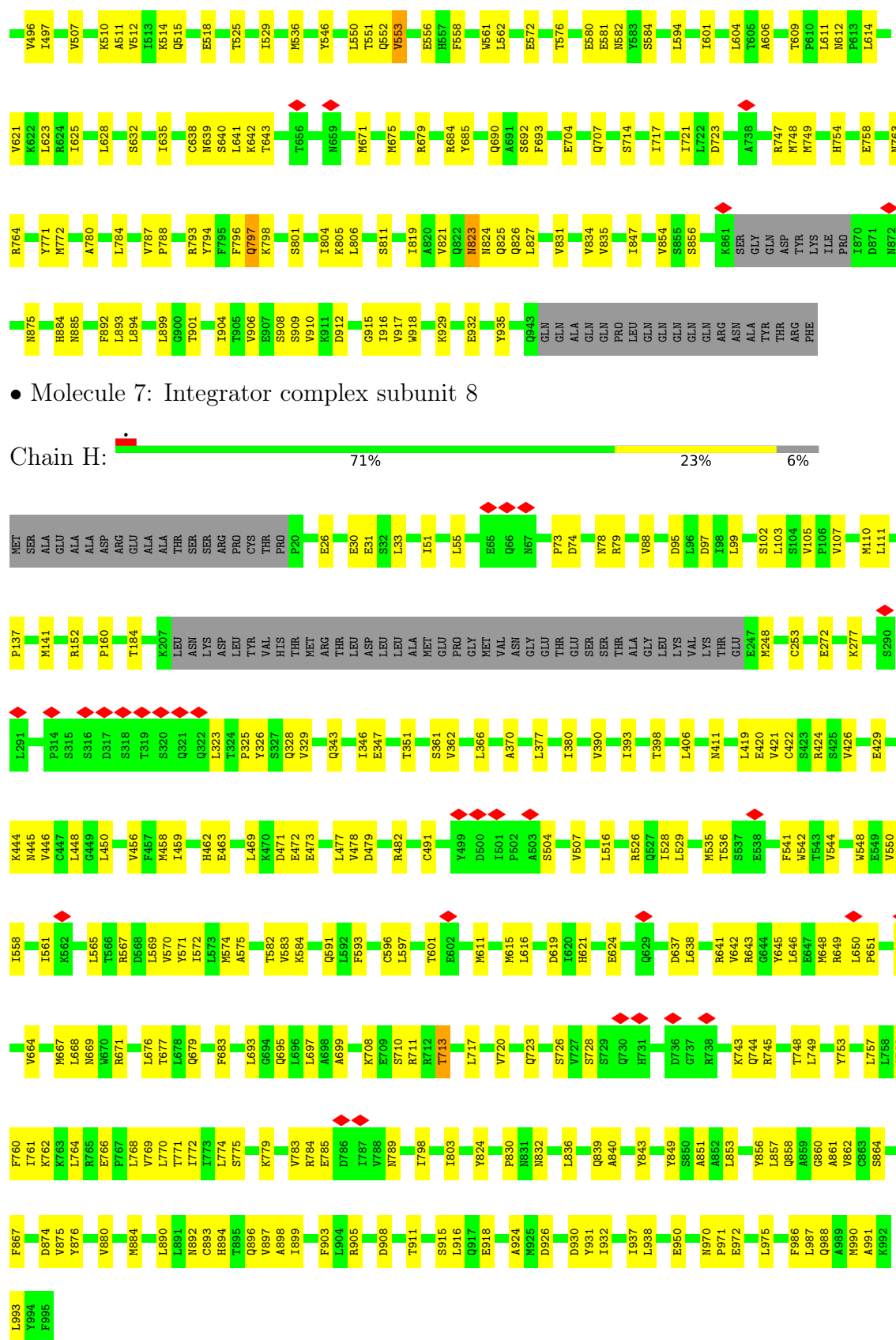


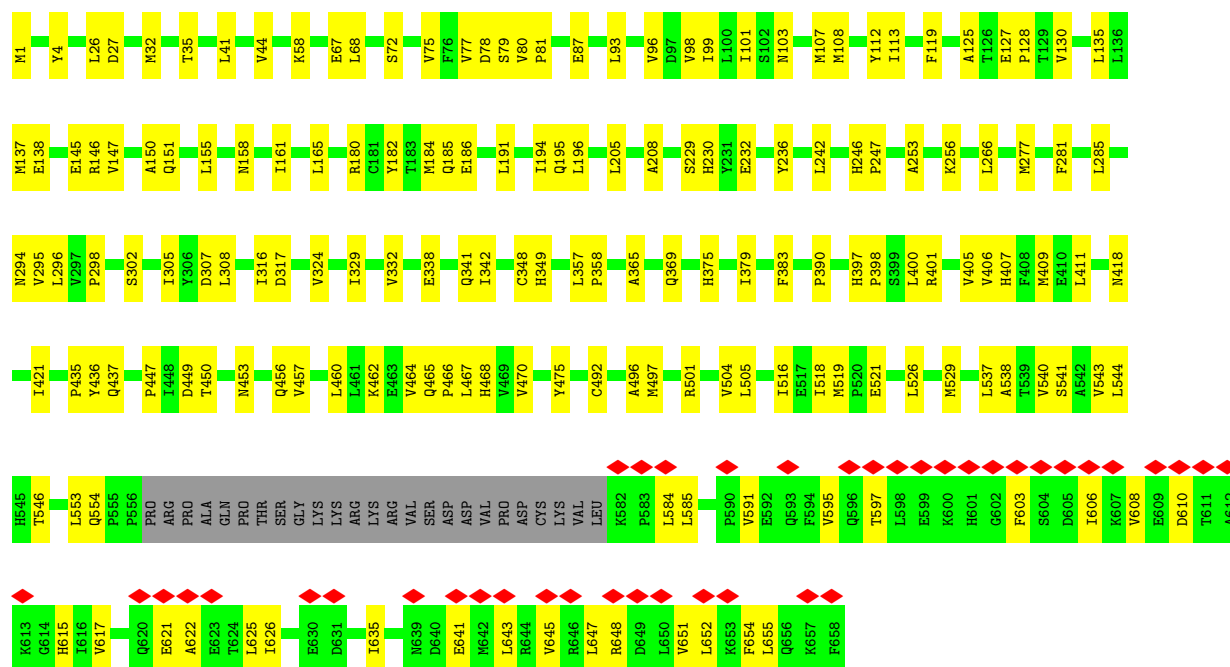
• Molecule 4: Integrator complex subunit 5



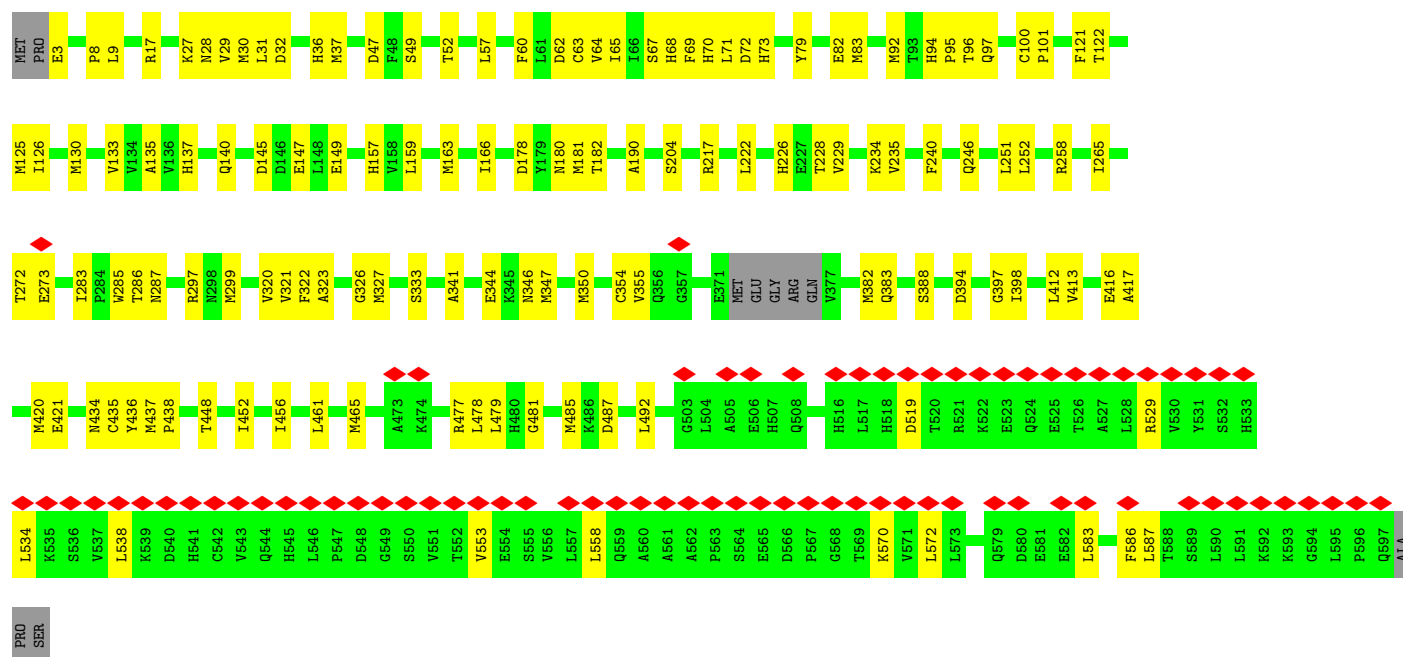
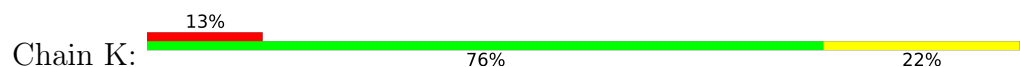
• Molecule 5: Integrator complex subunit 6







• Molecule 9: Integrator complex subunit 11

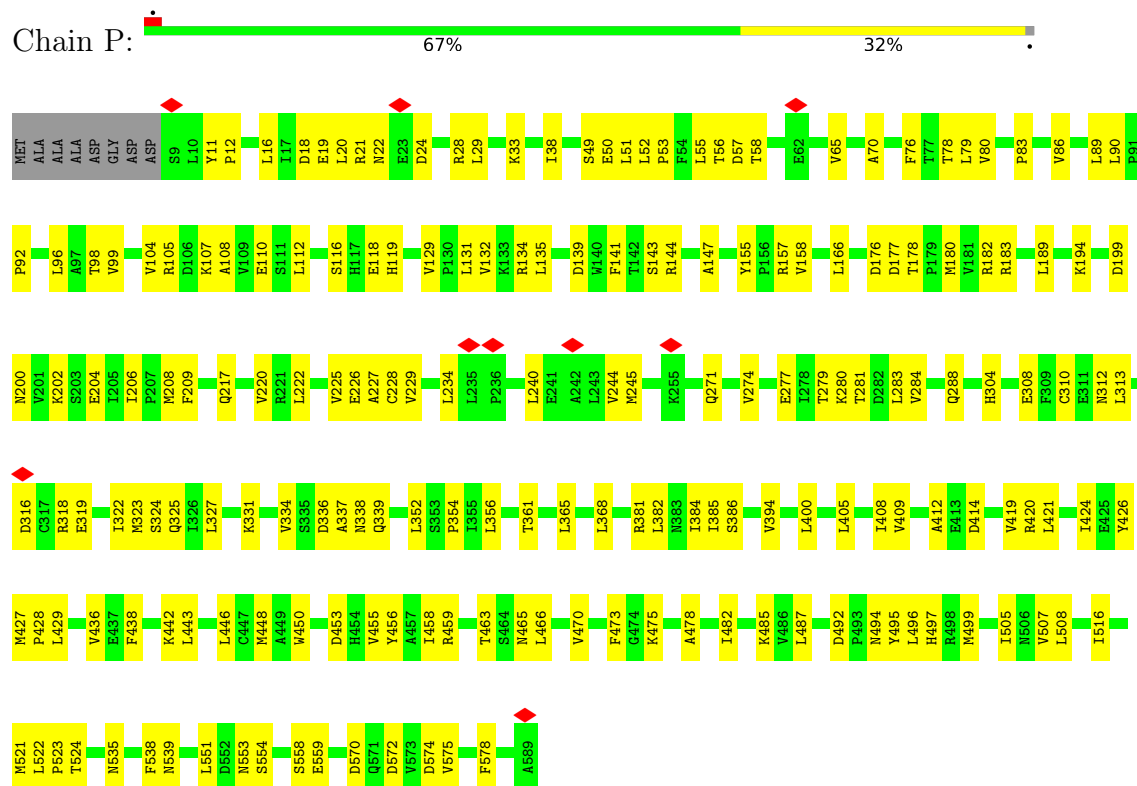


• Molecule 10: Unknown2

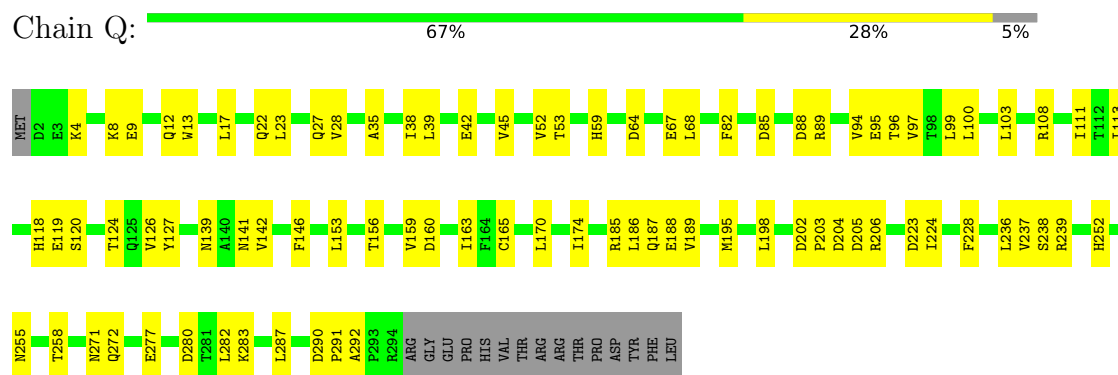


There are no outlier residues recorded for this chain.

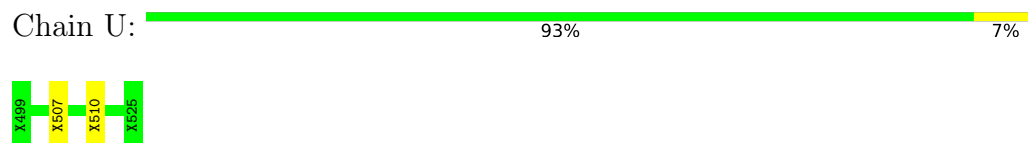
- Molecule 11: Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform



- Molecule 12: Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform



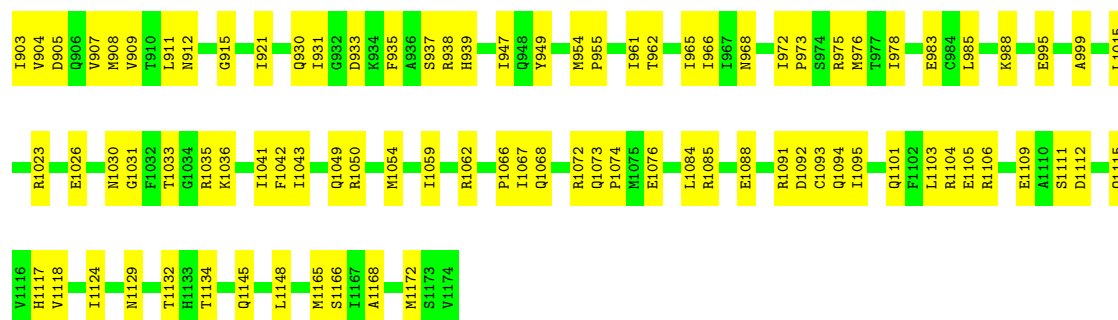
- Molecule 13: Unknown



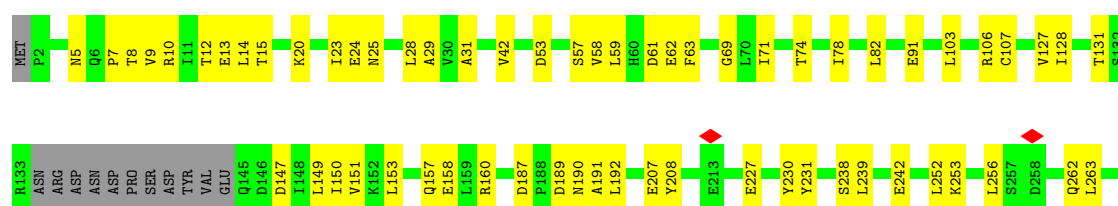
- Molecule 14: DNA-directed RNA polymerase II subunit RPB1, DNA-directed RNA polymerase II subunit RPB1, CTD1, CTD2, CTD3, CTD4



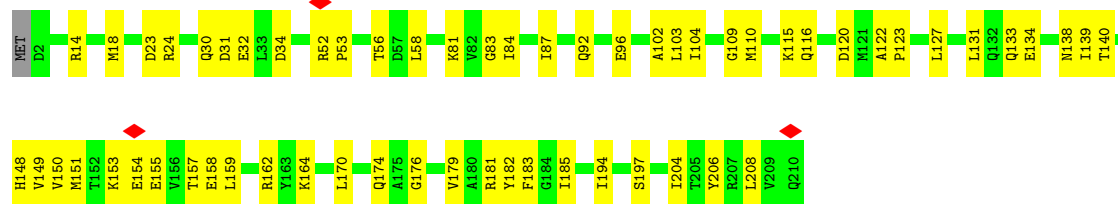




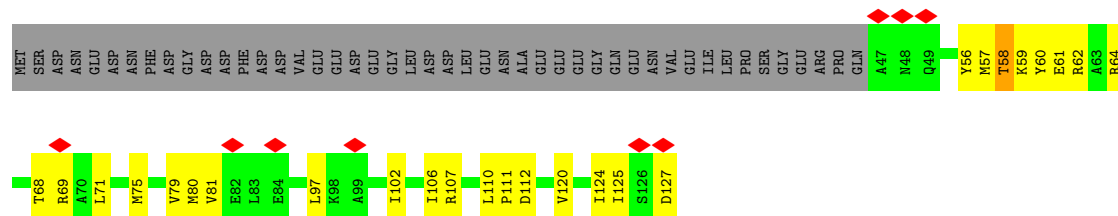
• Molecule 16: DNA-directed RNA polymerase II subunit RPB3



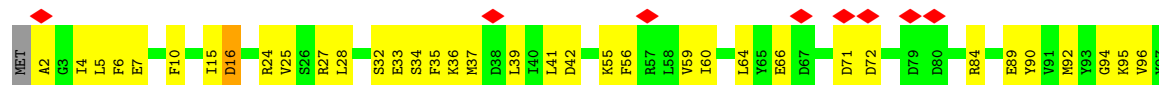
• Molecule 17: DNA-directed RNA polymerase II subunit E

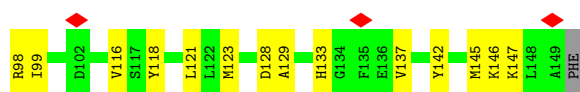


• Molecule 18: DNA-directed RNA polymerase II subunit F

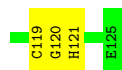
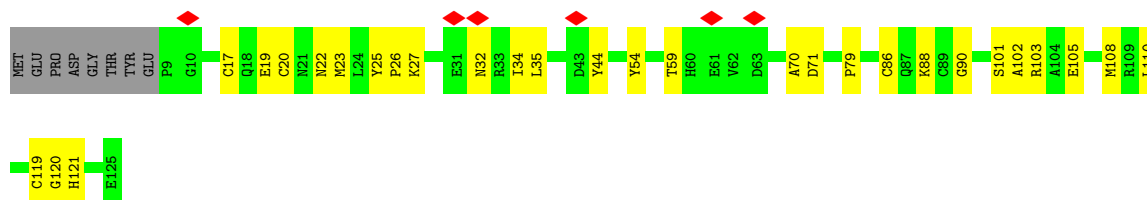


• Molecule 19: DNA-directed RNA polymerases I, II, and III subunit RPABC3





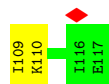
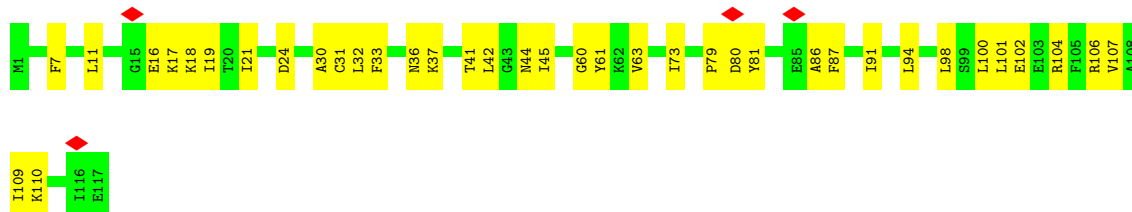
- Molecule 20: DNA-directed RNA polymerase II subunit RPB9



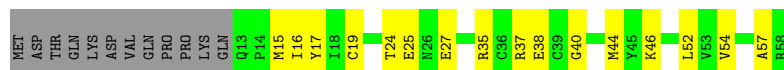
- Molecule 21: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 22: RNA_pol_L_2 domain-containing protein



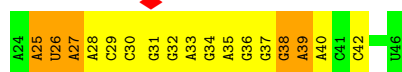
- Molecule 23: RPB12



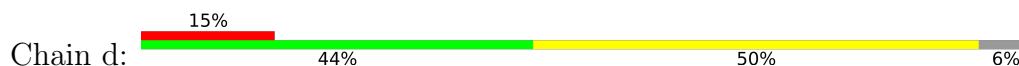
- Molecule 24: non-template DNA



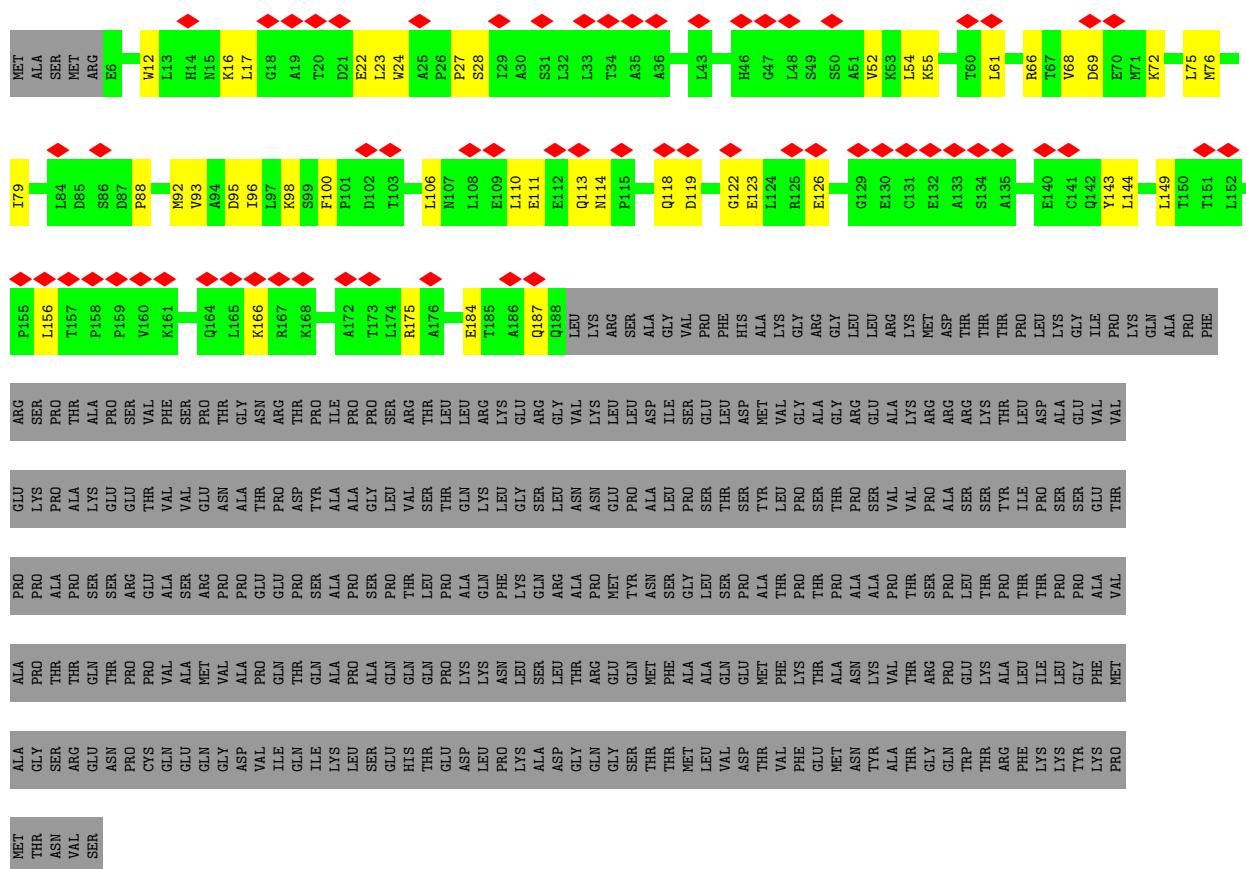
- Molecule 25: RNA



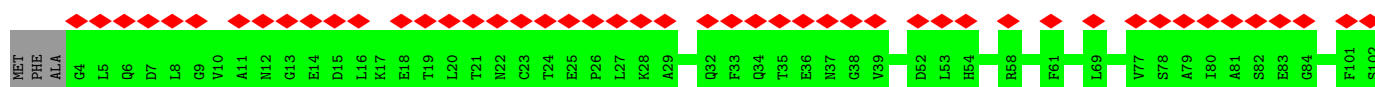
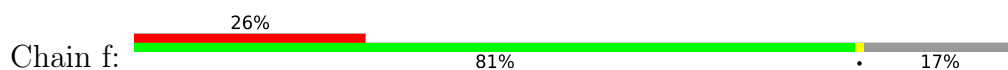
- Molecule 26: template DNA



- Molecule 27: Negative elongation factor A

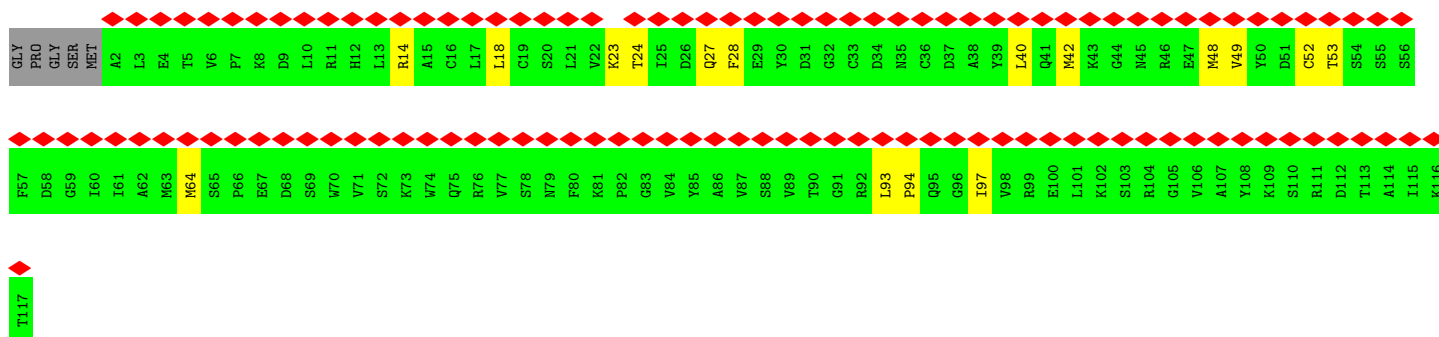
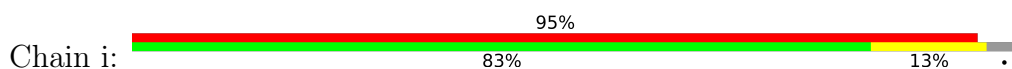


- Molecule 28: Negative elongation factor B

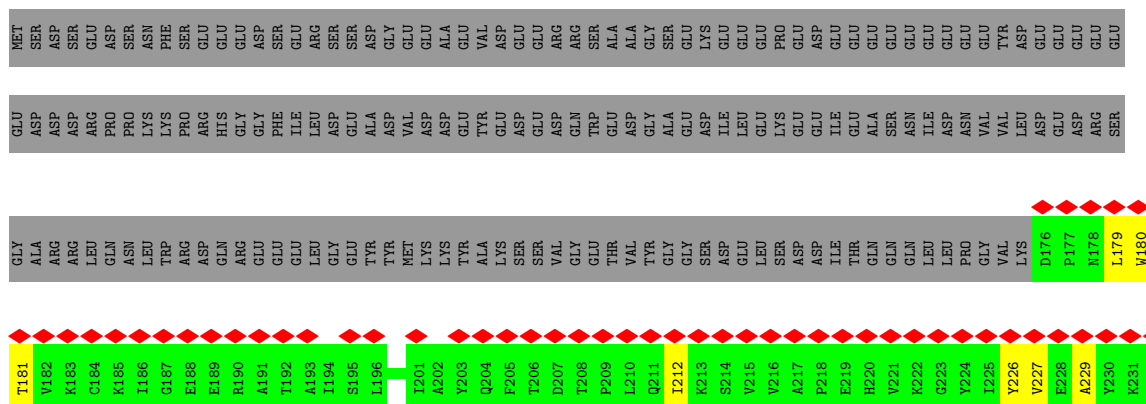
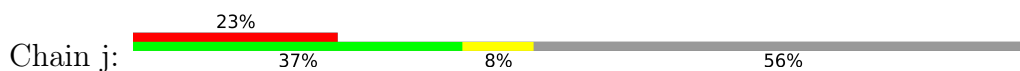


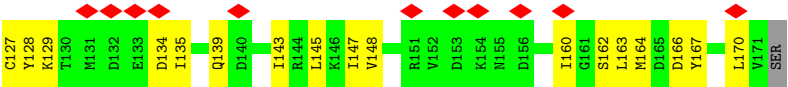


- Molecule 31: Transcription elongation factor SPT4

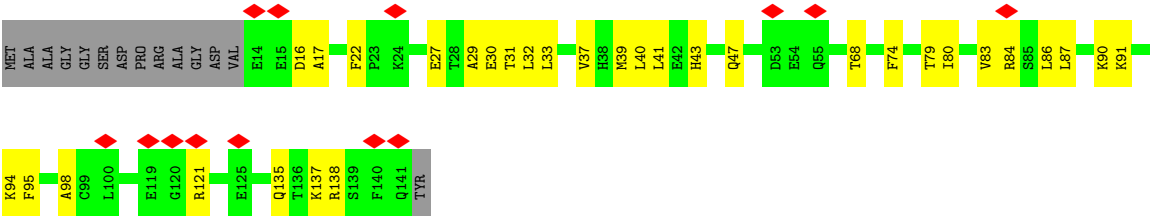


- Molecule 32: Transcription elongation factor SPT5





● Molecule 34: DNA-directed RNA polymerase II subunit RPB4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41201	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.124	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	442.68002, 442.68002, 442.68002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.054, 1.054, 1.054	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.16	0/13264	0.33	0/18049
2	B	0.24	0/8474	0.39	0/11498
3	D	0.23	0/6315	0.39	0/8583
4	E	0.16	0/5344	0.35	0/7312
5	F	0.19	0/4508	0.35	0/6131
6	G	0.26	0/7038	0.45	2/9532 (0.0%)
7	H	0.17	0/7583	0.34	0/10280
8	I	0.23	0/5110	0.39	0/6959
9	K	0.22	0/4747	0.38	0/6412
11	P	0.20	0/4601	0.39	0/6246
12	Q	0.22	0/2423	0.40	0/3285
14	1	0.28	0/11492	0.43	0/15525
15	2	0.25	0/8823	0.40	0/11947
16	3	0.23	0/2091	0.38	0/2843
17	4	0.15	0/1752	0.35	0/2366
18	5	0.33	0/659	0.54	1/889 (0.1%)
19	6	0.20	0/1207	0.42	1/1628 (0.1%)
20	7	0.14	0/973	0.35	0/1316
21	8	0.30	0/542	0.41	0/730
22	9	0.18	0/956	0.38	0/1294
23	a	0.19	0/395	0.42	0/524
24	b	0.26	0/846	0.35	0/1304
25	c	0.55	0/450	0.87	2/696 (0.3%)
26	d	0.31	0/1014	0.48	0/1560
27	e	0.13	0/1434	0.34	0/1948
28	f	0.10	0/1913	0.28	0/2379
29	g	0.15	0/3830	0.35	2/5236 (0.0%)
30	h	0.22	0/108	0.94	2/149 (1.3%)
31	i	0.24	0/927	0.42	0/1250
32	j	0.19	0/3920	0.33	0/5276
33	k	0.11	0/1330	0.26	0/1813
34	l	0.14	0/1011	0.33	0/1364

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.22	0/115080	0.38	10/156324 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	g	76	PRO	N-CA-CB	9.72	109.33	102.81
6	G	275	ASP	CA-CB-CG	7.96	120.56	112.60
30	h	5	PRO	N-CA-CB	7.18	110.05	103.08
29	g	60	PRO	N-CA-CB	6.19	110.14	103.33
25	c	38	G	C2'-C3'-O3'	6.13	122.90	113.70
30	h	6	PRO	N-CA-CB	6.07	110.01	103.33
6	G	275	ASP	CB-CA-C	5.33	119.14	110.24
25	c	27	A	C2'-C3'-O3'	-5.24	105.84	113.70
19	6	16	ASP	CA-CB-CG	5.13	117.73	112.60
18	5	69	ARG	N-CA-C	-5.13	105.58	111.07

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	13054	0	12233	218	0
2	B	8328	0	8566	230	0
3	D	6205	0	5907	166	0
4	E	5244	0	4501	101	0
5	F	4395	0	4372	70	0
6	G	6928	0	6913	192	0
7	H	7440	0	7530	164	0
8	I	4985	0	5013	136	0
9	K	4646	0	4665	113	0
10	M	85	0	19	0	0
11	P	4527	0	4633	132	0
12	Q	2366	0	2269	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	U	135	0	30	1	0
14	1	11345	0	11343	340	0
15	2	8649	0	8462	271	0
16	3	2048	0	1985	52	0
17	4	1721	0	1737	42	0
18	5	649	0	676	21	0
19	6	1186	0	1147	47	0
20	7	950	0	879	21	0
21	8	533	0	553	20	0
22	9	937	0	959	36	0
23	a	389	0	393	15	0
24	b	752	0	401	24	0
25	c	406	0	207	12	0
26	d	909	0	506	25	0
27	e	1410	0	1455	36	0
28	f	1920	0	504	4	0
29	g	3764	0	3378	79	0
30	h	109	0	45	0	0
31	i	911	0	908	11	0
32	j	3854	0	3913	58	0
33	k	1299	0	1258	38	0
34	l	997	0	953	34	0
35	1	2	0	0	0	0
35	2	1	0	0	0	0
35	3	1	0	0	0	0
35	7	2	0	0	0	0
35	8	1	0	0	0	0
35	K	2	0	0	0	0
35	a	1	0	0	0	0
36	Q	2	0	0	0	0
37	1	1	0	0	0	0
All	All	113089	0	108313	2592	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 12.

All (2592) 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)
33:k:1:MET:HE2	34:l:95:PHE:CE1	1.82	1.14
33:k:1:MET:CE	34:l:95:PHE:HE1	1.61	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:k:1:MET:HE2	34:l:95:PHE:HE1	0.98	1.12
33:k:1:MET:CE	34:l:95:PHE:CE1	2.31	1.11
2:B:850:GLN:NE2	2:B:854:MET:SD	2.33	1.02
9:K:37:MET:HG3	25:c:25:A:N6	1.75	1.01
3:D:525:LEU:HD11	3:D:551:ILE:HD11	1.41	1.00
33:k:78:ARG:NH1	33:k:79:PRO:O	1.98	0.97
9:K:31:LEU:HD21	9:K:166:ILE:HD11	1.45	0.95
2:B:437:LEU:HD23	2:B:517:MET:HE1	1.51	0.92
11:P:522:LEU:HD21	11:P:551:LEU:HD21	1.52	0.91
33:k:4:HIS:HB2	34:l:32:LEU:HD11	1.50	0.91
22:9:45:ILE:HD12	22:9:94:LEU:HD21	1.55	0.89
18:5:71:LEU:HD23	18:5:75:MET:HE2	1.52	0.87
4:E:798:CYS:SG	7:H:411:ASN:ND2	2.48	0.86
3:D:688:LYS:NZ	3:D:689:GLN:OE1	2.09	0.85
15:2:91:ILE:HD13	15:2:126:VAL:HG12	1.58	0.85
1:A:1746:ARG:HD2	1:A:1754:ALA:HB2	1.57	0.85
14:1:350:VAL:HG11	14:1:1435:THR:HG21	1.58	0.84
12:Q:38:ILE:HD11	12:Q:108:ARG:HG3	1.60	0.83
14:1:103:THR:OG1	14:1:248:MET:SD	2.35	0.83
9:K:297:ARG:NH1	9:K:299:MET:SD	2.51	0.83
31:i:18:LEU:HD11	31:i:93:LEU:HD11	1.62	0.81
11:P:141:PHE:HB3	11:P:180:MET:HE3	1.63	0.81
1:A:146:VAL:HG11	1:A:183:ALA:HB1	1.63	0.80
14:1:1798:SER:OG	14:1:1799:PRO:HD3	1.81	0.80
14:1:1329:LYS:NZ	14:1:1330:ALA:O	2.14	0.79
33:k:1:MET:CE	34:l:95:PHE:CZ	2.65	0.79
1:A:339:ARG:NH1	1:A:340:ARG:O	2.16	0.79
2:B:409:GLU:OE1	2:B:410:GLN:NE2	2.15	0.79
5:F:543:ASN:OD1	5:F:544:ALA:N	2.16	0.79
5:F:35:PHE:HB2	5:F:220:LEU:HD11	1.65	0.78
6:G:854:VAL:HG12	6:G:906:VAL:HG12	1.65	0.78
1:A:1074:THR:HG21	1:A:1085:LEU:HD22	1.64	0.78
2:B:1182:ASP:OD1	2:B:1183:VAL:N	2.15	0.78
6:G:621:VAL:O	6:G:625:ILE:HD12	1.83	0.78
9:K:163:MET:HE1	9:K:190:ALA:HB1	1.63	0.78
1:A:904:VAL:HG12	1:A:906:PRO:HD2	1.65	0.78
9:K:121:PHE:HD1	9:K:126:ILE:HD11	1.48	0.77
14:1:668:PHE:CZ	14:1:672:ILE:HD11	2.20	0.77
2:B:921:VAL:HG12	2:B:925:GLU:OE1	1.84	0.77
7:H:648:MET:SD	7:H:649:ARG:N	2.57	0.77
16:3:12:THR:OG1	16:3:13:GLU:OE2	2.02	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:a:52:LEU:HD11	32:j:721:ILE:HG21	1.66	0.77
9:K:37:MET:CG	25:c:25:A:N6	2.48	0.77
14:1:668:PHE:CE1	14:1:672:ILE:HD11	2.20	0.76
14:1:1083:PRO:HD2	18:5:58:THR:HG21	1.65	0.76
31:i:40:LEU:HB3	31:i:42:MET:HE3	1.67	0.76
27:e:17:LEU:HD13	27:e:55:LYS:HB2	1.67	0.76
15:2:985:LEU:HD11	15:2:1015:LEU:HD11	1.68	0.76
22:9:42:LEU:HD13	22:9:45:ILE:HD11	1.67	0.76
14:1:467:MET:HE1	14:1:534:VAL:HG11	1.68	0.76
14:1:111:CYS:SG	14:1:112:PHE:N	2.58	0.75
16:3:61:ASP:OD1	16:3:62:GLU:N	2.20	0.75
23:a:19:CYS:HA	23:a:44:MET:HE1	1.67	0.75
1:A:1076:VAL:O	1:A:1130:ARG:NH1	2.20	0.75
3:D:450:ASP:OD1	3:D:451:THR:N	2.19	0.75
15:2:817:GLN:OE1	15:2:912:ASN:ND2	2.20	0.75
8:I:195:GLN:NE2	8:I:196:LEU:O	2.20	0.75
33:k:1:MET:HE3	34:l:95:PHE:CE1	2.21	0.75
27:e:22:GLU:O	27:e:55:LYS:NZ	2.20	0.74
2:B:649:LEU:HB3	2:B:706:LEU:HD21	1.69	0.74
15:2:663:GLU:OE2	15:2:695:HIS:NE2	2.20	0.74
7:H:857:LEU:HD21	7:H:990:MET:HG3	1.68	0.74
16:3:59:LEU:HD12	16:3:63:PHE:CD2	2.23	0.74
15:2:403:LEU:HD23	15:2:407:MET:HE1	1.69	0.74
14:1:71:CYS:SG	14:1:84:HIS:CD2	2.81	0.74
1:A:1662:THR:HG22	6:G:187:LEU:HD12	1.70	0.73
15:2:739:ASN:OD1	15:2:743:ARG:NH2	2.22	0.73
6:G:525:THR:O	6:G:529:ILE:HD12	1.88	0.73
2:B:426:VAL:HG13	2:B:476:PHE:CE1	2.24	0.73
5:F:283:TRP:NE1	5:F:323:PRO:O	2.21	0.73
14:1:933:THR:O	14:1:1002:SER:N	2.21	0.73
15:2:1068:GLN:NE2	15:2:1074:PRO:O	2.22	0.73
2:B:201:LEU:HD11	2:B:210:PHE:HD2	1.53	0.73
1:A:446:ILE:HG21	1:A:480:VAL:HG11	1.70	0.73
14:1:67:ARG:HG2	14:1:68:THR:HG23	1.71	0.73
27:e:68:VAL:HG13	27:e:75:LEU:HD12	1.71	0.73
7:H:784:ARG:NH2	7:H:789:ASN:OD1	2.22	0.73
7:H:930:ASP:OD1	7:H:931:TYR:N	2.21	0.73
8:I:87:GLU:OE2	8:I:501:ARG:NE	2.22	0.72
15:2:193:VAL:HG21	15:2:470:LEU:HD13	1.71	0.72
1:A:2167:MET:HE2	2:B:1129:GLY:HA3	1.72	0.72
9:K:327:MET:HE2	9:K:355:VAL:HG23	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:102:GLU:OE2	6:G:106:ARG:NE	2.22	0.72
7:H:669:ASN:O	7:H:671:ARG:NH1	2.23	0.72
21:8:10:CYS:SG	21:8:42:ARG:NH2	2.63	0.72
5:F:458:LYS:O	5:F:462:GLN:NE2	2.23	0.72
14:1:479:TRP:HB2	15:2:931:ILE:HD11	1.70	0.72
17:4:176:GLY:O	17:4:181:ARG:NH1	2.22	0.72
15:2:584:MET:HE2	15:2:588:ARG:NH1	2.05	0.72
27:e:69:ASP:OD1	27:e:72:LYS:NZ	2.23	0.72
32:j:479:LYS:N	32:j:519:GLN:O	2.22	0.72
3:D:536:GLU:OE1	14:1:1767:PRO:HD3	1.89	0.72
4:E:658:SER:OG	4:E:667:VAL:HG12	1.89	0.72
9:K:9:LEU:O	9:K:17:ARG:NH1	2.21	0.72
22:9:21:ILE:HD11	22:9:31:CYS:HB3	1.71	0.72
2:B:937:ALA:O	2:B:941:ILE:HD12	1.90	0.72
6:G:819:ILE:O	6:G:929:LYS:N	2.22	0.72
14:1:998:PRO:O	14:1:1059:ARG:NH1	2.23	0.72
2:B:433:PHE:HD2	2:B:479:MET:HE1	1.55	0.72
15:2:309:PHE:O	15:2:312:GLN:NE2	2.22	0.72
12:Q:119:GLU:OE1	12:Q:119:GLU:N	2.22	0.71
12:Q:223:ASP:OD1	12:Q:224:ILE:N	2.23	0.71
23:a:17:TYR:HB3	23:a:44:MET:SD	2.30	0.71
4:E:881:LEU:HD22	4:E:910:LEU:HD22	1.71	0.71
32:j:427:GLU:OE2	32:j:469:ARG:NH2	2.23	0.71
11:P:308:GLU:O	11:P:312:ASN:ND2	2.23	0.71
6:G:556:GLU:OE1	6:G:556:GLU:N	2.23	0.71
7:H:471:ASP:OD1	7:H:472:GLU:N	2.23	0.71
15:2:628:VAL:HG21	15:2:683:GLN:OE1	1.91	0.71
27:e:68:VAL:HG13	27:e:75:LEU:CD1	2.20	0.71
15:2:625:LEU:HD12	15:2:665:ILE:HG13	1.71	0.71
7:H:51:ILE:HD11	7:H:88:VAL:HB	1.73	0.71
15:2:505:LEU:HD22	15:2:509:VAL:HB	1.72	0.71
1:A:814:ALA:O	1:A:819:LYS:N	2.23	0.71
14:1:384:ILE:HD11	15:2:1059:ILE:HD11	1.73	0.71
21:8:36:ASP:OD1	21:8:46:ARG:NH1	2.24	0.70
14:1:1149:ARG:NH1	29:g:524:ASP:OD2	2.24	0.70
14:1:415:GLY:O	14:1:449:HIS:ND1	2.24	0.70
7:H:646:LEU:O	7:H:649:ARG:NE	2.24	0.70
9:K:122:THR:O	9:K:126:ILE:HD12	1.91	0.70
5:F:221:GLU:O	5:F:225:GLN:NE2	2.24	0.70
14:1:559:GLU:OE1	14:1:559:GLU:N	2.23	0.70
6:G:835:VAL:HG21	6:G:847:ILE:HD13	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:467:MET:CE	14:1:534:VAL:HG21	2.22	0.70
32:j:419:ASN:OD1	32:j:421:GLN:NE2	2.24	0.70
12:Q:204:ASP:OD1	12:Q:205:ASP:N	2.24	0.70
6:G:453:LEU:HD22	6:G:496:VAL:HG23	1.71	0.70
11:P:322:ILE:HG21	11:P:356:LEU:HD21	1.74	0.70
17:4:159:LEU:HD11	17:4:206:TYR:CE2	2.27	0.70
2:B:702:GLU:OE1	2:B:702:GLU:N	2.25	0.70
3:D:395:VAL:CG1	3:D:419:MET:HE1	2.21	0.70
3:D:622:TYR:OH	3:D:811:LEU:N	2.25	0.70
6:G:183:MET:SD	6:G:189:THR:HG21	2.31	0.70
32:j:416:ARG:NH2	32:j:446:ASN:OD1	2.25	0.70
1:A:2072:GLU:OE1	1:A:2075:ARG:NH1	2.25	0.69
9:K:265:ILE:HG22	9:K:320:VAL:HB	1.74	0.69
15:2:388:TYR:HE2	15:2:505:LEU:HD21	1.58	0.69
2:B:489:SER:O	2:B:491:GLN:NE2	2.26	0.69
1:A:702:ILE:HD11	1:A:752:ILE:HG23	1.73	0.69
3:D:479:LYS:HG3	3:D:521:LEU:HD11	1.73	0.69
3:D:624:LEU:O	3:D:625:GLN:NE2	2.25	0.69
3:D:882:PHE:CE1	3:D:892:LEU:HD13	2.27	0.69
15:2:677:MET:HG3	15:2:678:THR:HG23	1.74	0.69
8:I:135:LEU:HD12	8:I:332:VAL:HB	1.73	0.69
11:P:453:ASP:O	11:P:459:ARG:NH1	2.25	0.69
14:1:718:GLU:OE2	14:1:722:ASN:ND2	2.26	0.69
16:3:13:GLU:OE2	16:3:13:GLU:N	2.26	0.69
6:G:30:ASP:OD1	6:G:34:ARG:NH2	2.26	0.69
12:Q:42:GLU:O	12:Q:185:ARG:NH2	2.26	0.69
4:E:565:THR:HG22	4:E:566:LEU:H	1.58	0.69
6:G:260:LEU:O	6:G:269:LYS:NZ	2.26	0.69
11:P:572:ASP:HB3	11:P:575:VAL:HG12	1.75	0.69
14:1:367:ILE:HD13	14:1:501:MET:HE3	1.75	0.69
33:k:35:GLU:OE2	33:k:48:VAL:N	2.26	0.69
14:1:600:ILE:HD11	14:1:660:MET:SD	2.33	0.68
15:2:1062:ARG:NH2	15:2:1066:PRO:O	2.26	0.68
2:B:670:ALA:O	2:B:673:GLN:NE2	2.26	0.68
14:1:1430:CYS:O	14:1:1435:THR:HG22	1.93	0.68
2:B:437:LEU:CD2	2:B:517:MET:HE1	2.22	0.68
14:1:517:GLU:O	14:1:523:ARG:NE	2.27	0.68
19:6:56:PHE:CD2	19:6:145:MET:HE1	2.28	0.68
6:G:369:ASN:OD1	6:G:418:LYS:NZ	2.23	0.68
32:j:577:ARG:NH1	32:j:578:LYS:O	2.27	0.68
2:B:1107:LEU:HD22	2:B:1121:ILE:HD12	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:461:GLN:HG3	26:d:26:DG:H2''	1.76	0.68
16:3:263:LEU:HD13	22:9:87:PHE:CE2	2.29	0.68
2:B:239:GLU:O	2:B:244:ARG:NH2	2.27	0.68
2:B:1029:VAL:HG12	2:B:1035:MET:HE1	1.75	0.68
2:B:87:LEU:HD12	2:B:139:LEU:HD21	1.76	0.68
5:F:551:ASN:OD1	5:F:555:HIS:ND1	2.27	0.68
14:1:354:LEU:O	14:1:357:LYS:NZ	2.27	0.68
32:j:311:ILE:O	32:j:338:ARG:NH1	2.26	0.68
34:l:43:HIS:O	34:l:47:GLN:NE2	2.27	0.68
1:A:1292:VAL:O	2:B:73:ARG:NH1	2.27	0.67
2:B:201:LEU:HD21	2:B:210:PHE:HB2	1.75	0.67
8:I:253:ALA:O	8:I:256:LYS:NZ	2.26	0.67
23:a:16:ILE:HG23	23:a:25:GLU:OE2	1.95	0.67
34:l:79:THR:O	34:l:83:VAL:HG23	1.94	0.67
9:K:147:GLU:OE1	9:K:147:GLU:N	2.28	0.67
14:1:966:LEU:HA	14:1:969:ILE:HG22	1.77	0.67
1:A:2149:LEU:HD12	1:A:2183:ILE:HG21	1.76	0.67
3:D:418:ASP:OD1	3:D:419:MET:N	2.28	0.67
6:G:901:THR:HG22	6:G:929:LYS:HD3	1.77	0.67
14:1:549:THR:O	14:1:549:THR:HG22	1.94	0.67
15:2:89:GLU:OE1	15:2:89:GLU:N	2.26	0.67
4:E:985:LEU:HD13	4:E:1009:PRO:HG3	1.77	0.67
11:P:487:LEU:HD11	11:P:524:THR:HG21	1.75	0.67
11:P:76:PHE:O	11:P:80:VAL:HG23	1.94	0.67
15:2:275:ALA:O	15:2:314:GLN:NE2	2.27	0.67
6:G:551:THR:O	6:G:552:GLN:NE2	2.27	0.67
33:k:126:PRO:O	33:k:139:GLN:NE2	2.27	0.67
1:A:1721:GLU:OE2	1:A:1724:VAL:HG13	1.93	0.67
6:G:639:ASN:O	6:G:642:LYS:NZ	2.27	0.67
15:2:584:MET:SD	15:2:585:ASN:N	2.68	0.67
34:l:33:LEU:HD11	34:l:84:ARG:NH1	2.09	0.67
5:F:265:HIS:O	5:F:266:LYS:NZ	2.22	0.67
7:H:55:LEU:HD13	7:H:110:MET:SD	2.35	0.67
11:P:324:SER:OG	11:P:325:GLN:OE1	2.12	0.67
15:2:865:VAL:HG12	15:2:895:PHE:CE1	2.30	0.67
1:A:644:SER:O	1:A:682:ARG:NE	2.29	0.66
9:K:204:SER:OG	9:K:420:MET:HE2	1.95	0.66
11:P:277:GLU:O	11:P:281:THR:HG23	1.96	0.66
15:2:596:ILE:HG23	15:2:597:ILE:HD12	1.76	0.66
17:4:24:ARG:NH2	17:4:182:TYR:O	2.28	0.66
22:9:106:ARG:O	22:9:109:ILE:HG22	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:g:442:GLN:N	29:g:442:GLN:OE1	2.28	0.66
5:F:100:ASN:ND2	5:F:161:PRO:O	2.28	0.66
9:K:149:GLU:OE1	9:K:149:GLU:N	2.28	0.66
11:P:202:LYS:HA	11:P:206:ILE:HD12	1.77	0.66
15:2:533:SER:OG	15:2:620:ARG:N	2.28	0.66
11:P:16:LEU:HD21	11:P:38:ILE:HD13	1.78	0.66
14:1:485:ASN:OD1	14:1:486:LEU:N	2.28	0.66
5:F:74:MET:HA	5:F:74:MET:HE3	1.77	0.66
19:6:33:GLU:OE1	19:6:33:GLU:N	2.28	0.66
7:H:621:HIS:ND1	7:H:624:GLU:OE2	2.29	0.66
7:H:708:LYS:NZ	7:H:710:SER:OG	2.26	0.66
12:Q:9:GLU:OE2	12:Q:13:TRP:NE1	2.28	0.66
15:2:1118:VAL:HG23	15:2:1124:ILE:O	1.96	0.66
6:G:482:ALA:O	6:G:486:GLN:NE2	2.28	0.66
6:G:484:ASP:OD1	6:G:485:LYS:N	2.29	0.66
1:A:485:LEU:O	1:A:536:ARG:NH2	2.28	0.66
5:F:268:ILE:HD13	5:F:379:LEU:CD2	2.26	0.66
11:P:49:SER:OG	11:P:50:GLU:OE1	2.14	0.66
29:g:218:GLU:OE1	29:g:222:LYS:NZ	2.29	0.66
8:I:648:ARG:O	8:I:652:LEU:HD23	1.96	0.66
15:2:590:LEU:HD23	15:2:597:ILE:CD1	2.26	0.66
31:i:42:MET:HE2	31:i:48:MET:HE1	1.78	0.66
2:B:1002:HIS:NE2	2:B:1006:ILE:HD11	2.11	0.65
4:E:754:ILE:HD11	12:Q:282:LEU:HD21	1.78	0.65
4:E:893:ARG:HD3	12:Q:186:LEU:HD11	1.78	0.65
9:K:69:PHE:HA	9:K:100:CYS:SG	2.36	0.65
11:P:155:TYR:CD1	11:P:166:LEU:HD11	2.31	0.65
18:5:102:ILE:HB	18:5:120:VAL:HG21	1.77	0.65
1:A:2181:LEU:HD13	2:B:1118:TYR:OH	1.96	0.65
11:P:499:MET:HA	11:P:499:MET:HE3	1.79	0.65
34:l:37:VAL:HG12	34:l:68:THR:HG21	1.78	0.65
2:B:1135:ASP:O	2:B:1138:THR:HG22	1.96	0.65
6:G:402:SER:O	6:G:406:GLN:NE2	2.29	0.65
14:1:296:ASN:OD1	14:1:297:GLY:N	2.29	0.65
14:1:1143:LEU:HB2	14:1:1148:ALA:HB2	1.77	0.65
15:2:591:ARG:NH2	15:2:664:TYR:O	2.30	0.65
29:g:329:ARG:NE	29:g:363:ALA:O	2.27	0.65
7:H:102:SER:C	7:H:103:LEU:HD12	2.22	0.65
14:1:702:ILE:HD12	14:1:752:THR:HG23	1.79	0.65
14:1:1313:GLN:O	14:1:1318:LYS:NZ	2.29	0.65
1:A:777:TYR:CZ	1:A:791:MET:HE2	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:903:PHE:O	7:H:905:ARG:NH2	2.28	0.65
9:K:28:ASN:N	9:K:62:ASP:OD2	2.30	0.65
34:l:33:LEU:HD11	34:l:84:ARG:HH11	1.60	0.65
4:E:935:ALA:N	4:E:938:GLU:OE1	2.30	0.65
34:l:83:VAL:HG22	34:l:137:LYS:CD	2.26	0.65
7:H:30:GLU:OE1	7:H:33:LEU:N	2.30	0.65
7:H:73:PRO:O	7:H:78:ASN:ND2	2.30	0.65
17:4:84:ILE:HD13	24:b:39:DA:OP1	1.97	0.65
2:B:1147:ILE:HD12	2:B:1147:ILE:H	1.62	0.64
34:l:83:VAL:HG22	34:l:137:LYS:HD3	1.78	0.64
6:G:138:ASN:OD1	6:G:139:ALA:N	2.31	0.64
11:P:558:SER:OG	11:P:559:GLU:OE1	2.10	0.64
14:1:381:PRO:HD2	14:1:384:ILE:HD12	1.78	0.64
14:1:885:GLN:OE1	14:1:1408:ARG:NH1	2.30	0.64
15:2:90:GLN:NE2	15:2:91:ILE:O	2.30	0.64
6:G:305:ASP:OD1	6:G:306:SER:N	2.31	0.64
14:1:104:MET:HE2	14:1:198:LEU:HD11	1.78	0.64
14:1:555:LEU:HD23	14:1:560:VAL:HG22	1.79	0.64
15:2:789:ASN:O	15:2:968:ASN:ND2	2.29	0.64
17:4:194:ILE:CD1	17:4:204:ILE:HG22	2.27	0.64
27:e:96:ILE:HD13	27:e:110:LEU:HD11	1.78	0.64
1:A:2122:LEU:HD22	1:A:2154:HIS:ND1	2.13	0.64
4:E:769:GLN:HE22	4:E:773:ILE:HD11	1.62	0.64
6:G:835:VAL:HG21	6:G:847:ILE:CD1	2.28	0.64
33:k:1:MET:HE3	34:l:95:PHE:CZ	2.32	0.64
4:E:642:SER:OG	7:H:858:GLN:NE2	2.31	0.64
8:I:460:LEU:O	8:I:464:VAL:HG22	1.98	0.64
11:P:538:PHE:HA	11:P:575:VAL:HG23	1.80	0.64
22:9:16:GLU:OE1	22:9:16:GLU:N	2.29	0.64
15:2:508:MET:HE3	15:2:667:THR:HG22	1.80	0.64
15:2:790:GLN:O	15:2:968:ASN:ND2	2.31	0.64
1:A:520:MET:HE3	1:A:545:LEU:HD11	1.80	0.64
1:A:1668:SER:O	2:B:807:ARG:NH1	2.30	0.64
2:B:201:LEU:HD11	2:B:210:PHE:CD2	2.31	0.64
3:D:868:PRO:HB2	6:G:893:LEU:HD23	1.80	0.64
3:D:209:PRO:O	3:D:213:THR:HG23	1.98	0.64
4:E:585:GLU:OE2	4:E:598:HIS:N	2.31	0.64
6:G:749:MET:HA	6:G:749:MET:HE3	1.79	0.64
14:1:404:GLU:OE2	14:1:407:ARG:NH2	2.28	0.64
16:3:263:LEU:HD13	22:9:87:PHE:HE2	1.63	0.64
26:d:17:DT:H2"	26:d:18:DG:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:e:66:ARG:NH2	27:e:69:ASP:OD2	2.29	0.64
2:B:508:VAL:O	2:B:509:ILE:HD13	1.97	0.64
7:H:582:THR:O	7:H:584:LYS:NZ	2.31	0.64
11:P:194:LYS:HD3	11:P:234:LEU:HD21	1.80	0.64
14:1:1292:MET:HA	14:1:1296:MET:HE3	1.78	0.64
15:2:285:LEU:O	15:2:289:ILE:HG22	1.98	0.64
1:A:471:GLU:N	1:A:471:GLU:OE1	2.31	0.63
15:2:310:VAL:HG13	15:2:311:ILE:HD12	1.79	0.63
9:K:69:PHE:CB	9:K:100:CYS:SG	2.86	0.63
12:Q:170:LEU:HD21	12:Q:228:PHE:CE2	2.33	0.63
17:4:81:LYS:NZ	17:4:109:GLY:O	2.31	0.63
22:9:21:ILE:HD13	22:9:33:PHE:CD2	2.33	0.63
7:H:711:ARG:NH1	7:H:798:ILE:O	2.29	0.63
11:P:352:LEU:HD12	11:P:352:LEU:O	1.99	0.63
14:1:726:GLU:OE1	14:1:726:GLU:N	2.30	0.63
14:1:153:ILE:HG22	14:1:187:TYR:HA	1.80	0.63
19:6:89:GLU:OE2	19:6:147:LYS:N	2.30	0.63
1:A:852:GLN:NE2	1:A:853:VAL:HG23	2.13	0.63
12:Q:35:ALA:HA	12:Q:38:ILE:HG22	1.81	0.63
5:F:38:LEU:HD23	5:F:41:ARG:HH21	1.64	0.63
14:1:489:THR:HG21	14:1:496:PHE:CZ	2.33	0.63
15:2:752:TYR:O	21:8:1:MET:N	2.32	0.63
3:D:482:ILE:HD11	3:D:514:HIS:NE2	2.13	0.63
4:E:573:ARG:O	4:E:577:ASN:ND2	2.32	0.63
5:F:115:ARG:NH2	5:F:302:THR:O	2.31	0.63
14:1:520:MET:HG2	14:1:522:PRO:HD2	1.80	0.63
15:2:1101:GLN:N	15:2:1101:GLN:OE1	2.32	0.63
1:A:1255:VAL:HA	1:A:1258:MET:HE2	1.79	0.63
3:D:253:VAL:HG11	3:D:290:MET:HE2	1.81	0.63
15:2:168:ASP:OD1	15:2:169:ARG:N	2.31	0.63
1:A:1918:LEU:O	1:A:1921:HIS:N	2.32	0.62
9:K:326:GLY:O	9:K:350:MET:HE1	1.99	0.62
11:P:522:LEU:HD21	11:P:551:LEU:CD2	2.25	0.62
14:1:571:ASP:OD1	14:1:572:GLY:N	2.32	0.62
16:3:238:SER:C	16:3:239:LEU:HD12	2.24	0.62
2:B:747:ASN:OD1	2:B:748:ASN:N	2.32	0.62
8:I:603:PHE:HB3	8:I:606:ILE:HD11	1.80	0.62
17:4:174:GLN:OE1	17:4:176:GLY:N	2.32	0.62
32:j:424:ASP:HB2	32:j:440:ILE:HD12	1.81	0.62
34:l:84:ARG:NH2	34:l:87:LEU:HD12	2.14	0.62
34:l:135:GLN:OE1	34:l:138:ARG:NH1	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:552:ASP:O	19:6:24:ARG:NH2	2.31	0.62
2:B:426:VAL:HG13	2:B:476:PHE:CD1	2.35	0.62
3:D:525:LEU:CD1	3:D:551:ILE:HD11	2.25	0.62
9:K:519:ASP:OD1	9:K:570:LYS:NZ	2.31	0.62
15:2:665:ILE:HG23	15:2:669:GLU:OE1	2.00	0.62
15:2:826:GLU:N	15:2:872:THR:OG1	2.33	0.62
11:P:116:SER:O	11:P:157:ARG:NH1	2.33	0.62
11:P:424:ILE:O	11:P:465:ASN:ND2	2.32	0.62
14:1:1091:ALA:O	14:1:1095:LEU:HD23	1.99	0.62
1:A:1680:LEU:HD21	1:A:1694:SER:HB2	1.82	0.62
2:B:262:LEU:HD12	2:B:265:ARG:NH2	2.14	0.62
32:j:474:MET:HG3	33:k:148:VAL:HG21	1.80	0.62
1:A:633:GLU:OE1	1:A:636:ARG:NH1	2.33	0.62
2:B:436:LEU:HD11	2:B:452:MET:HG3	1.81	0.62
4:E:896:ASP:OD1	4:E:897:THR:N	2.32	0.62
8:I:492:CYS:SG	8:I:496:ALA:N	2.72	0.62
11:P:131:LEU:HD23	11:P:134:ARG:HH21	1.63	0.62
32:j:236:LYS:NZ	32:j:249:TYR:O	2.33	0.62
1:A:1623:GLU:OE2	2:B:808:ARG:NH2	2.33	0.62
2:B:625:LEU:HD22	2:B:683:LEU:HD13	1.81	0.62
9:K:394:ASP:O	9:K:398:ILE:HD12	2.00	0.62
15:2:23:GLN:OE1	15:2:23:GLN:N	2.33	0.62
15:2:126:VAL:HG22	15:2:149:ILE:HD11	1.81	0.62
28:f:152:ASP:O	28:f:157:PHE:N	2.33	0.62
29:g:470:LEU:HD22	29:g:508:TYR:HE2	1.65	0.62
2:B:1136:VAL:HG22	2:B:1182:ASP:OD2	2.00	0.62
1:A:2159:LEU:HD12	1:A:2177:ILE:HG23	1.81	0.62
2:B:103:GLN:HG2	2:B:147:LEU:HD23	1.82	0.62
4:E:537:GLN:NE2	7:H:491:CYS:SG	2.71	0.62
6:G:453:LEU:HD22	6:G:496:VAL:CG2	2.29	0.62
7:H:616:LEU:HD11	7:H:642:VAL:HG22	1.81	0.62
34:l:86:LEU:O	34:l:90:LYS:NZ	2.33	0.62
1:A:493:ARG:NH1	1:A:627:TRP:O	2.33	0.61
2:B:62:GLN:O	2:B:66:GLN:NE2	2.33	0.61
2:B:390:ARG:NH1	6:G:556:GLU:OE2	2.32	0.61
2:B:457:SER:O	2:B:461:LYS:NZ	2.29	0.61
11:P:494:ASN:OD1	11:P:495:TYR:N	2.33	0.61
14:1:155:GLU:O	14:1:181:HIS:ND1	2.33	0.61
2:B:15:LEU:HD11	2:B:174:LEU:CD2	2.30	0.61
11:P:52:LEU:O	11:P:56:THR:HG23	2.00	0.61
15:2:1111:SER:OG	15:2:1112:ASP:OD1	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:9:11:LEU:O	22:9:37:LYS:NZ	2.29	0.61
24:b:25:DC:H2"	24:b:26:DG:C8	2.35	0.61
2:B:482:LEU:HD23	2:B:498:LEU:HD22	1.82	0.61
15:2:350:HIS:CE1	15:2:351:VAL:HG13	2.35	0.61
1:A:899:GLU:OE2	1:A:946:LYS:NZ	2.33	0.61
2:B:72:LEU:HD13	2:B:75:LEU:HD12	1.81	0.61
9:K:52:THR:HG21	9:K:57:LEU:HA	1.82	0.61
12:Q:88:ASP:OD2	12:Q:118:HIS:ND1	2.34	0.61
14:1:388:MET:HB3	14:1:450:MET:HE1	1.81	0.61
8:I:449:ASP:OD1	8:I:450:THR:N	2.33	0.61
14:1:1054:MET:HE3	14:1:1054:MET:O	2.00	0.61
15:2:626:LEU:HD23	15:2:662:VAL:HG12	1.81	0.61
27:e:106:LEU:HD12	29:g:283:LEU:HD22	1.82	0.61
1:A:767:MET:O	1:A:771:MET:HE3	2.01	0.61
8:I:281:PHE:CE2	8:I:308:LEU:HD21	2.35	0.61
15:2:91:ILE:HD13	15:2:126:VAL:CG1	2.28	0.61
20:7:23:MET:HE2	20:7:25:TYR:CD1	2.36	0.61
1:A:252:ASN:OD1	1:A:317:ARG:NE	2.33	0.61
3:D:645:ARG:HH12	3:D:649:LEU:HD13	1.65	0.61
8:I:597:THR:HG21	8:I:654:PHE:CZ	2.35	0.61
4:E:966:ARG:NH1	7:H:370:ALA:O	2.34	0.61
6:G:417:VAL:HA	6:G:456:ILE:HD11	1.82	0.61
14:1:760:LEU:HD12	14:1:767:LYS:HE2	1.83	0.61
15:2:388:TYR:CE2	15:2:505:LEU:HD21	2.35	0.61
15:2:677:MET:HE1	15:2:700:PRO:HB3	1.82	0.61
15:2:1091:ARG:HG2	15:2:1103:LEU:HD11	1.83	0.61
4:E:517:GLU:O	4:E:521:HIS:ND1	2.34	0.61
4:E:769:GLN:NE2	4:E:773:ILE:HD11	2.15	0.61
32:j:367:SER:HB2	32:j:372:LEU:HD23	1.82	0.61
6:G:363:GLY:O	6:G:366:VAL:HG12	2.00	0.60
21:8:1:MET:O	21:8:2:ILE:HD13	2.01	0.60
32:j:604:ASP:OD1	32:j:605:GLY:N	2.34	0.60
3:D:962:ARG:NH1	16:3:91:GLU:OE2	2.33	0.60
6:G:110:VAL:HG23	6:G:122:THR:OG1	2.01	0.60
7:H:535:MET:SD	7:H:536:THR:HG23	2.41	0.60
1:A:767:MET:C	1:A:771:MET:HE3	2.26	0.60
11:P:426:TYR:CE1	11:P:429:LEU:HD22	2.37	0.60
14:1:191:ILE:HG22	14:1:198:LEU:HD12	1.83	0.60
14:1:770:VAL:HG21	14:1:781:ILE:HD11	1.82	0.60
15:2:403:LEU:CD2	15:2:407:MET:HE1	2.32	0.60
19:6:34:SER:O	19:6:36:LYS:NZ	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:32:MET:HE3	8:I:397:HIS:CE1	2.35	0.60
25:c:39:A:H2'	25:c:40:A:C8	2.37	0.60
32:j:536:TRP:CZ2	32:j:635:MET:HE1	2.37	0.60
2:B:227:ARG:HA	2:B:267:MET:HE1	1.84	0.60
2:B:936:SER:CB	2:B:1014:LEU:HD22	2.32	0.60
11:P:277:GLU:OE1	11:P:277:GLU:N	2.33	0.60
14:1:1365:ILE:HG13	14:1:1374:VAL:HG12	1.83	0.60
32:j:433:LEU:HD13	32:j:461:LEU:HD13	1.83	0.60
1:A:2087:ASN:O	1:A:2090:ARG:NH1	2.35	0.60
3:D:525:LEU:HD12	3:D:526:LEU:N	2.16	0.60
5:F:545:TYR:HE2	14:1:1795:PRO:C	2.09	0.60
14:1:256:PRO:O	14:1:261:ARG:NH1	2.33	0.60
14:1:760:LEU:O	14:1:761:SER:OG	2.17	0.60
24:b:24:DC:H2''	24:b:25:DC:H5''	1.81	0.60
33:k:8:GLU:OE2	33:k:70:VAL:N	2.34	0.60
2:B:517:MET:HA	2:B:520:ILE:HD12	1.84	0.60
5:F:273:ASN:O	5:F:277:GLY:N	2.34	0.60
11:P:408:ILE:O	11:P:412:ALA:N	2.34	0.60
15:2:764:MET:SD	15:2:765:GLU:N	2.75	0.60
27:e:17:LEU:HD12	27:e:52:VAL:HG13	1.84	0.60
27:e:110:LEU:O	27:e:114:ASN:ND2	2.35	0.60
2:B:83:SER:O	2:B:87:LEU:HD23	2.02	0.60
4:E:865:ALA:HA	4:E:871:LEU:HD21	1.84	0.60
15:2:59:VAL:HG23	15:2:408:PHE:CZ	2.37	0.60
29:g:393:VAL:HG21	29:g:423:VAL:HG13	1.84	0.60
32:j:179:LEU:HD22	32:j:226:TYR:HB3	1.84	0.60
2:B:347:LEU:HD11	2:B:414:LEU:HD22	1.84	0.60
3:D:161:ASP:OD1	3:D:163:SER:N	2.32	0.60
4:E:643:GLN:O	4:E:647:LEU:HD23	2.02	0.60
7:H:444:LYS:HE3	7:H:477:LEU:HD21	1.83	0.60
11:P:189:LEU:HD22	11:P:227:ALA:HB1	1.83	0.60
14:1:511:THR:HG21	15:2:1105:GLU:OE1	2.02	0.60
14:1:1149:ARG:NH2	29:g:525:THR:O	2.34	0.60
15:2:898:THR:O	15:2:899:SER:OG	2.15	0.60
16:3:9:VAL:HG21	22:9:101:LEU:HD11	1.84	0.60
4:E:659:LEU:CD2	4:E:667:VAL:HG11	2.32	0.60
26:d:26:DG:H2'	26:d:26:DG:N3	2.17	0.60
14:1:934:LEU:HD23	14:1:938:LEU:HB3	1.84	0.59
6:G:232:ILE:HG23	6:G:271:LEU:HD12	1.84	0.59
29:g:416:GLN:OE1	29:g:419:ARG:NH2	2.35	0.59
8:I:348:CYS:SG	8:I:349:HIS:N	2.76	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:1066:ASP:OD1	14:1:1067:TRP:N	2.34	0.59
12:Q:8:LYS:O	12:Q:12:GLN:NE2	2.35	0.59
12:Q:39:LEU:HD21	12:Q:153:LEU:HD23	1.84	0.59
14:1:459:ASN:HD22	14:1:469:MET:HE1	1.66	0.59
1:A:231:ILE:HG21	1:A:332:MET:SD	2.43	0.59
3:D:290:MET:HE1	3:D:302:ALA:HB2	1.84	0.59
11:P:538:PHE:CA	11:P:575:VAL:HG23	2.32	0.59
26:d:30:DG:H2'	26:d:31:DT:H71	1.85	0.59
1:A:2160:HIS:ND1	2:B:1194:ILE:HD11	2.18	0.59
15:2:237:VAL:HG23	15:2:269:ILE:HD11	1.84	0.59
29:g:308:ALA:O	29:g:311:THR:OG1	2.20	0.59
32:j:259:GLU:O	32:j:263:VAL:HG23	2.02	0.59
1:A:782:LEU:O	1:A:788:ARG:NH1	2.35	0.59
2:B:485:MET:HA	2:B:485:MET:HE3	1.84	0.59
2:B:558:TYR:HE1	2:B:598:VAL:HG21	1.68	0.59
4:E:659:LEU:HD23	4:E:667:VAL:HG11	1.85	0.59
7:H:570:VAL:HG23	7:H:596:CYS:SG	2.43	0.59
7:H:832:ASN:O	7:H:836:LEU:HD23	2.03	0.59
4:E:864:VAL:HG12	4:E:871:LEU:HD22	1.84	0.59
12:Q:271:ASN:ND2	12:Q:272:GLN:O	2.36	0.59
22:9:18:LYS:HB3	22:9:19:ILE:HD12	1.84	0.59
1:A:523:ARG:NH2	1:A:528:TYR:OH	2.35	0.59
6:G:912:ASP:OD2	6:G:918:TRP:NE1	2.36	0.59
15:2:783:ALA:HB2	15:2:1041:ILE:HG23	1.85	0.59
3:D:878:LYS:N	3:D:881:ASP:OD2	2.36	0.58
11:P:466:LEU:HD23	11:P:508:LEU:HD21	1.84	0.58
15:2:377:LEU:O	20:7:103:ARG:NH1	2.36	0.58
6:G:81:LEU:O	6:G:81:LEU:HD23	2.03	0.58
8:I:519:MET:HE1	8:I:521:GLU:HB3	1.84	0.58
1:A:1079:GLN:OE1	1:A:1130:ARG:NE	2.36	0.58
4:E:757:GLY:HA2	12:Q:282:LEU:HD23	1.84	0.58
29:g:504:LEU:HG	29:g:509:VAL:HG23	1.85	0.58
4:E:817:VAL:HG22	4:E:877:LEU:HD23	1.85	0.58
6:G:103:PHE:HE2	6:G:129:LEU:HD21	1.69	0.58
6:G:478:ILE:HD12	6:G:489:LEU:HD13	1.85	0.58
12:Q:159:VAL:HG12	12:Q:160:ASP:OD1	2.03	0.58
15:2:661:VAL:HG13	15:2:662:VAL:HG13	1.84	0.58
15:2:1050:ARG:NH2	15:2:1054:MET:SD	2.77	0.58
22:9:21:ILE:HD12	22:9:32:LEU:O	2.03	0.58
6:G:915:GLY:C	6:G:916:ILE:HD12	2.29	0.58
8:I:504:VAL:C	8:I:505:LEU:HD22	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:47:ASP:OD1	9:K:49:SER:N	2.35	0.58
9:K:180:ASN:OD1	9:K:182:THR:N	2.33	0.58
12:Q:99:LEU:O	12:Q:103:LEU:HD23	2.04	0.58
15:2:333:GLU:O	15:2:334:LYS:HG2	2.03	0.58
1:A:153:ARG:HA	1:A:204:VAL:HG21	1.86	0.58
3:D:535:ALA:HA	14:1:1765:THR:HG23	1.85	0.58
9:K:456:ILE:HG21	9:K:461:LEU:HD11	1.85	0.58
14:1:126:ILE:O	14:1:130:LEU:HD23	2.04	0.58
14:1:376:ASP:OD2	14:1:473:ARG:NH2	2.36	0.58
1:A:501:GLU:O	1:A:505:GLN:OE1	2.21	0.58
3:D:258:VAL:O	3:D:261:GLN:NE2	2.34	0.58
3:D:868:PRO:CB	6:G:893:LEU:HD23	2.34	0.58
5:F:168:LEU:HB3	5:F:203:THR:HG21	1.85	0.58
7:H:643:ARG:NH2	7:H:679:GLN:OE1	2.36	0.58
22:9:17:LYS:O	22:9:36:ASN:ND2	2.37	0.58
27:e:96:ILE:CD1	27:e:110:LEU:HD11	2.33	0.58
3:D:779:LYS:CB	3:D:802:MET:HE1	2.34	0.58
6:G:856:SER:HB3	6:G:875:ASN:OD1	2.04	0.58
8:I:246:HIS:O	8:I:348:CYS:N	2.37	0.58
20:7:20:CYS:SG	20:7:22:ASN:ND2	2.76	0.58
29:g:292:ALA:HB2	29:g:316:MET:HE2	1.85	0.58
2:B:832:THR:HG21	2:B:880:MET:HE1	1.86	0.58
9:K:3:GLU:HA	9:K:448:THR:HG23	1.86	0.58
11:P:139:ASP:O	11:P:144:ARG:NH2	2.37	0.58
14:1:587:THR:HG23	14:1:590:GLN:H	1.69	0.58
21:8:20:ALA:O	21:8:24:LEU:HD23	2.03	0.58
23:a:52:LEU:CD1	32:j:721:ILE:HG21	2.34	0.58
6:G:558:PHE:O	6:G:562:LEU:HD23	2.03	0.57
14:1:24:GLY:O	15:2:1168:ALA:N	2.36	0.57
14:1:1224:ARG:HB2	14:1:1226:LEU:HD23	1.84	0.57
16:3:71:ILE:HD11	16:3:150:ILE:HD11	1.86	0.57
29:g:362:TYR:O	29:g:366:VAL:HG22	2.03	0.57
32:j:602:VAL:HG22	32:j:643:LEU:CD2	2.34	0.57
2:B:764:VAL:HG13	2:B:765:PRO:HD3	1.86	0.57
3:D:395:VAL:HG12	3:D:419:MET:HE1	1.85	0.57
14:1:966:LEU:HD21	14:1:1043:ILE:HG21	1.85	0.57
14:1:1227:THR:O	14:1:1230:GLN:N	2.33	0.57
15:2:796:MET:HE1	15:2:935:PHE:CZ	2.39	0.57
15:2:1094:GLN:HB3	15:2:1103:LEU:HD12	1.85	0.57
19:6:16:ASP:N	19:6:27:ARG:O	2.36	0.57
2:B:310:ASN:O	2:B:314:ARG:NH2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:P:108:ALA:O	11:P:112:LEU:HD23	2.04	0.57
14:1:957:GLU:OE2	14:1:960:ARG:NH2	2.37	0.57
1:A:703:ASP:O	1:A:707:ASN:ND2	2.38	0.57
1:A:2126:MET:HE1	1:A:2158:LEU:HD13	1.86	0.57
4:E:881:LEU:CD2	4:E:910:LEU:HD22	2.35	0.57
6:G:46:VAL:O	6:G:46:VAL:HG22	2.03	0.57
7:H:898:ALA:HB2	7:H:916:LEU:HD21	1.87	0.57
8:I:595:VAL:HG11	8:I:608:VAL:HG21	1.86	0.57
8:I:622:ALA:HB2	8:I:643:LEU:HD13	1.86	0.57
14:1:1211:LEU:HD21	14:1:1258:ARG:HB3	1.87	0.57
14:1:1474:LEU:HD11	18:5:107:ARG:HH11	1.68	0.57
15:2:155:MET:HE2	15:2:185:PHE:CE1	2.39	0.57
18:5:97:LEU:HA	18:5:102:ILE:HD11	1.86	0.57
27:e:54:LEU:HD21	29:g:236:HIS:CG	2.40	0.57
1:A:1624:MET:SD	1:A:1625:LEU:N	2.77	0.57
9:K:180:ASN:OD1	9:K:181:MET:N	2.37	0.57
19:6:35:PHE:HB2	19:6:37:MET:HE1	1.86	0.57
32:j:508:MET:HA	32:j:508:MET:HE3	1.87	0.57
3:D:420:PHE:O	3:D:428:ARG:NE	2.36	0.57
15:2:780:VAL:HG12	15:2:965:ILE:HB	1.87	0.57
17:4:138:ASN:OD1	17:4:139:ILE:N	2.38	0.57
21:8:8:PHE:H	21:8:48:MET:HE1	1.70	0.57
33:k:34:VAL:HG21	33:k:72:TYR:OH	2.05	0.57
1:A:1728:GLN:OE1	1:A:1728:GLN:N	2.38	0.57
4:E:487:GLU:OE1	4:E:490:ARG:NH1	2.35	0.57
4:E:522:LEU:HD22	4:E:535:ALA:HB2	1.86	0.57
8:I:1:MET:HE2	8:I:1:MET:N	2.20	0.57
15:2:771:GLU:C	15:2:772:LEU:HD12	2.29	0.57
15:2:848:LEU:HD11	15:2:852:GLY:C	2.29	0.57
1:A:835:SER:OG	1:A:843:ARG:NH1	2.38	0.57
7:H:699:ALA:HB3	7:H:713:THR:HG21	1.86	0.57
14:1:1211:LEU:HD12	14:1:1260:ARG:HG3	1.87	0.57
15:2:715:ASP:OD1	15:2:716:HIS:ND1	2.37	0.57
15:2:985:LEU:HD11	15:2:1015:LEU:CD1	2.34	0.57
19:6:5:LEU:N	19:6:60:ILE:O	2.38	0.57
1:A:893:ASP:OD1	1:A:894:LEU:N	2.37	0.57
1:A:1695:LEU:HD13	1:A:1739:ILE:HD13	1.86	0.57
7:H:362:VAL:O	7:H:366:LEU:HD23	2.03	0.57
7:H:458:MET:SD	7:H:459:ILE:N	2.78	0.57
8:I:35:THR:HG23	8:I:81:PRO:HB3	1.86	0.57
14:1:192:ARG:NH1	14:1:199:TYR:HB2	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:k:108:ILE:HD11	33:k:145:LEU:HD22	1.87	0.57
3:D:168:ASN:OD1	3:D:169:LYS:N	2.38	0.56
11:P:466:LEU:CD2	11:P:508:LEU:HD21	2.35	0.56
1:A:1296:ARG:CZ	2:B:76:SER:HB2	2.36	0.56
7:H:429:GLU:OE1	7:H:429:GLU:N	2.37	0.56
8:I:497:MET:CE	8:I:505:LEU:HD12	2.36	0.56
11:P:22:ASN:ND2	11:P:24:ASP:OD1	2.37	0.56
15:2:83:ARG:NH1	15:2:132:VAL:O	2.38	0.56
15:2:594:MET:HE1	15:2:658:ALA:HA	1.87	0.56
15:2:939:HIS:NE2	15:2:983:GLU:OE1	2.38	0.56
2:B:426:VAL:HG13	2:B:476:PHE:HE1	1.68	0.56
3:D:518:VAL:HA	3:D:521:LEU:HD13	1.87	0.56
4:E:773:ILE:HG23	7:H:398:THR:HA	1.87	0.56
4:E:857:LEU:O	4:E:861:LEU:HD23	2.04	0.56
11:P:52:LEU:HD11	11:P:89:LEU:HA	1.86	0.56
11:P:98:THR:O	11:P:98:THR:HG23	2.06	0.56
11:P:382:LEU:O	11:P:386:SER:OG	2.23	0.56
14:1:133:SER:OG	14:1:140:ARG:NE	2.33	0.56
14:1:1221:MET:HE3	14:1:1226:LEU:O	2.04	0.56
29:g:307:PRO:HA	29:g:310:ILE:HG22	1.87	0.56
1:A:221:ASN:ND2	1:A:320:GLU:OE2	2.38	0.56
7:H:105:VAL:HB	7:H:184:THR:HG23	1.86	0.56
14:1:87:HIS:NE2	14:1:89:GLU:OE2	2.37	0.56
14:1:1143:LEU:CB	14:1:1148:ALA:HB2	2.35	0.56
1:A:686:VAL:O	1:A:686:VAL:HG12	2.06	0.56
2:B:103:GLN:CG	2:B:147:LEU:HD23	2.34	0.56
3:D:484:LEU:O	3:D:488:GLU:OE1	2.23	0.56
15:2:509:VAL:HG11	15:2:524:LYS:HB3	1.87	0.56
32:j:519:GLN:NE2	32:j:520:LEU:O	2.39	0.56
4:E:851:PHE:HZ	4:E:877:LEU:HD12	1.71	0.56
7:H:648:MET:HE1	7:H:651:PRO:HD3	1.86	0.56
14:1:457:ILE:HD12	14:1:470:MET:O	2.05	0.56
14:1:522:PRO:HA	14:1:525:ILE:HD11	1.86	0.56
15:2:420:GLN:NE2	15:2:424:ASP:OD1	2.39	0.56
27:e:88:PRO:C	27:e:92:MET:HE3	2.30	0.56
1:A:328:TYR:CE2	1:A:332:MET:HE1	2.40	0.56
1:A:1911:VAL:O	1:A:1915:LEU:HD23	2.06	0.56
1:A:2117:ILE:O	1:A:2117:ILE:HG22	2.05	0.56
3:D:645:ARG:NH1	3:D:649:LEU:HD13	2.21	0.56
29:g:431:VAL:HG13	29:g:451:HIS:ND1	2.20	0.56
29:g:525:THR:HG22	29:g:526:ASP:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:g:566:ILE:HD11	29:g:575:VAL:HG22	1.88	0.56
1:A:2146:GLU:OE1	1:A:2146:GLU:N	2.36	0.56
8:I:101:ILE:HD12	8:I:107:MET:HB3	1.86	0.56
8:I:108:MET:HA	8:I:108:MET:HE2	1.87	0.56
15:2:760:THR:O	15:2:999:ALA:N	2.38	0.56
1:A:1694:SER:O	1:A:1698:LEU:HD23	2.06	0.56
2:B:265:ARG:O	2:B:268:VAL:HG12	2.05	0.56
2:B:436:LEU:HD11	2:B:452:MET:CG	2.36	0.56
7:H:772:ILE:O	7:H:775:SER:OG	2.20	0.56
7:H:857:LEU:HD23	7:H:991:ALA:HA	1.88	0.56
14:1:599:HIS:O	14:1:600:ILE:HD13	2.05	0.56
17:4:14:ARG:HG3	17:4:18:MET:HE1	1.87	0.56
32:j:627:LYS:NZ	33:k:105:SER:OG	2.35	0.56
2:B:43:ARG:NH1	2:B:43:ARG:O	2.38	0.56
3:D:201:GLY:O	3:D:236:GLN:NE2	2.39	0.56
3:D:216:ILE:HG21	3:D:251:ALA:CB	2.36	0.56
5:F:192:ASP:OD1	5:F:197:THR:OG1	2.23	0.56
6:G:793:ARG:O	6:G:796:PHE:N	2.39	0.56
7:H:565:LEU:O	7:H:569:LEU:HD13	2.06	0.56
7:H:593:PHE:HB3	7:H:615:MET:HE1	1.88	0.56
15:2:509:VAL:HG13	15:2:525:ASN:O	2.06	0.56
6:G:465:ASP:OD1	6:G:466:GLY:N	2.39	0.55
6:G:884:HIS:ND1	6:G:885:ASN:N	2.54	0.55
1:A:2074:SER:HB3	1:A:2081:LEU:HD21	1.87	0.55
4:E:571:THR:O	4:E:575:LEU:HD23	2.07	0.55
14:1:1316:ASN:OD1	14:1:1317:LYS:N	2.39	0.55
14:1:1759:SER:HB2	14:1:1762:TYR:HB2	1.87	0.55
15:2:59:VAL:HG11	15:2:91:ILE:HD11	1.88	0.55
15:2:455:ASP:OD1	15:2:456:GLN:N	2.33	0.55
15:2:1117:HIS:CE1	15:2:1148:LEU:HD12	2.41	0.55
6:G:609:THR:OG1	6:G:611:LEU:O	2.24	0.55
14:1:95:PHE:O	14:1:311:GLN:NE2	2.38	0.55
15:2:1132:THR:HG23	15:2:1134:THR:HG23	1.88	0.55
26:d:21:DT:H2''	26:d:22:DC:H5'	1.87	0.55
2:B:1038:CYS:HB2	2:B:1064:LEU:HD11	1.88	0.55
14:1:457:ILE:O	14:1:503:LEU:HD12	2.06	0.55
1:A:1253:ILE:HG22	1:A:1257:SER:HB2	1.88	0.55
3:D:253:VAL:CG1	3:D:290:MET:HE2	2.36	0.55
7:H:550:VAL:HG22	7:H:574:MET:SD	2.46	0.55
7:H:611:MET:HE3	7:H:615:MET:HE3	1.87	0.55
7:H:840:ALA:HB1	7:H:856:TYR:CE2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Q:45:VAL:HG23	12:Q:45:VAL:O	2.06	0.55
17:4:148:HIS:CD2	17:4:179:VAL:HG11	2.42	0.55
27:e:92:MET:HE1	29:g:198:LEU:HD22	1.87	0.55
4:E:585:GLU:OE1	4:E:599:PHE:N	2.40	0.55
4:E:753:VAL:HG12	12:Q:283:LYS:HD3	1.89	0.55
6:G:420:ALA:CB	6:G:456:ILE:HD12	2.36	0.55
17:4:102:ALA:HB3	17:4:127:LEU:HD22	1.88	0.55
5:F:235:PHE:HZ	5:F:268:ILE:HD11	1.71	0.55
7:H:867:PHE:CE1	7:H:987:LEU:HD13	2.41	0.55
9:K:485:MET:SD	9:K:487:ASP:N	2.80	0.55
11:P:119:HIS:O	11:P:157:ARG:NH1	2.40	0.55
14:1:962:ASP:O	14:1:966:LEU:HD23	2.07	0.55
29:g:310:ILE:HD13	29:g:356:TYR:CD1	2.42	0.55
2:B:15:LEU:HD11	2:B:174:LEU:HD21	1.89	0.55
11:P:199:ASP:OD1	11:P:200:ASN:N	2.39	0.55
15:2:838:GLN:O	15:2:890:ARG:NH2	2.37	0.55
29:g:514:SER:OG	29:g:518:LYS:NZ	2.40	0.55
1:A:547:VAL:O	1:A:551:LEU:HD23	2.07	0.55
2:B:588:LEU:HD11	2:B:593:LEU:HD11	1.89	0.55
2:B:899:THR:O	2:B:899:THR:HG22	2.06	0.55
2:B:1029:VAL:HG12	2:B:1035:MET:CE	2.37	0.55
14:1:723:ASN:ND2	20:7:108:MET:O	2.36	0.55
15:2:600:GLU:OE2	15:2:620:ARG:NH1	2.40	0.55
18:5:71:LEU:HD23	18:5:75:MET:CE	2.31	0.55
1:A:1205:LEU:O	1:A:1209:SER:N	2.37	0.55
2:B:15:LEU:HD12	2:B:209:TRP:NE1	2.21	0.55
3:D:478:THR:HG23	3:D:481:GLY:H	1.72	0.55
9:K:52:THR:HG22	9:K:60:PHE:CD2	2.42	0.55
15:2:239:MET:HB2	15:2:372:LEU:HD21	1.88	0.55
1:A:428:ARG:NH2	1:A:467:GLN:OE1	2.41	0.54
1:A:466:LEU:HD21	1:A:509:GLU:O	2.07	0.54
4:E:565:THR:HG22	4:E:566:LEU:N	2.21	0.54
7:H:419:LEU:HD22	7:H:462:HIS:CG	2.42	0.54
7:H:529:LEU:HD23	7:H:569:LEU:HD12	1.88	0.54
8:I:401:ARG:NH2	8:I:435:PRO:HG2	2.21	0.54
27:e:175:ARG:NE	29:g:457:GLU:OE1	2.40	0.54
33:k:143:ILE:HG22	33:k:170:LEU:HA	1.89	0.54
3:D:287:ILE:O	3:D:291:VAL:HG23	2.07	0.54
8:I:27:ASP:OD1	8:I:236:TYR:OH	2.25	0.54
11:P:334:VAL:HG11	11:P:368:LEU:HD11	1.89	0.54
14:1:366:VAL:O	14:1:481:THR:OG1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2:540:PRO:HB3	15:2:596:ILE:HD11	1.89	0.54
16:3:5:ASN:ND2	16:3:25:ASN:OD1	2.40	0.54
29:g:129:PRO:O	29:g:133:ASP:N	2.40	0.54
2:B:1025:LEU:O	2:B:1029:VAL:HG13	2.07	0.54
5:F:556:LEU:HD21	5:F:560:ARG:NH2	2.21	0.54
8:I:626:ILE:HD11	8:I:647:LEU:HD11	1.88	0.54
14:1:57:LEU:HD11	14:1:281:ALA:N	2.22	0.54
14:1:458:PHE:HD1	14:1:503:LEU:HD13	1.72	0.54
24:b:42:DT:H3	26:d:7:DA:H61	1.55	0.54
7:H:74:ASP:O	7:H:79:ARG:NH2	2.38	0.54
8:I:591:VAL:HG21	8:I:615:HIS:HB2	1.90	0.54
15:2:25:ALA:O	15:2:28:ILE:HG22	2.07	0.54
29:g:305:LEU:HD12	29:g:310:ILE:HD12	1.90	0.54
7:H:856:TYR:CD2	7:H:884:MET:HE1	2.43	0.54
29:g:228:ALA:HA	29:g:231:VAL:HG22	1.88	0.54
34:l:33:LEU:HD12	34:l:80:ILE:HG23	1.88	0.54
3:D:484:LEU:O	3:D:487:VAL:HG22	2.08	0.54
6:G:135:GLU:OE1	6:G:135:GLU:N	2.40	0.54
6:G:155:VAL:HG11	6:G:193:LEU:HD21	1.90	0.54
22:9:42:LEU:CD1	22:9:45:ILE:HD11	2.36	0.54
1:A:895:VAL:HG13	1:A:913:PHE:CE2	2.43	0.54
1:A:1167:VAL:HA	1:A:1170:MET:HE2	1.89	0.54
7:H:347:GLU:O	7:H:351:THR:HG23	2.08	0.54
11:P:51:LEU:HD23	11:P:55:LEU:HD23	1.90	0.54
11:P:448:MET:HE2	11:P:485:LYS:HB2	1.90	0.54
14:1:672:ILE:HG23	14:1:676:ILE:HD12	1.90	0.54
14:1:1343:LEU:HD23	14:1:1344:MET:N	2.23	0.54
15:2:628:VAL:HG22	15:2:630:LYS:O	2.07	0.54
1:A:375:LEU:HD22	1:A:384:ALA:HB1	1.89	0.54
1:A:441:THR:O	1:A:445:VAL:HG23	2.07	0.54
1:A:1788:GLN:OE1	1:A:1790:TRP:NE1	2.37	0.54
1:A:2163:PHE:CE2	1:A:2167:MET:HE3	2.43	0.54
2:B:577:ILE:CD1	2:B:595:LEU:HD21	2.37	0.54
2:B:1061:LEU:HD21	2:B:1076:VAL:HG12	1.89	0.54
3:D:500:ARG:NH1	3:D:501:ASP:OD1	2.41	0.54
8:I:32:MET:HE3	8:I:397:HIS:HE1	1.73	0.54
15:2:383:ASP:OD1	15:2:384:ASP:N	2.41	0.54
6:G:478:ILE:HG23	6:G:489:LEU:HD11	1.90	0.54
6:G:507:VAL:HG23	6:G:510:LYS:HD2	1.89	0.54
6:G:604:LEU:HD11	6:G:614:LEU:HD22	1.89	0.54
7:H:26:GLU:HB3	7:H:33:LEU:HD13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:419:LEU:HD21	7:H:459:ILE:HD12	1.89	0.54
8:I:470:VAL:HG22	8:I:497:MET:SD	2.47	0.54
12:Q:159:VAL:C	12:Q:160:ASP:OD1	2.50	0.54
15:2:1095:ILE:CD1	15:2:1103:LEU:HD13	2.38	0.54
17:4:84:ILE:H	17:4:84:ILE:HD12	1.72	0.54
11:P:492:ASP:OD2	11:P:497:HIS:ND1	2.38	0.54
14:1:51:ARG:HH22	32:j:530:VAL:HG12	1.73	0.54
14:1:486:LEU:HB3	14:1:538:VAL:HG21	1.89	0.54
15:2:837:CYS:SG	15:2:838:GLN:N	2.81	0.54
32:j:737:HIS:ND1	32:j:737:HIS:O	2.40	0.54
3:D:452:VAL:O	3:D:455:VAL:HG12	2.08	0.53
4:E:917:GLY:O	4:E:918:SER:OG	2.14	0.53
6:G:340:ARG:NH2	6:G:378:ASP:O	2.41	0.53
7:H:504:SER:HB2	7:H:507:VAL:HG12	1.89	0.53
8:I:205:LEU:O	8:I:208:ALA:N	2.41	0.53
11:P:361:THR:HG22	11:P:365:LEU:HD12	1.90	0.53
15:2:300:MET:HG3	15:2:377:LEU:HD21	1.88	0.53
18:5:71:LEU:CD2	18:5:75:MET:HE2	2.33	0.53
1:A:488:LYS:NZ	1:A:532:GLU:OE2	2.35	0.53
1:A:648:ILE:HG22	1:A:694:LEU:HD23	1.90	0.53
2:B:771:VAL:O	2:B:775:ILE:HD12	2.08	0.53
3:D:197:GLN:OE1	3:D:230:HIS:ND1	2.40	0.53
9:K:341:ALA:HA	9:K:382:MET:HE3	1.90	0.53
14:1:373:LEU:HD23	14:1:373:LEU:H	1.73	0.53
15:2:159:THR:HG23	15:2:160:TYR:CD1	2.44	0.53
15:2:736:TYR:CE2	15:2:737:ILE:HG22	2.42	0.53
15:2:786:THR:O	15:2:786:THR:HG22	2.08	0.53
14:1:1465:PRO:HA	14:1:1470:CYS:HA	1.90	0.53
15:2:411:LEU:HD13	15:2:439:ILE:CG2	2.39	0.53
15:2:702:MET:HA	15:2:702:MET:HE2	1.89	0.53
3:D:384:GLU:O	3:D:384:GLU:HG2	2.07	0.53
6:G:356:ASN:HB3	6:G:359:ILE:HD12	1.91	0.53
7:H:803:ILE:HG23	7:H:803:ILE:O	2.09	0.53
12:Q:39:LEU:CD2	12:Q:153:LEU:HD23	2.39	0.53
14:1:1417:HIS:CG	24:b:28:DA:H4'	2.44	0.53
17:4:194:ILE:HD12	17:4:204:ILE:HG22	1.90	0.53
20:7:19:GLU:N	20:7:19:GLU:OE2	2.39	0.53
6:G:261:LYS:NZ	6:G:262:ASN:OD1	2.38	0.53
9:K:534:LEU:HD13	9:K:553:VAL:HG21	1.90	0.53
11:P:183:ARG:HG2	11:P:220:VAL:HG12	1.90	0.53
14:1:1061:SER:OG	14:1:1063:GLU:OE1	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2:1030:ASN:OD1	15:2:1031:GLY:N	2.41	0.53
16:3:69:GLY:HA3	23:a:57:ALA:HB1	1.90	0.53
27:e:166:LYS:NZ	29:g:539:ASP:O	2.42	0.53
33:k:39:THR:HG23	33:k:42:TYR:H	1.74	0.53
33:k:134:ASP:OD1	33:k:135:ILE:N	2.41	0.53
34:l:16:ASP:OD1	34:l:17:ALA:N	2.42	0.53
2:B:452:MET:HE1	2:B:520:ILE:HG21	1.89	0.53
6:G:420:ALA:HB3	6:G:456:ILE:HD12	1.91	0.53
7:H:419:LEU:HD22	7:H:462:HIS:ND1	2.24	0.53
7:H:830:PRO:O	7:H:836:LEU:HD21	2.09	0.53
9:K:37:MET:CG	25:c:25:A:C6	2.91	0.53
12:Q:290:ASP:CG	12:Q:291:PRO:HD2	2.33	0.53
14:1:1169:VAL:HG12	14:1:1216:LEU:HD12	1.91	0.53
26:d:28:DG:H5"	26:d:28:DG:H8	1.73	0.53
2:B:142:VAL:O	2:B:146:LEU:HD23	2.09	0.53
2:B:1009:PRO:O	2:B:1012:ALA:N	2.42	0.53
11:P:494:ASN:OD1	11:P:496:LEU:N	2.30	0.53
12:Q:223:ASP:OD1	12:Q:223:ASP:C	2.51	0.53
33:k:87:ALA:N	33:k:143:ILE:O	2.38	0.53
1:A:1866:CYS:SG	1:A:1867:ARG:N	2.81	0.53
6:G:111:ILE:HD11	6:G:123:LEU:HD21	1.91	0.53
7:H:343:GLN:NE2	7:H:347:GLU:OE2	2.41	0.53
9:K:31:LEU:HD23	9:K:65:ILE:HB	1.91	0.53
14:1:67:ARG:HA	14:1:78:MET:HE3	1.90	0.53
15:2:266:GLU:OE1	15:2:266:GLU:N	2.42	0.53
1:A:457:ASN:O	1:A:461:VAL:HG23	2.07	0.53
4:E:841:VAL:HG22	4:E:845:LEU:HD23	1.91	0.53
6:G:453:LEU:C	6:G:453:LEU:HD23	2.34	0.53
6:G:580:GLU:OE2	6:G:581:GLU:N	2.41	0.53
6:G:763:ASN:OD1	6:G:764:ARG:N	2.41	0.53
6:G:780:ALA:O	6:G:784:LEU:HD23	2.09	0.53
7:H:377:LEU:HA	7:H:380:ILE:HD12	1.91	0.53
7:H:593:PHE:HB3	7:H:615:MET:CE	2.39	0.53
7:H:667:MET:SD	7:H:668:LEU:N	2.81	0.53
9:K:92:MET:HE2	9:K:97:GLN:N	2.24	0.53
14:1:232:GLU:O	14:1:236:LEU:HD23	2.09	0.53
14:1:340:LYS:HZ2	14:1:1436:VAL:HG11	1.74	0.53
14:1:364:ARG:NH1	14:1:502:ASN:OD1	2.42	0.53
14:1:367:ILE:HD13	14:1:501:MET:CE	2.37	0.53
17:4:138:ASN:OD1	17:4:140:THR:N	2.42	0.53
25:c:42:C:H42	26:d:29:DG:H1	1.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1277:GLU:HA	1:A:1280:ILE:HD12	1.90	0.53
1:A:1719:ARG:NH2	2:B:1204:ILE:HD12	2.23	0.53
8:I:338:GLU:O	8:I:342:ILE:HG23	2.09	0.53
8:I:554:GLN:OE1	8:I:554:GLN:N	2.42	0.53
15:2:853:LEU:O	23:a:46:LYS:NZ	2.42	0.53
23:a:38:GLU:OE1	23:a:38:GLU:N	2.42	0.53
1:A:958:LEU:HD12	1:A:997:VAL:HG11	1.89	0.52
1:A:2069:ASP:O	1:A:2073:MET:SD	2.67	0.52
2:B:658:TYR:CE1	2:B:662:LEU:HD21	2.44	0.52
12:Q:120:SER:O	12:Q:124:THR:HG23	2.09	0.52
14:1:118:LEU:O	14:1:118:LEU:HD23	2.09	0.52
14:1:600:ILE:HD11	14:1:660:MET:CE	2.39	0.52
24:b:44:DG:H2''	24:b:45:DG:C8	2.44	0.52
29:g:485:ASP:OD1	29:g:486:VAL:N	2.42	0.52
34:l:84:ARG:HH22	34:l:87:LEU:HD12	1.74	0.52
6:G:48:PHE:O	6:G:51:LEU:N	2.42	0.52
6:G:105:LYS:HE3	14:1:1769:TYR:CE1	2.43	0.52
6:G:236:HIS:O	6:G:239:THR:HG22	2.08	0.52
11:P:141:PHE:CB	11:P:180:MET:HE3	2.37	0.52
14:1:1366:PHE:HA	14:1:1374:VAL:HG11	1.91	0.52
2:B:1014:LEU:HD21	2:B:1018:GLN:NE2	2.23	0.52
3:D:515:PRO:O	3:D:518:VAL:HG12	2.10	0.52
4:E:531:GLU:OE1	4:E:531:GLU:N	2.39	0.52
7:H:272:GLU:OE1	7:H:272:GLU:N	2.42	0.52
7:H:558:ILE:HD11	7:H:570:VAL:HG22	1.90	0.52
8:I:146:ARG:O	8:I:147:VAL:HG23	2.09	0.52
8:I:191:LEU:HD13	8:I:194:ILE:HD12	1.91	0.52
14:1:621:ILE:HG23	14:1:621:ILE:O	2.10	0.52
14:1:629:VAL:HG12	14:1:631:GLU:OE1	2.09	0.52
15:2:601:VAL:CG2	15:2:616:THR:HG22	2.40	0.52
15:2:1112:ASP:OD1	15:2:1112:ASP:N	2.43	0.52
23:a:54:VAL:HG23	23:a:54:VAL:O	2.09	0.52
1:A:1225:ARG:NH2	1:A:1251:PHE:O	2.42	0.52
1:A:1888:LEU:HD12	1:A:1888:LEU:O	2.09	0.52
2:B:732:GLU:O	2:B:733:ILE:HD13	2.10	0.52
3:D:561:MET:HA	3:D:564:LEU:HD13	1.90	0.52
3:D:779:LYS:HB2	3:D:802:MET:HE1	1.90	0.52
6:G:273:ILE:HD11	6:G:311:MET:SD	2.49	0.52
12:Q:252:HIS:O	12:Q:255:ASN:ND2	2.43	0.52
27:e:61:LEU:HD11	27:e:106:LEU:HD21	1.92	0.52
27:e:119:ASP:O	27:e:123:GLU:OE1	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:LEU:HD12	1:A:419:LEU:HD11	1.92	0.52
2:B:265:ARG:HD3	2:B:301:PHE:CE1	2.45	0.52
2:B:1070:LEU:HD11	14:1:1764:PRO:HB2	1.89	0.52
6:G:107:ILE:HD12	6:G:125:MET:SD	2.50	0.52
20:7:32:ASN:OD1	20:7:34:ILE:HG22	2.10	0.52
29:g:338:MET:HE1	29:g:426:GLY:HA2	1.91	0.52
1:A:515:PHE:CZ	1:A:519:LEU:HD11	2.44	0.52
1:A:531:MET:HA	1:A:531:MET:HE2	1.91	0.52
3:D:815:GLU:OE1	3:D:816:GLN:N	2.41	0.52
4:E:937:PHE:O	4:E:941:LEU:HD23	2.09	0.52
5:F:238:ALA:HB2	5:F:308:LYS:HB3	1.91	0.52
11:P:405:LEU:O	11:P:408:ILE:HG22	2.09	0.52
14:1:861:GLN:HE22	14:1:865:ILE:HD12	1.74	0.52
14:1:1400:LEU:O	14:1:1404:THR:HG23	2.09	0.52
15:2:772:LEU:N	15:2:773:PRO:HD3	2.25	0.52
26:d:11:DC:H2''	26:d:12:DC:H5'	1.92	0.52
1:A:1304:PHE:CE2	1:A:1308:LEU:HD11	2.45	0.52
1:A:1836:ASP:HA	1:A:1862:ALA:HB1	1.92	0.52
2:B:1115:PRO:N	2:B:1116:PRO:HD2	2.24	0.52
3:D:791:LYS:N	3:D:794:GLU:OE2	2.42	0.52
7:H:783:VAL:HG23	7:H:783:VAL:O	2.10	0.52
11:P:570:ASP:OD2	11:P:575:VAL:HG11	2.10	0.52
17:4:83:GLY:O	17:4:87:ILE:HG23	2.10	0.52
29:g:562:ILE:HD12	29:g:562:ILE:H	1.74	0.52
1:A:593:LEU:O	1:A:598:PRO:HD3	2.10	0.52
2:B:578:TYR:HE1	2:B:627:ILE:HD11	1.75	0.52
2:B:1091:LEU:HD11	2:B:1095:LYS:CB	2.40	0.52
9:K:327:MET:CE	9:K:355:VAL:HG23	2.40	0.52
11:P:240:LEU:O	11:P:244:VAL:HG22	2.09	0.52
15:2:564:ALA:HB3	15:2:576:ILE:HD12	1.92	0.52
29:g:279:ILE:O	29:g:283:LEU:HD23	2.10	0.52
32:j:498:ASN:OD1	32:j:499:PHE:N	2.43	0.52
2:B:508:VAL:C	2:B:509:ILE:HD13	2.35	0.52
6:G:806:LEU:HD23	6:G:806:LEU:O	2.10	0.52
7:H:55:LEU:HD12	7:H:107:VAL:HG13	1.91	0.52
7:H:843:TYR:CD2	7:H:851:ALA:HB1	2.45	0.52
14:1:232:GLU:HA	14:1:235:VAL:HG12	1.91	0.52
14:1:239:GLU:OE1	14:1:241:ARG:N	2.42	0.52
29:g:427:VAL:O	29:g:431:VAL:HG23	2.10	0.52
2:B:191:LEU:C	2:B:192:LEU:HD22	2.35	0.52
2:B:621:GLU:O	2:B:625:LEU:HD23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:834:ASN:OD1	2:B:848:TYR:N	2.43	0.52
3:D:659:PHE:CE2	3:D:811:LEU:HD21	2.45	0.52
7:H:839:GLN:NE2	7:H:839:GLN:O	2.42	0.52
11:P:99:VAL:O	11:P:105:ARG:NH1	2.43	0.52
14:1:432:HIS:CE1	32:j:728:THR:HG22	2.44	0.52
14:1:977:VAL:HG13	14:1:979:LEU:HD23	1.91	0.52
32:j:751:THR:O	32:j:753:VAL:N	2.42	0.52
1:A:130:GLU:HA	1:A:138:ILE:HD11	1.92	0.51
1:A:2111:MET:HE1	1:A:2118:ALA:N	2.25	0.51
3:D:915:LEU:HB2	3:D:948:PHE:CE1	2.45	0.51
19:6:64:LEU:HD23	19:6:142:TYR:CE2	2.45	0.51
29:g:533:PHE:O	29:g:537:VAL:HG23	2.10	0.51
33:k:94:LYS:O	33:k:110:ARG:NH1	2.43	0.51
2:B:35:ALA:HA	2:B:74:LEU:HD21	1.92	0.51
14:1:1208:SER:OG	14:1:1210:TRP:O	2.22	0.51
15:2:844:ILE:HG21	32:j:725:LYS:HZ2	1.75	0.51
16:3:149:LEU:HD23	16:3:150:ILE:N	2.24	0.51
16:3:187:ASP:OD1	16:3:191:ALA:N	2.43	0.51
22:9:102:GLU:O	22:9:106:ARG:HG3	2.11	0.51
27:e:100:PHE:HB2	27:e:106:LEU:HD23	1.93	0.51
1:A:594:HIS:HB2	1:A:659:ILE:HD11	1.92	0.51
2:B:91:ASP:OD1	2:B:92:PHE:N	2.43	0.51
2:B:314:ARG:HD3	2:B:398:ILE:HD11	1.91	0.51
6:G:188:ALA:O	6:G:189:THR:OG1	2.15	0.51
6:G:390:LEU:O	6:G:394:LEU:HD23	2.11	0.51
14:1:702:ILE:CD1	14:1:752:THR:HG23	2.41	0.51
15:2:732:ALA:HB1	15:2:1049:GLN:HB3	1.93	0.51
27:e:27:PRO:O	27:e:28:SER:OG	2.21	0.51
4:E:568:PRO:HA	4:E:571:THR:HG22	1.92	0.51
4:E:690:GLN:OE1	7:H:988:GLN:NE2	2.42	0.51
8:I:99:ILE:HD12	8:I:119:PHE:CE2	2.45	0.51
8:I:329:ILE:HD13	8:I:379:ILE:HG22	1.91	0.51
15:2:746:THR:HG22	15:2:747:LEU:HD23	1.91	0.51
15:2:1165:MET:O	15:2:1166:SER:OG	2.26	0.51
17:4:131:LEU:HD23	17:4:133:GLN:H	1.75	0.51
2:B:1149:ARG:HE	2:B:1150:LEU:HD21	1.74	0.51
3:D:561:MET:N	3:D:562:PRO:HD2	2.25	0.51
9:K:71:LEU:C	9:K:73:HIS:H	2.18	0.51
14:1:450:MET:HE2	14:1:505:LEU:HD22	1.93	0.51
14:1:652:LEU:C	14:1:652:LEU:HD23	2.35	0.51
15:2:420:GLN:HA	15:2:423:ILE:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:9:60:GLY:O	22:9:73:ILE:HG23	2.10	0.51
28:f:235:CYS:N	28:f:306:CYS:O	2.44	0.51
33:k:1:MET:N	33:k:78:ARG:O	2.44	0.51
7:H:420:GLU:OE2	7:H:424:ARG:HD2	2.11	0.51
14:1:30:GLU:HB3	14:1:34:MET:HE1	1.93	0.51
14:1:402:LEU:O	14:1:406:VAL:HG23	2.11	0.51
14:1:1157:ILE:HD13	14:1:1160:ARG:HD3	1.92	0.51
15:2:903:ILE:HG22	15:2:904:VAL:N	2.26	0.51
16:3:71:ILE:HD11	16:3:150:ILE:CD1	2.40	0.51
19:6:6:PHE:CZ	19:6:37:MET:HE3	2.45	0.51
21:8:2:ILE:HG22	21:8:3:ILE:N	2.25	0.51
6:G:221:LEU:HD23	6:G:221:LEU:C	2.36	0.51
7:H:529:LEU:CD2	7:H:569:LEU:HD12	2.41	0.51
12:Q:22:GLN:N	12:Q:22:GLN:OE1	2.41	0.51
15:2:803:ARG:NH1	21:8:8:PHE:O	2.44	0.51
19:6:95:LYS:C	19:6:116:VAL:HG23	2.36	0.51
24:b:27:DG:H2''	24:b:28:DA:C8	2.46	0.51
29:g:477:PHE:O	29:g:493:LYS:NZ	2.30	0.51
1:A:616:LEU:O	1:A:682:ARG:NH1	2.41	0.51
1:A:1868:LYS:NZ	1:A:2151:CYS:O	2.44	0.51
2:B:832:THR:CG2	2:B:880:MET:HE1	2.40	0.51
3:D:301:GLN:OE1	3:D:301:GLN:N	2.44	0.51
6:G:225:TYR:N	6:G:226:PRO:HD3	2.26	0.51
6:G:552:GLN:O	6:G:553:VAL:HG22	2.10	0.51
8:I:145:GLU:O	8:I:146:ARG:HB3	2.09	0.51
12:Q:4:LYS:HB3	12:Q:8:LYS:HZ1	1.75	0.51
15:2:523:VAL:O	15:2:523:VAL:HG12	2.10	0.51
33:k:93:ASN:OD1	33:k:94:LYS:N	2.44	0.51
2:B:50:VAL:HG11	2:B:84:ILE:HG21	1.92	0.51
2:B:764:VAL:HG23	2:B:771:VAL:HG21	1.93	0.51
7:H:899:ILE:HG21	7:H:986:PHE:CD1	2.46	0.51
14:1:540:ASP:OD2	15:2:790:GLN:HA	2.11	0.51
15:2:370:HIS:O	15:2:374:LEU:HD23	2.11	0.51
1:A:649:LEU:HB2	1:A:652:THR:HG23	1.93	0.51
2:B:600:ILE:HD11	2:B:658:TYR:CG	2.46	0.51
2:B:772:MET:HE2	2:B:772:MET:HA	1.93	0.51
3:D:840:GLY:HA3	8:I:411:LEU:HD11	1.93	0.51
6:G:671:MET:HE2	6:G:671:MET:HA	1.92	0.51
7:H:463:GLU:OE1	7:H:463:GLU:N	2.35	0.51
8:I:242:LEU:HD23	8:I:242:LEU:H	1.74	0.51
14:1:978:VAL:O	14:1:979:LEU:HD22	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:1304:ILE:O	14:1:1304:ILE:HG23	2.11	0.51
15:2:41:ARG:NH2	15:2:45:ASP:OD1	2.44	0.51
29:g:411:LEU:HD11	29:g:454:LEU:HD21	1.93	0.51
2:B:201:LEU:HD23	2:B:211:LEU:HD13	1.91	0.50
15:2:779:ILE:HG13	15:2:779:ILE:O	2.11	0.50
16:3:262:GLN:OE1	16:3:262:GLN:HA	2.10	0.50
17:4:23:ASP:OD2	17:4:182:TYR:OH	2.28	0.50
20:7:26:PRO:HB2	20:7:35:LEU:HD11	1.93	0.50
29:g:525:THR:HG22	29:g:526:ASP:N	2.25	0.50
2:B:669:LEU:HD11	2:B:676:PRO:HD3	1.92	0.50
3:D:626:HIS:ND1	3:D:626:HIS:O	2.44	0.50
4:E:517:GLU:OE1	4:E:517:GLU:N	2.42	0.50
6:G:675:MET:HE1	6:G:679:ARG:HH12	1.75	0.50
6:G:787:VAL:HG23	6:G:787:VAL:O	2.10	0.50
8:I:621:GLU:HG2	8:I:643:LEU:HD11	1.93	0.50
19:6:98:ARG:O	19:6:99:ILE:HD13	2.11	0.50
2:B:927:LYS:O	2:B:931:LEU:HD23	2.11	0.50
2:B:1148:THR:HG22	2:B:1148:THR:O	2.11	0.50
3:D:539:MET:O	3:D:545:ILE:HD11	2.11	0.50
6:G:435:LEU:HD21	6:G:453:LEU:HD11	1.92	0.50
1:A:393:MET:SD	1:A:394:ASN:ND2	2.84	0.50
1:A:1722:GLU:C	1:A:1723:LEU:HD12	2.36	0.50
1:A:1870:ALA:HB1	1:A:1918:LEU:HD21	1.93	0.50
1:A:2097:GLU:OE1	1:A:2097:GLU:N	2.41	0.50
11:P:338:ASN:OD1	11:P:339:GLN:N	2.44	0.50
14:1:1401:LEU:HG	14:1:1405:MET:HE3	1.94	0.50
18:5:80:MET:SD	18:5:80:MET:N	2.76	0.50
20:7:101:SER:N	20:7:105:GLU:OE2	2.44	0.50
22:9:106:ARG:HB3	22:9:110:LYS:NZ	2.26	0.50
2:B:15:LEU:HD12	2:B:209:TRP:CD1	2.46	0.50
2:B:874:MET:O	2:B:878:LEU:HD13	2.12	0.50
4:E:699:ARG:O	4:E:702:THR:HG22	2.12	0.50
5:F:165:ASP:N	5:F:165:ASP:OD1	2.44	0.50
6:G:218:LEU:HB2	6:G:238:PHE:CD2	2.47	0.50
6:G:824:ASN:OD1	6:G:825:GLN:N	2.45	0.50
6:G:826:GLN:HG3	6:G:827:LEU:N	2.27	0.50
7:H:390:VAL:HA	7:H:393:ILE:HD12	1.92	0.50
9:K:70:HIS:CE1	9:K:157:HIS:NE2	2.79	0.50
14:1:912:SER:N	14:1:1327:GLU:OE2	2.43	0.50
14:1:1286:ARG:O	14:1:1289:GLU:HG3	2.11	0.50
18:5:110:LEU:HG	18:5:111:PRO:HD2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:383:VAL:O	2:B:386:SER:OG	2.21	0.50
2:B:666:THR:O	2:B:901:GLN:NE2	2.44	0.50
3:D:560:THR:HG23	3:D:560:THR:O	2.12	0.50
6:G:204:MET:HE2	6:G:204:MET:HA	1.92	0.50
7:H:469:LEU:HD11	7:H:473:GLU:CB	2.41	0.50
7:H:785:GLU:OE1	7:H:785:GLU:N	2.36	0.50
9:K:287:ASN:C	9:K:287:ASN:OD1	2.54	0.50
9:K:413:VAL:CA	9:K:420:MET:HE1	2.41	0.50
14:1:864:LEU:O	14:1:868:MET:SD	2.70	0.50
15:2:37:LYS:NZ	15:2:664:TYR:OH	2.31	0.50
22:9:87:PHE:CE2	22:9:91:ILE:HD11	2.46	0.50
1:A:1706:ARG:NE	2:B:992:GLU:OE1	2.42	0.50
1:A:2149:LEU:O	1:A:2152:GLN:NE2	2.45	0.50
2:B:645:ILE:HG23	2:B:646:THR:N	2.26	0.50
2:B:921:VAL:O	2:B:925:GLU:OE1	2.30	0.50
2:B:936:SER:HB3	2:B:1014:LEU:HD22	1.91	0.50
5:F:32:VAL:HG11	5:F:77:LEU:HD11	1.94	0.50
15:2:549:SER:OG	15:2:577:HIS:NE2	2.42	0.50
19:6:2:ALA:O	19:6:84:ARG:NH1	2.45	0.50
3:D:570:PHE:CE1	3:D:589:LEU:HD12	2.47	0.50
4:E:754:ILE:HD12	12:Q:163:ILE:HD11	1.94	0.50
4:E:823:ASP:OD1	4:E:824:ALA:N	2.45	0.50
8:I:158:ASN:HB3	8:I:161:ILE:HG22	1.94	0.50
9:K:234:LYS:N	9:K:346:ASN:OD1	2.32	0.50
14:1:274:ASP:OD1	14:1:274:ASP:N	2.45	0.50
14:1:551:ARG:HA	14:1:589:LYS:HZ1	1.76	0.50
19:6:56:PHE:HB2	19:6:146:LYS:O	2.12	0.50
1:A:2070:ILE:HA	1:A:2073:MET:SD	2.52	0.50
2:B:764:VAL:CG2	2:B:771:VAL:HG21	2.42	0.50
2:B:1014:LEU:HD23	2:B:1014:LEU:C	2.37	0.50
3:D:689:GLN:NE2	6:G:690:GLN:OE1	2.45	0.50
7:H:874:ASP:OD1	7:H:875:VAL:N	2.45	0.50
8:I:68:LEU:HD23	8:I:75:VAL:HG21	1.94	0.50
8:I:541:SER:HB3	9:K:478:LEU:HD11	1.94	0.50
11:P:313:LEU:O	11:P:318:ARG:NH2	2.44	0.50
11:P:414:ASP:O	11:P:420:ARG:NH1	2.45	0.50
14:1:1288:ILE:C	14:1:1292:MET:HE3	2.36	0.50
14:1:1379:GLU:HG2	14:1:1398:LEU:HD22	1.94	0.50
15:2:116:ARG:NH2	15:2:911:LEU:O	2.41	0.50
24:b:25:DC:H2"	24:b:26:DG:H8	1.76	0.50
29:g:476:LEU:O	29:g:479:THR:OG1	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:j:712:ILE:HG21	32:j:717:TYR:HB2	1.94	0.50
5:F:223:LEU:O	5:F:227:VAL:HG23	2.12	0.49
6:G:875:ASN:OD1	6:G:875:ASN:O	2.29	0.49
7:H:574:MET:SD	7:H:575:ALA:N	2.85	0.49
8:I:1:MET:HE2	8:I:1:MET:H2	1.77	0.49
8:I:546:THR:HG21	9:K:465:MET:CE	2.42	0.49
12:Q:59:HIS:N	12:Q:85:ASP:O	2.39	0.49
14:1:388:MET:HA	14:1:388:MET:HE2	1.94	0.49
14:1:781:ILE:CG2	14:1:785:ILE:HD12	2.41	0.49
16:3:25:ASN:N	16:3:227:GLU:OE1	2.45	0.49
32:j:506:LEU:HD21	32:j:536:TRP:CD2	2.47	0.49
1:A:476:PHE:O	1:A:480:VAL:HG23	2.12	0.49
2:B:304:GLY:O	2:B:308:GLY:N	2.45	0.49
2:B:1091:LEU:HD11	2:B:1095:LYS:HB3	1.93	0.49
3:D:758:VAL:HG11	3:D:780:LEU:HD22	1.94	0.49
5:F:317:MET:HE1	5:F:387:PRO:HA	1.95	0.49
12:Q:165:CYS:SG	12:Q:238:SER:OG	2.68	0.49
14:1:955:GLU:OE1	14:1:1010:VAL:HG22	2.12	0.49
20:7:88:LYS:NZ	20:7:119:CYS:HB2	2.27	0.49
31:i:48:MET:SD	31:i:49:VAL:HG23	2.52	0.49
2:B:467:GLU:HB2	2:B:474:ALA:HB2	1.93	0.49
3:D:301:GLN:O	3:D:305:LEU:HD23	2.12	0.49
5:F:125:ILE:O	5:F:168:LEU:HD12	2.11	0.49
6:G:246:LEU:HG	6:G:246:LEU:O	2.12	0.49
7:H:31:GLU:OE1	7:H:31:GLU:N	2.45	0.49
7:H:583:VAL:O	7:H:583:VAL:HG12	2.11	0.49
7:H:677:THR:HG22	7:H:695:GLN:HB3	1.94	0.49
8:I:467:LEU:O	8:I:468:HIS:ND1	2.45	0.49
9:K:344:GLU:O	9:K:383:GLN:NE2	2.41	0.49
12:Q:67:GLU:OE1	12:Q:292:ALA:N	2.45	0.49
1:A:565:ASP:OD2	1:A:641:ARG:NH2	2.43	0.49
2:B:213:LEU:HD23	2:B:217:ASN:OD1	2.13	0.49
2:B:930:LEU:HD23	2:B:930:LEU:C	2.38	0.49
4:E:801:ALA:HB2	7:H:406:LEU:HD13	1.93	0.49
7:H:840:ALA:HB1	7:H:856:TYR:CD2	2.47	0.49
8:I:137:MET:HE1	8:I:191:LEU:HD21	1.94	0.49
12:Q:96:THR:O	12:Q:100:LEU:HD23	2.12	0.49
14:1:593:SER:OG	14:1:634:GLU:OE2	2.23	0.49
14:1:1175:ILE:HD11	20:7:54:TYR:HB3	1.94	0.49
24:b:34:DC:H2"	24:b:35:DA:H8	1.77	0.49
27:e:23:LEU:HD12	29:g:233:HIS:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:745:ALA:HB1	1:A:753:GLY:HA2	1.93	0.49
2:B:394:ALA:O	2:B:398:ILE:HG22	2.13	0.49
2:B:408:ALA:O	2:B:412:LEU:HD23	2.11	0.49
2:B:824:MET:O	2:B:824:MET:HG3	2.13	0.49
4:E:779:LEU:O	4:E:783:LEU:HD23	2.12	0.49
15:2:310:VAL:CG1	15:2:311:ILE:HD12	2.42	0.49
15:2:395:LEU:HD11	15:2:532:ILE:HG21	1.94	0.49
1:A:168:ALA:HB2	1:A:211:LEU:HD23	1.95	0.49
1:A:520:MET:CE	1:A:545:LEU:HD11	2.42	0.49
2:B:239:GLU:OE1	2:B:239:GLU:N	2.45	0.49
2:B:785:GLU:OE1	2:B:785:GLU:N	2.39	0.49
5:F:5:LEU:HA	5:F:51:MET:HB2	1.95	0.49
6:G:892:PHE:C	6:G:893:LEU:HD22	2.38	0.49
6:G:894:LEU:HD13	6:G:904:ILE:HD12	1.94	0.49
7:H:619:ASP:OD2	7:H:641:ARG:NH1	2.43	0.49
8:I:308:LEU:O	8:I:308:LEU:HD23	2.12	0.49
11:P:310:CYS:SG	11:P:322:ILE:HD11	2.53	0.49
14:1:450:MET:CE	14:1:505:LEU:HD22	2.42	0.49
14:1:1158:LEU:HD22	14:1:1309:MET:CE	2.42	0.49
15:2:1115:GLN:N	15:2:1115:GLN:OE1	2.46	0.49
32:j:440:ILE:HG23	32:j:450:ILE:HD11	1.95	0.49
34:l:91:LYS:O	34:l:121:ARG:NH2	2.46	0.49
2:B:646:THR:HG22	2:B:650:LEU:HD23	1.93	0.49
2:B:1115:PRO:O	2:B:1118:TYR:HB2	2.12	0.49
14:1:625:ASP:OD1	14:1:638:GLY:N	2.45	0.49
14:1:979:LEU:HD21	14:1:1040:LEU:HD21	1.95	0.49
15:2:962:THR:HG23	15:2:962:THR:O	2.12	0.49
29:g:524:ASP:N	29:g:524:ASP:OD1	2.45	0.49
31:i:42:MET:CE	31:i:48:MET:HE1	2.42	0.49
1:A:190:ARG:NH1	1:A:232:GLU:O	2.46	0.49
2:B:575:ASP:O	2:B:579:ARG:NE	2.39	0.49
4:E:739:VAL:O	4:E:740:PRO:CB	2.59	0.49
4:E:850:ARG:NE	4:E:854:GLN:OE1	2.44	0.49
5:F:233:ILE:HD12	5:F:268:ILE:HD12	1.95	0.49
6:G:747:ARG:HD2	6:G:787:VAL:HG12	1.95	0.49
8:I:546:THR:HG21	9:K:465:MET:HE1	1.94	0.49
11:P:466:LEU:HD11	11:P:482:ILE:HG12	1.95	0.49
11:P:505:ILE:HD12	11:P:521:MET:HG2	1.95	0.49
17:4:110:MET:SD	17:4:115:LYS:HG3	2.53	0.49
22:9:81:TYR:CE2	22:9:86:ALA:HB2	2.48	0.49
1:A:767:MET:O	1:A:770:VAL:HG22	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:606:PRO:HG3	2:B:672:MET:SD	2.53	0.49
2:B:868:HIS:HA	2:B:874:MET:HE3	1.94	0.49
3:D:956:ILE:HG22	3:D:958:PRO:HD3	1.95	0.49
7:H:728:SER:HA	7:H:749:LEU:HD22	1.95	0.49
8:I:79:SER:OG	8:I:80:VAL:N	2.45	0.49
9:K:394:ASP:OD1	9:K:397:GLY:N	2.43	0.49
9:K:434:ASN:OD1	9:K:435:CYS:N	2.46	0.49
11:P:155:TYR:HD1	11:P:166:LEU:HD11	1.76	0.49
11:P:177:ASP:O	11:P:182:ARG:NH2	2.46	0.49
14:1:400:ASP:N	14:1:400:ASP:OD1	2.46	0.49
15:2:797:ASN:OD1	15:2:799:SER:N	2.45	0.49
19:6:27:ARG:NH1	19:6:42:ASP:OD1	2.45	0.49
19:6:129:ALA:O	19:6:133:HIS:ND1	2.46	0.49
29:g:351:ASP:OD1	29:g:352:HIS:N	2.45	0.49
32:j:181:THR:HG22	32:j:226:TYR:CE1	2.47	0.49
8:I:540:VAL:HG22	9:K:481:GLY:C	2.38	0.49
9:K:52:THR:HG22	9:K:60:PHE:HD2	1.78	0.49
2:B:761:PHE:O	2:B:764:VAL:HG12	2.13	0.48
6:G:771:TYR:CE2	6:G:772:MET:HE3	2.48	0.48
9:K:92:MET:HE3	9:K:96:THR:HG22	1.95	0.48
12:Q:38:ILE:HG23	12:Q:39:LEU:HD12	1.93	0.48
14:1:861:GLN:NE2	14:1:865:ILE:HD12	2.28	0.48
15:2:159:THR:HG23	15:2:160:TYR:CE1	2.48	0.48
19:6:28:LEU:HD12	19:6:28:LEU:O	2.13	0.48
20:7:23:MET:HE2	20:7:25:TYR:CE1	2.48	0.48
32:j:254:MET:HA	32:j:254:MET:HE2	1.94	0.48
1:A:1396:PRO:O	1:A:1400:GLY:N	2.35	0.48
2:B:580:GLN:O	2:B:580:GLN:NE2	2.44	0.48
5:F:319:ILE:HB	5:F:322:LEU:HD12	1.94	0.48
7:H:637:ASP:OD1	7:H:638:LEU:N	2.45	0.48
8:I:185:GLN:NE2	8:I:186:GLU:HG3	2.27	0.48
11:P:80:VAL:HG21	11:P:89:LEU:HD23	1.94	0.48
14:1:728:THR:HG23	29:g:488:GLU:OE2	2.13	0.48
14:1:865:ILE:HD11	14:1:1093:GLN:HB2	1.95	0.48
15:2:930:GLN:N	15:2:933:ASP:OD2	2.46	0.48
17:4:159:LEU:HD11	17:4:206:TYR:CD2	2.48	0.48
22:9:87:PHE:CZ	22:9:91:ILE:HD11	2.47	0.48
1:A:1887:LEU:O	1:A:1888:LEU:HG	2.13	0.48
1:A:2067:LEU:HD11	1:A:2091:LEU:HD21	1.95	0.48
6:G:201:LEU:HD13	6:G:238:PHE:HZ	1.78	0.48
12:Q:23:LEU:HD23	12:Q:27:GLN:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Q:202:ASP:C	12:Q:202:ASP:OD1	2.56	0.48
14:1:456:VAL:CG2	14:1:503:LEU:HD11	2.44	0.48
15:2:22:TRP:HH2	15:2:626:LEU:HD11	1.78	0.48
15:2:432:GLU:N	15:2:432:GLU:OE1	2.45	0.48
16:3:9:VAL:HG12	16:3:10:ARG:N	2.28	0.48
16:3:106:ARG:NH1	16:3:107:CYS:O	2.47	0.48
16:3:189:ASP:OD1	16:3:189:ASP:N	2.45	0.48
24:b:25:DC:N4	26:d:23:DC:H42	2.11	0.48
26:d:20:DC:H2''	26:d:21:DT:C5	2.48	0.48
1:A:473:ALA:HB3	1:A:474:PRO:HD3	1.95	0.48
3:D:460:SER:O	3:D:463:ILE:N	2.47	0.48
4:E:692:LEU:CD2	4:E:782:LEU:HD22	2.44	0.48
4:E:831:TRP:O	4:E:951:ARG:NH1	2.47	0.48
4:E:927:MET:CE	4:E:942:LEU:HB3	2.43	0.48
6:G:377:LYS:O	6:G:380:LEU:HD13	2.12	0.48
6:G:472:MET:CE	6:G:511:ALA:HB3	2.43	0.48
7:H:762:LYS:O	7:H:824:TYR:OH	2.31	0.48
14:1:334:ARG:NH1	25:c:39:A:O2'	2.47	0.48
14:1:1366:PHE:CA	14:1:1374:VAL:HG11	2.43	0.48
14:1:1366:PHE:HB2	14:1:1374:VAL:HG11	1.96	0.48
15:2:541:ILE:O	15:2:545:LEU:HD23	2.13	0.48
27:e:88:PRO:O	27:e:92:MET:HE3	2.13	0.48
4:E:842:GLU:OE1	4:E:842:GLU:N	2.33	0.48
12:Q:236:LEU:HD12	12:Q:255:ASN:O	2.13	0.48
12:Q:280:ASP:OD1	12:Q:280:ASP:N	2.45	0.48
15:2:1084:LEU:HD23	15:2:1085:ARG:N	2.29	0.48
19:6:6:PHE:HZ	19:6:37:MET:HE3	1.78	0.48
32:j:180:TRP:CD1	32:j:235:VAL:HG21	2.48	0.48
32:j:227:VAL:HG11	32:j:235:VAL:HG13	1.95	0.48
1:A:851:ASP:O	1:A:854:LYS:HG2	2.13	0.48
3:D:687:LEU:HD11	6:G:704:GLU:OE1	2.13	0.48
3:D:822:ALA:HB2	3:D:948:PHE:CE2	2.48	0.48
3:D:908:GLN:NE2	3:D:955:TYR:CE1	2.78	0.48
5:F:33:GLU:OE2	5:F:74:MET:HE1	2.14	0.48
6:G:271:LEU:HD23	6:G:271:LEU:C	2.38	0.48
7:H:770:LEU:O	7:H:774:LEU:HG	2.13	0.48
8:I:409:MET:HE3	8:I:436:TYR:CD2	2.49	0.48
9:K:37:MET:HG3	25:c:25:A:H62	1.69	0.48
14:1:1211:LEU:HD11	14:1:1258:ARG:HB3	1.94	0.48
3:D:166:VAL:O	3:D:169:LYS:N	2.47	0.48
6:G:232:ILE:HA	6:G:271:LEU:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:597:LEU:HD11	7:H:615:MET:SD	2.53	0.48
7:H:932:ILE:CG2	7:H:938:LEU:HD11	2.44	0.48
9:K:69:PHE:CA	9:K:100:CYS:SG	3.00	0.48
11:P:538:PHE:CB	11:P:575:VAL:HG23	2.43	0.48
14:1:909:LEU:O	14:1:910:LYS:CB	2.62	0.48
15:2:790:GLN:HA	15:2:968:ASN:ND2	2.29	0.48
32:j:543:ASP:N	32:j:543:ASP:OD1	2.44	0.48
2:B:35:ALA:CA	2:B:74:LEU:HD21	2.44	0.48
3:D:422:ASP:OD2	3:D:427:VAL:HG11	2.13	0.48
4:E:823:ASP:OD2	4:E:843:ARG:NE	2.46	0.48
5:F:419:MET:HE3	5:F:427:LEU:HD11	1.95	0.48
9:K:137:HIS:ND1	9:K:140:GLN:OE1	2.46	0.48
11:P:129:VAL:O	11:P:132:VAL:HG22	2.14	0.48
11:P:442:LYS:HG3	11:P:443:LEU:HD22	1.94	0.48
11:P:535:ASN:HA	11:P:538:PHE:CE2	2.49	0.48
11:P:553:ASN:OD1	11:P:554:SER:N	2.47	0.48
14:1:350:VAL:HG13	14:1:351:ARG:HG3	1.96	0.48
14:1:595:ILE:HD11	14:1:675:VAL:HG21	1.94	0.48
14:1:864:LEU:HB3	14:1:1092:ALA:HB1	1.95	0.48
14:1:1123:ARG:O	14:1:1127:LEU:HD23	2.13	0.48
14:1:1124:LEU:O	14:1:1128:ILE:HG12	2.12	0.48
29:g:261:ILE:O	29:g:265:VAL:HG23	2.14	0.48
32:j:264:LEU:HD23	32:j:264:LEU:H	1.79	0.48
1:A:2074:SER:CB	1:A:2081:LEU:HD21	2.44	0.48
3:D:410:GLU:OE1	3:D:410:GLU:N	2.38	0.48
3:D:577:ARG:NH1	3:D:584:VAL:O	2.46	0.48
9:K:27:LYS:NZ	9:K:145:ASP:OD2	2.45	0.48
14:1:868:MET:SD	14:1:1092:ALA:HB2	2.54	0.48
15:2:98:HIS:ND1	15:2:108:MET:SD	2.83	0.48
15:2:1026:GLU:OE1	15:2:1043:ILE:HG22	2.14	0.48
16:3:208:TYR:CD2	16:3:230:TYR:CD2	3.02	0.48
27:e:114:ASN:O	27:e:118:GLN:NE2	2.46	0.48
31:i:94:PRO:HD2	31:i:97:ILE:HD12	1.95	0.48
1:A:1769:CYS:SG	1:A:1770:CYS:N	2.87	0.48
3:D:223:HIS:HB2	3:D:229:LEU:HD11	1.96	0.48
6:G:218:LEU:HB2	6:G:238:PHE:CE2	2.47	0.48
8:I:585:LEU:HD23	8:I:585:LEU:H	1.79	0.48
11:P:354:PRO:HA	11:P:394:VAL:HG21	1.95	0.48
11:P:455:VAL:O	11:P:459:ARG:NH1	2.47	0.48
12:Q:239:ARG:NH1	12:Q:258:THR:OG1	2.47	0.48
14:1:22:GLN:NE2	14:1:1447:GLU:O	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:891:TYR:CE1	14:1:1087:VAL:HG11	2.48	0.48
19:6:4:ILE:HG21	19:6:7:GLU:CG	2.43	0.48
19:6:118:TYR:N	19:6:121:LEU:O	2.36	0.48
22:9:17:LYS:NZ	22:9:19:ILE:O	2.38	0.48
1:A:445:VAL:HG11	1:A:462:LEU:HG	1.95	0.47
2:B:123:GLN:OE1	2:B:123:GLN:N	2.38	0.47
3:D:460:SER:HB3	3:D:463:ILE:HB	1.96	0.47
8:I:294:ASN:N	8:I:418:ASN:OD1	2.45	0.47
9:K:240:PHE:HB2	25:c:26:U:OP1	2.13	0.47
11:P:436:VAL:HG22	11:P:473:PHE:CD2	2.49	0.47
14:1:104:MET:HE2	14:1:198:LEU:HD21	1.96	0.47
14:1:305:GLU:O	14:1:309:LEU:HD23	2.14	0.47
21:8:41:LYS:HG3	21:8:42:ARG:HD3	1.96	0.47
29:g:292:ALA:HB2	29:g:316:MET:CE	2.43	0.47
3:D:717:LYS:O	3:D:720:VAL:HG12	2.14	0.47
4:E:929:GLU:OE2	7:H:361:SER:OG	2.28	0.47
8:I:4:TYR:CE1	8:I:504:VAL:HG13	2.49	0.47
8:I:543:VAL:HG13	9:K:477:ARG:NH1	2.30	0.47
11:P:29:LEU:HD21	11:P:33:LYS:HE2	1.95	0.47
14:1:479:TRP:CB	15:2:931:ILE:HD11	2.41	0.47
16:3:131:THR:HG21	16:3:147:ASP:HA	1.96	0.47
17:4:149:VAL:HG12	17:4:150:VAL:O	2.14	0.47
28:f:476:PHE:O	28:f:480:ASP:N	2.47	0.47
29:g:432:ASP:CG	29:g:472:LEU:HD13	2.40	0.47
1:A:1077:GLU:O	1:A:1130:ARG:NH2	2.45	0.47
2:B:896:LEU:HD11	2:B:927:LYS:HB2	1.95	0.47
3:D:773:GLN:O	3:D:774:ASP:OD1	2.31	0.47
7:H:561:ILE:HB	7:H:567:ARG:HB3	1.96	0.47
14:1:388:MET:CB	14:1:450:MET:HE1	2.43	0.47
14:1:848:ILE:HD11	15:2:499:ARG:HG3	1.95	0.47
15:2:220:GLU:OE2	15:2:234:THR:HG23	2.14	0.47
15:2:346:GLU:OE1	15:2:346:GLU:N	2.47	0.47
18:5:102:ILE:H	18:5:102:ILE:HD12	1.80	0.47
1:A:520:MET:HA	1:A:520:MET:HE2	1.95	0.47
1:A:849:ILE:O	1:A:852:GLN:NE2	2.44	0.47
2:B:220:ASP:OD1	2:B:221:SER:N	2.46	0.47
3:D:566:SER:OG	3:D:567:ASP:N	2.47	0.47
4:E:664:PRO:N	4:E:665:PRO:HD2	2.30	0.47
5:F:101:LEU:HD21	5:F:467:SER:HA	1.96	0.47
6:G:748:MET:SD	6:G:787:VAL:HG21	2.55	0.47
8:I:232:GLU:OE1	8:I:232:GLU:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:121:PHE:CD1	9:K:126:ILE:HD11	2.37	0.47
12:Q:159:VAL:HB	12:Q:163:ILE:HB	1.96	0.47
21:8:8:PHE:N	21:8:48:MET:HE1	2.29	0.47
27:e:76:MET:HE2	27:e:79:ILE:HD12	1.96	0.47
32:j:561:LEU:HD11	32:j:565:GLY:C	2.39	0.47
1:A:610:HIS:ND1	1:A:619:GLU:OE2	2.47	0.47
1:A:1253:ILE:O	1:A:1258:MET:HE1	2.15	0.47
2:B:726:ASP:C	2:B:726:ASP:OD1	2.56	0.47
8:I:610:ASP:OD1	8:I:615:HIS:ND1	2.44	0.47
15:2:48:ASP:OD1	15:2:159:THR:HG22	2.15	0.47
15:2:851:ASP:OD1	23:a:15:MET:HE1	2.15	0.47
16:3:9:VAL:HG22	16:3:23:ILE:HD12	1.97	0.47
23:a:35:ARG:HB3	23:a:40:GLY:HA2	1.96	0.47
1:A:1881:LEU:O	1:A:1884:ILE:HG22	2.14	0.47
1:A:2134:PHE:HD2	7:H:851:ALA:HB2	1.79	0.47
1:A:2149:LEU:CD1	1:A:2183:ILE:HG21	2.43	0.47
2:B:463:GLU:OE1	2:B:464:ALA:N	2.48	0.47
3:D:499:ASP:OD1	3:D:499:ASP:N	2.47	0.47
3:D:718:GLN:O	3:D:722:ILE:HG12	2.15	0.47
5:F:10:THR:HG22	5:F:80:LEU:HD21	1.97	0.47
6:G:489:LEU:HD12	6:G:490:LEU:N	2.30	0.47
6:G:493:LEU:HA	6:G:496:VAL:HG12	1.95	0.47
7:H:548:TRP:CZ3	7:H:572:ILE:HD12	2.49	0.47
9:K:37:MET:HG2	25:c:25:A:C6	2.49	0.47
9:K:92:MET:CE	9:K:96:THR:HG22	2.45	0.47
9:K:100:CYS:N	9:K:101:PRO:HD2	2.29	0.47
12:Q:28:VAL:HG11	12:Q:142:VAL:HG13	1.95	0.47
14:1:550:LYS:O	14:1:589:LYS:NZ	2.48	0.47
14:1:556:GLU:O	14:1:560:VAL:HG23	2.14	0.47
14:1:693:ILE:HD13	15:2:1023:ARG:CZ	2.45	0.47
15:2:378:GLY:HA3	20:7:102:ALA:HB3	1.96	0.47
15:2:643:LEU:HD22	15:2:656:LEU:HD11	1.96	0.47
16:3:149:LEU:HD22	21:8:2:ILE:HG21	1.96	0.47
17:4:131:LEU:O	17:4:134:GLU:HG2	2.14	0.47
29:g:236:HIS:CE1	29:g:237:THR:HG23	2.49	0.47
31:i:14:ARG:NH1	31:i:53:THR:OG1	2.48	0.47
1:A:231:ILE:HD11	1:A:329:VAL:HG22	1.96	0.47
1:A:409:LEU:HA	1:A:412:ILE:HD12	1.96	0.47
1:A:1076:VAL:O	1:A:1076:VAL:HG12	2.14	0.47
2:B:462:GLU:HA	2:B:465:TYR:HB3	1.95	0.47
2:B:775:ILE:HG23	2:B:816:LEU:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:921:VAL:O	2:B:922:THR:C	2.58	0.47
3:D:572:HIS:O	3:D:576:LEU:HD23	2.14	0.47
3:D:815:GLU:OE1	3:D:816:GLN:HG3	2.15	0.47
4:E:501:GLN:O	4:E:505:LEU:HD23	2.14	0.47
5:F:10:THR:HG21	5:F:54:THR:HB	1.95	0.47
5:F:235:PHE:CZ	5:F:268:ILE:HD11	2.49	0.47
5:F:268:ILE:HD13	5:F:379:LEU:HD23	1.97	0.47
6:G:361:ALA:O	6:G:364:VAL:HG12	2.15	0.47
7:H:768:LEU:O	7:H:771:THR:HG22	2.14	0.47
8:I:72:SER:OG	8:I:437:GLN:O	2.32	0.47
8:I:93:LEU:HD23	8:I:113:ILE:HG23	1.95	0.47
8:I:229:SER:OG	8:I:230:HIS:N	2.48	0.47
8:I:464:VAL:HG23	8:I:466:PRO:HD3	1.97	0.47
8:I:504:VAL:O	8:I:505:LEU:HD22	2.15	0.47
9:K:435:CYS:SG	9:K:436:TYR:N	2.88	0.47
11:P:78:THR:HG23	11:P:79:LEU:HD12	1.96	0.47
11:P:217:GLN:O	11:P:220:VAL:HG22	2.14	0.47
11:P:522:LEU:O	11:P:523:PRO:C	2.57	0.47
12:Q:139:ASN:OD1	12:Q:141:ASN:ND2	2.47	0.47
14:1:29:ASP:OD1	14:1:29:ASP:N	2.47	0.47
14:1:384:ILE:CD1	15:2:1059:ILE:HD11	2.44	0.47
14:1:419:ILE:HD12	14:1:445:LYS:O	2.14	0.47
14:1:457:ILE:HD12	14:1:470:MET:C	2.40	0.47
14:1:539:GLN:NE2	15:2:791:GLU:OE1	2.48	0.47
14:1:601:ASN:OD1	14:1:631:GLU:HA	2.15	0.47
15:2:483:ARG:NH2	15:2:527:ALA:O	2.46	0.47
15:2:760:THR:OG1	15:2:761:THR:N	2.47	0.47
16:3:14:LEU:O	16:3:15:THR:OG1	2.30	0.47
16:3:158:GLU:N	16:3:158:GLU:OE1	2.48	0.47
24:b:25:DC:H42	26:d:23:DC:N4	2.11	0.47
32:j:588:ASP:O	32:j:589:SER:OG	2.23	0.47
1:A:543:ASP:O	1:A:547:VAL:HG23	2.15	0.47
6:G:183:MET:HE1	6:G:197:LEU:CD1	2.45	0.47
7:H:849:TYR:OH	7:H:890:LEU:HD13	2.15	0.47
9:K:217:ARG:NH1	9:K:388:SER:O	2.48	0.47
15:2:289:ILE:HD13	15:2:297:MET:CE	2.45	0.47
15:2:771:GLU:C	15:2:773:PRO:HD3	2.40	0.47
15:2:1104:ARG:NH1	15:2:1109:GLU:OE2	2.47	0.47
22:9:41:THR:HG22	22:9:42:LEU:HD22	1.97	0.47
1:A:1042:VAL:HG22	1:A:1042:VAL:O	2.15	0.47
3:D:443:THR:C	3:D:444:LEU:HD12	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:842:VAL:HG12	3:D:899:SER:HB3	1.96	0.47
4:E:851:PHE:CZ	4:E:877:LEU:HD12	2.49	0.47
8:I:369:GLN:OE1	8:I:369:GLN:HA	2.14	0.47
11:P:56:THR:HG22	11:P:92:PRO:HB3	1.96	0.47
14:1:549:THR:O	14:1:549:THR:CG2	2.63	0.47
15:2:344:GLN:O	15:2:353:VAL:HG13	2.15	0.47
15:2:1033:THR:HA	22:9:44:ASN:ND2	2.30	0.47
19:6:41:LEU:HD13	19:6:123:MET:SD	2.55	0.47
1:A:1088:ASP:OD1	1:A:1091:ARG:NH1	2.48	0.47
6:G:104:VAL:HG21	6:G:133:ILE:HG21	1.96	0.47
6:G:246:LEU:HD23	6:G:246:LEU:H	1.80	0.47
14:1:290:LEU:HD21	14:1:306:ASP:HB3	1.97	0.47
15:2:288:ILE:CD1	15:2:369:VAL:HG23	2.45	0.47
16:3:13:GLU:OE1	16:3:20:LYS:HE2	2.15	0.47
29:g:559:ASN:N	29:g:562:ILE:HD11	2.30	0.47
2:B:35:ALA:N	2:B:74:LEU:HD21	2.30	0.46
2:B:1092:THR:HA	7:H:926:ASP:OD2	2.15	0.46
6:G:417:VAL:HG23	6:G:452:CYS:SG	2.55	0.46
6:G:916:ILE:HG22	6:G:917:VAL:N	2.30	0.46
11:P:458:ILE:O	11:P:459:ARG:C	2.58	0.46
12:Q:174:ILE:HD13	12:Q:198:LEU:HD21	1.97	0.46
14:1:909:LEU:C	14:1:911:PRO:HD2	2.41	0.46
14:1:1212:LEU:CD2	14:1:1214:VAL:HG13	2.45	0.46
14:1:1359:SER:OG	14:1:1361:ASP:OD1	2.27	0.46
21:8:54:ASP:OD1	21:8:56:ILE:HG22	2.15	0.46
29:g:289:TYR:HB2	29:g:292:ALA:HB3	1.96	0.46
29:g:310:ILE:HD13	29:g:356:TYR:HD1	1.79	0.46
2:B:268:VAL:CG2	2:B:273:HIS:O	2.63	0.46
2:B:1193:VAL:HA	2:B:1196:ILE:HG22	1.97	0.46
3:D:795:VAL:HA	3:D:798:ILE:HD12	1.97	0.46
6:G:233:VAL:O	6:G:237:THR:HG23	2.15	0.46
7:H:858:GLN:O	7:H:862:VAL:HG23	2.15	0.46
9:K:29:VAL:HG12	9:K:63:CYS:SG	2.54	0.46
9:K:69:PHE:HB3	9:K:100:CYS:SG	2.55	0.46
9:K:272:THR:HG23	9:K:273:GLU:N	2.30	0.46
9:K:350:MET:HE3	9:K:354:CYS:SG	2.55	0.46
11:P:83:PRO:HA	11:P:86:VAL:HG13	1.97	0.46
12:Q:170:LEU:HD11	12:Q:228:PHE:CD2	2.50	0.46
14:1:1173:THR:OG1	14:1:1214:VAL:HG12	2.15	0.46
15:2:873:LEU:HD23	15:2:873:LEU:H	1.80	0.46
15:2:1067:ILE:HA	15:2:1073:GLN:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:3:59:LEU:HD23	16:3:151:VAL:HG23	1.97	0.46
20:7:27:LYS:O	20:7:35:LEU:HD12	2.15	0.46
29:g:490:LEU:HD21	29:g:494:LYS:HE2	1.96	0.46
34:l:31:THR:HG21	34:l:98:ALA:HB2	1.98	0.46
1:A:1397:GLU:O	1:A:1401:ILE:N	2.40	0.46
1:A:2177:ILE:HG22	1:A:2181:LEU:HD12	1.95	0.46
2:B:733:ILE:HG22	2:B:734:THR:H	1.79	0.46
2:B:1088:LEU:O	2:B:1088:LEU:HD23	2.15	0.46
3:D:459:SER:O	3:D:460:SER:C	2.57	0.46
3:D:545:ILE:HD12	3:D:576:LEU:HD11	1.96	0.46
6:G:551:THR:O	6:G:551:THR:HG22	2.16	0.46
7:H:849:TYR:CZ	7:H:890:LEU:HD13	2.50	0.46
15:2:590:LEU:CD2	15:2:597:ILE:CD1	2.93	0.46
16:3:74:THR:O	16:3:127:VAL:HG12	2.15	0.46
19:6:28:LEU:HD12	19:6:28:LEU:C	2.40	0.46
27:e:24:TRP:NE1	29:g:232:CYS:O	2.48	0.46
32:j:426:VAL:HG21	32:j:468:LEU:HD13	1.97	0.46
33:k:162:SER:C	33:k:163:LEU:HD12	2.40	0.46
2:B:479:MET:HG2	2:B:498:LEU:HD21	1.97	0.46
3:D:166:VAL:O	3:D:167:ARG:C	2.59	0.46
14:1:542:LEU:O	14:1:545:VAL:HG12	2.16	0.46
15:2:47:PHE:HB2	15:2:155:MET:HE3	1.96	0.46
15:2:285:LEU:HA	15:2:288:ILE:HG22	1.98	0.46
19:6:64:LEU:O	19:6:84:ARG:N	2.36	0.46
5:F:78:LYS:HB2	12:Q:206:ARG:HG3	1.96	0.46
6:G:37:LYS:HB2	6:G:40:GLU:OE1	2.16	0.46
6:G:48:PHE:O	6:G:49:PRO:C	2.57	0.46
6:G:561:TRP:HD1	6:G:562:LEU:HD22	1.80	0.46
6:G:594:LEU:HD11	6:G:628:LEU:HB3	1.97	0.46
7:H:110:MET:SD	7:H:111:LEU:N	2.89	0.46
9:K:421:GLU:HA	9:K:437:MET:HE1	1.96	0.46
12:Q:45:VAL:HG12	12:Q:156:THR:OG1	2.15	0.46
14:1:848:ILE:HG23	14:1:849:ASP:N	2.30	0.46
14:1:1022:ILE:HD11	14:1:1076:PHE:HE1	1.81	0.46
15:2:551:GLU:OE1	15:2:551:GLU:N	2.49	0.46
17:4:154:GLU:OE1	17:4:154:GLU:N	2.39	0.46
32:j:602:VAL:O	32:j:609:GLY:N	2.47	0.46
5:F:268:ILE:HG21	5:F:379:LEU:HD21	1.96	0.46
6:G:105:LYS:NZ	14:1:1771:PRO:HG2	2.31	0.46
8:I:544:LEU:HD23	9:K:479:LEU:HG	1.98	0.46
11:P:70:ALA:HB2	11:P:96:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2:601:VAL:HG21	15:2:616:THR:HG22	1.97	0.46
19:6:4:ILE:HG21	19:6:7:GLU:HG3	1.97	0.46
27:e:143:TYR:HA	29:g:425:MET:HE1	1.98	0.46
34:l:37:VAL:HB	34:l:68:THR:OG1	2.16	0.46
1:A:647:PRO:HA	1:A:693:VAL:HG13	1.98	0.46
1:A:903:ASP:O	1:A:904:VAL:O	2.34	0.46
1:A:2133:ASP:OD2	1:A:2136:VAL:HG22	2.15	0.46
2:B:65:ALA:O	2:B:69:LYS:HG3	2.16	0.46
2:B:540:VAL:HG12	2:B:576:TRP:CE2	2.51	0.46
3:D:216:ILE:HG21	3:D:251:ALA:HB1	1.98	0.46
6:G:54:LYS:HG2	6:G:55:TYR:CE1	2.51	0.46
6:G:723:ASP:N	6:G:723:ASP:OD1	2.48	0.46
7:H:759:SER:HA	7:H:762:LYS:HG2	1.98	0.46
11:P:280:LYS:NZ	11:P:316:ASP:OD2	2.48	0.46
14:1:388:MET:HB3	14:1:450:MET:CE	2.46	0.46
14:1:689:ILE:HG22	15:2:1042:PHE:HE2	1.81	0.46
15:2:218:THR:HG23	15:2:218:THR:O	2.16	0.46
15:2:596:ILE:CG2	15:2:597:ILE:HD12	2.45	0.46
17:4:155:GLU:O	17:4:158:GLU:OE1	2.34	0.46
18:5:61:GLU:O	18:5:65:VAL:HG22	2.15	0.46
19:6:7:GLU:HG2	19:6:59:VAL:HG22	1.97	0.46
27:e:93:VAL:O	27:e:96:ILE:HG22	2.16	0.46
29:g:349:ASN:ND2	29:g:351:ASP:OD2	2.49	0.46
29:g:451:HIS:O	29:g:455:LEU:HD23	2.16	0.46
1:A:431:LEU:HD22	1:A:438:LEU:HA	1.98	0.46
2:B:236:GLN:NE2	2:B:319:THR:HG22	2.31	0.46
2:B:250:LEU:CB	2:B:277:LEU:HD11	2.45	0.46
3:D:697:ALA:O	3:D:700:ILE:HG22	2.16	0.46
4:E:489:LEU:HD21	4:E:522:LEU:HG	1.97	0.46
4:E:528:SER:HB2	4:E:531:GLU:OE1	2.16	0.46
4:E:607:LEU:HD11	4:E:639:LEU:HD11	1.98	0.46
4:E:988:LEU:HD23	4:E:992:LEU:HD23	1.98	0.46
6:G:171:ASP:OD1	6:G:171:ASP:N	2.45	0.46
11:P:11:TYR:N	11:P:12:PRO:HD2	2.31	0.46
11:P:538:PHE:HB3	11:P:575:VAL:HG23	1.98	0.46
14:1:77:ASN:O	14:1:79:THR:N	2.49	0.46
14:1:635:LEU:HD23	14:1:635:LEU:C	2.41	0.46
14:1:876:ASP:CG	14:1:878:THR:HG22	2.40	0.46
14:1:893:GLU:OE2	17:4:197:SER:OG	2.25	0.46
14:1:990:ALA:HB2	14:1:1067:TRP:HZ3	1.81	0.46
14:1:1227:THR:O	14:1:1230:GLN:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:1369:LEU:O	14:1:1373:ALA:HB3	2.16	0.46
15:2:646:ARG:O	15:2:647:GLU:HG2	2.16	0.46
15:2:795:ILE:HD12	15:2:947:ILE:HG22	1.98	0.46
27:e:12:TRP:O	27:e:16:LYS:HG2	2.16	0.46
1:A:371:LEU:O	1:A:375:LEU:HD23	2.16	0.46
1:A:578:PHE:O	1:A:582:ILE:HG12	2.16	0.46
3:D:221:GLN:O	3:D:224:GLU:HG3	2.16	0.46
3:D:707:MET:SD	3:D:722:ILE:HD11	2.56	0.46
6:G:438:LEU:HD23	6:G:449:MET:HE2	1.98	0.46
7:H:97:ASP:OD1	7:H:152:ARG:NH2	2.49	0.46
8:I:281:PHE:CE1	8:I:421:ILE:HG21	2.50	0.46
8:I:324:VAL:HG13	8:I:324:VAL:O	2.15	0.46
9:K:30:MET:HE2	9:K:64:VAL:HG22	1.97	0.46
9:K:36:HIS:ND1	9:K:37:MET:O	2.49	0.46
9:K:92:MET:HE2	9:K:96:THR:C	2.41	0.46
9:K:413:VAL:N	9:K:420:MET:HE1	2.31	0.46
11:P:57:ASP:OD1	11:P:58:THR:N	2.49	0.46
11:P:155:TYR:O	11:P:158:VAL:HG22	2.16	0.46
14:1:200:ALA:HB2	14:1:216:LEU:HD21	1.98	0.46
14:1:510:GLU:OE2	14:1:511:THR:HG23	2.15	0.46
14:1:847:LEU:HD11	15:2:720:PRO:HB3	1.98	0.46
14:1:1797:TYR:HD1	14:1:1799:PRO:HD2	1.80	0.46
17:4:31:ASP:OD1	17:4:32:GLU:N	2.43	0.46
29:g:164:GLU:O	29:g:165:ALA:HB3	2.16	0.46
32:j:212:ILE:HG22	32:j:229:ALA:HB2	1.97	0.46
32:j:624:LEU:HD23	32:j:636:PHE:CZ	2.51	0.46
1:A:702:ILE:HG23	1:A:741:LEU:HD13	1.98	0.46
3:D:414:ASP:OD1	3:D:415:PHE:N	2.49	0.46
3:D:800:GLN:O	3:D:804:ARG:HG2	2.16	0.46
4:E:915:ALA:HB2	4:E:925:GLY:HA2	1.98	0.46
6:G:635:ILE:HA	6:G:638:CYS:SG	2.56	0.46
6:G:823:ASN:HD22	6:G:823:ASN:HA	1.60	0.46
7:H:325:PRO:O	7:H:329:VAL:HG23	2.15	0.46
8:I:341:GLN:NE2	8:I:365:ALA:HB2	2.31	0.46
14:1:1464:ALA:C	14:1:1466:ALA:H	2.24	0.46
15:2:389:GLY:O	15:2:668:LEU:HD21	2.16	0.46
1:A:807:LEU:HD11	1:A:824:GLU:OE2	2.16	0.45
3:D:948:PHE:CD2	3:D:948:PHE:O	2.68	0.45
4:E:522:LEU:C	4:E:522:LEU:HD23	2.42	0.45
4:E:961:ILE:N	4:E:970:ILE:O	2.45	0.45
8:I:281:PHE:CZ	8:I:308:LEU:HD21	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:516:ILE:HD11	8:I:553:LEU:CD2	2.45	0.45
14:1:927:GLU:O	14:1:931:ARG:HG2	2.16	0.45
14:1:1288:ILE:O	14:1:1292:MET:HE3	2.15	0.45
15:2:838:GLN:O	15:2:890:ARG:NH1	2.45	0.45
15:2:852:GLY:O	15:2:853:LEU:HD23	2.16	0.45
16:3:153:LEU:HD22	16:3:157:GLN:HG2	1.98	0.45
3:D:444:LEU:HD12	3:D:444:LEU:N	2.31	0.45
3:D:460:SER:OG	9:K:258:ARG:NH2	2.49	0.45
3:D:666:CYS:SG	3:D:700:ILE:HG13	2.56	0.45
4:E:568:PRO:CD	4:E:569:PRO:HD2	2.46	0.45
8:I:329:ILE:HD11	8:I:383:PHE:CZ	2.52	0.45
11:P:107:LYS:O	11:P:110:GLU:HG3	2.17	0.45
14:1:319:ASP:OD1	14:1:319:ASP:N	2.49	0.45
14:1:565:MET:SD	22:9:61:TYR:N	2.89	0.45
14:1:1423:ASP:N	14:1:1423:ASP:OD1	2.46	0.45
15:2:271:ILE:HD13	15:2:320:PHE:CD2	2.51	0.45
15:2:905:ASP:N	15:2:905:ASP:OD1	2.49	0.45
19:6:128:ASP:OD1	19:6:129:ALA:N	2.49	0.45
2:B:578:TYR:CZ	2:B:582:CYS:SG	3.10	0.45
2:B:809:ILE:H	2:B:809:ILE:HD12	1.81	0.45
2:B:1128:ILE:HA	2:B:1131:VAL:HG12	1.98	0.45
3:D:688:LYS:O	3:D:689:GLN:HB2	2.16	0.45
6:G:623:LEU:HD21	6:G:684:ARG:HB3	1.98	0.45
7:H:323:LEU:O	7:H:328:GLN:NE2	2.50	0.45
8:I:26:LEU:HD13	8:I:236:TYR:CG	2.52	0.45
8:I:462:LYS:O	8:I:465:GLN:NE2	2.50	0.45
8:I:526:LEU:HD11	8:I:538:ALA:HB1	1.99	0.45
9:K:286:THR:O	9:K:287:ASN:OD1	2.35	0.45
11:P:487:LEU:HD11	11:P:524:THR:CG2	2.44	0.45
12:Q:126:VAL:HG23	12:Q:127:TYR:CD2	2.51	0.45
14:1:460:ARG:NH1	14:1:492:TYR:O	2.49	0.45
14:1:552:ASP:O	19:6:24:ARG:NH1	2.49	0.45
14:1:832:THR:HB	14:1:833:PRO:HD2	1.98	0.45
14:1:1063:GLU:O	14:1:1066:ASP:OD1	2.33	0.45
14:1:1434:GLU:OE2	14:1:1437:ASP:N	2.32	0.45
15:2:237:VAL:O	15:2:237:VAL:HG13	2.16	0.45
15:2:413:LYS:O	15:2:416:ARG:HG2	2.16	0.45
19:6:24:ARG:HG2	19:6:24:ARG:O	2.16	0.45
21:8:2:ILE:HG22	21:8:3:ILE:H	1.81	0.45
33:k:4:HIS:N	34:l:30:GLU:O	2.43	0.45
3:D:407:SER:O	3:D:408:PHE:HB3	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:880:ALA:O	3:D:883:ARG:NH1	2.49	0.45
4:E:890:GLU:OE1	4:E:940:ARG:NH2	2.49	0.45
6:G:81:LEU:HD23	6:G:81:LEU:C	2.42	0.45
6:G:754:HIS:NE2	6:G:758:GLU:OE2	2.49	0.45
7:H:744:GLN:O	7:H:745:ARG:HG3	2.17	0.45
11:P:412:ALA:HB1	11:P:446:LEU:HD12	1.98	0.45
11:P:414:ASP:OD2	11:P:419:VAL:HG21	2.16	0.45
14:1:413:TYR:HB3	14:1:414:PRO:HD3	1.98	0.45
14:1:1422:GLN:N	14:1:1422:GLN:OE1	2.49	0.45
16:3:207:GLU:OE1	16:3:207:GLU:N	2.43	0.45
17:4:153:LYS:O	17:4:157:THR:HG23	2.16	0.45
21:8:50:LEU:C	21:8:50:LEU:HD23	2.41	0.45
22:9:79:PRO:O	22:9:80:ASP:CG	2.59	0.45
1:A:409:LEU:HD23	1:A:412:ILE:HD12	1.98	0.45
2:B:684:MET:O	2:B:684:MET:HE3	2.17	0.45
4:E:768:ASN:ND2	4:E:771:GLU:OE2	2.50	0.45
4:E:930:VAL:O	4:E:930:VAL:HG22	2.16	0.45
7:H:779:LYS:O	7:H:783:VAL:HG13	2.17	0.45
7:H:857:LEU:HD21	7:H:990:MET:CG	2.42	0.45
8:I:281:PHE:CD1	8:I:421:ILE:HG21	2.51	0.45
11:P:279:THR:HA	11:P:283:LEU:HB2	1.99	0.45
11:P:455:VAL:HG12	11:P:456:TYR:N	2.31	0.45
12:Q:17:LEU:HD21	12:Q:23:LEU:CD1	2.47	0.45
15:2:186:ILE:O	15:2:187:ILE:HD13	2.15	0.45
15:2:750:VAL:HG13	15:2:809:VAL:CG1	2.46	0.45
16:3:242:GLU:OE1	16:3:242:GLU:N	2.39	0.45
18:5:56:TYR:CD1	18:5:124:ILE:HD11	2.52	0.45
22:9:80:ASP:C	22:9:80:ASP:OD1	2.60	0.45
27:e:95:ASP:OD2	27:e:113:GLN:NE2	2.50	0.45
2:B:72:LEU:HA	2:B:75:LEU:HD12	1.98	0.45
4:E:985:LEU:HD13	4:E:1009:PRO:CG	2.45	0.45
6:G:825:GLN:O	6:G:826:GLN:HB2	2.16	0.45
6:G:831:VAL:HG13	6:G:831:VAL:O	2.16	0.45
12:Q:89:ARG:NH2	14:1:1860:UNK:O	2.48	0.45
14:1:969:ILE:HG23	14:1:970:PHE:CD1	2.52	0.45
14:1:1347:LEU:HA	14:1:1352:VAL:HG11	1.99	0.45
16:3:28:LEU:HD12	16:3:29:ALA:N	2.31	0.45
19:6:15:ILE:O	19:6:16:ASP:C	2.60	0.45
34:l:74:PHE:CZ	34:l:83:VAL:HG21	2.51	0.45
2:B:392:TYR:HB3	2:B:396:MET:HE1	1.98	0.45
2:B:1132:CYS:HG	2:B:1186:CYS:HG	1.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:179:SER:OG	3:D:196:VAL:HG11	2.17	0.45
4:E:511:ARG:HB2	4:E:512:PRO:HD3	1.99	0.45
7:H:664:VAL:O	7:H:667:MET:HG3	2.17	0.45
8:I:98:VAL:HG21	8:I:205:LEU:HD13	1.99	0.45
8:I:101:ILE:HG23	8:I:107:MET:HB3	1.98	0.45
14:1:1798:SER:HG	14:1:1799:PRO:HD3	1.79	0.45
15:2:529:MET:O	15:2:530:ALA:C	2.59	0.45
15:2:771:GLU:O	15:2:772:LEU:HD12	2.17	0.45
15:2:786:THR:HG21	15:2:949:TYR:OH	2.17	0.45
15:2:954:MET:HE3	15:2:955:PRO:HD2	1.99	0.45
18:5:79:VAL:HG22	18:5:81:VAL:H	1.81	0.45
24:b:25:DC:N4	26:d:24:DG:H1	2.15	0.45
1:A:1056:MET:HA	1:A:1096:ARG:NH2	2.31	0.45
1:A:1280:ILE:HG23	1:A:1286:MET:CE	2.47	0.45
2:B:599:TYR:CZ	2:B:603:ILE:HD11	2.51	0.45
2:B:936:SER:HB2	2:B:1014:LEU:HD22	1.97	0.45
3:D:770:PRO:O	3:D:773:GLN:NE2	2.50	0.45
5:F:110:ASN:ND2	5:F:114:GLY:O	2.49	0.45
5:F:136:THR:O	5:F:139:GLY:N	2.50	0.45
7:H:764:LEU:O	7:H:824:TYR:OH	2.34	0.45
7:H:972:GLU:HA	7:H:975:LEU:HB2	1.99	0.45
8:I:406:VAL:HG23	8:I:407:HIS:N	2.32	0.45
11:P:327:LEU:HD23	11:P:331:LYS:HZ2	1.82	0.45
12:Q:203:PRO:HD3	12:Q:239:ARG:CZ	2.47	0.45
14:1:303:ILE:O	14:1:307:VAL:HG23	2.17	0.45
14:1:876:ASP:OD1	14:1:876:ASP:N	2.47	0.45
15:2:787:GLY:C	15:2:790:GLN:OE1	2.59	0.45
15:2:800:ALA:HB1	15:2:805:PHE:HB2	1.99	0.45
17:4:58:LEU:HD23	17:4:58:LEU:H	1.82	0.45
19:6:4:ILE:HG23	19:6:59:VAL:HG13	1.98	0.45
21:8:7:CYS:HA	21:8:48:MET:SD	2.57	0.45
29:g:310:ILE:HG21	29:g:356:TYR:CE1	2.52	0.45
2:B:684:MET:HE2	2:B:718:TYR:OH	2.16	0.45
3:D:167:ARG:O	3:D:171:LEU:HG	2.17	0.45
4:E:834:GLU:HG2	4:E:944:LEU:HD11	1.99	0.45
6:G:266:LYS:HD2	6:G:307:LEU:HD21	1.99	0.45
7:H:649:ARG:NH2	7:H:683:PHE:O	2.50	0.45
8:I:27:ASP:CG	8:I:236:TYR:HH	2.24	0.45
8:I:626:ILE:HG23	8:I:635:ILE:HG13	1.99	0.45
9:K:71:LEU:O	9:K:73:HIS:N	2.49	0.45
11:P:99:VAL:HG21	11:P:104:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:P:405:LEU:HD21	11:P:438:PHE:CZ	2.52	0.45
14:1:865:ILE:HG21	15:2:1092:ASP:CG	2.41	0.45
19:6:32:SER:HB3	19:6:37:MET:H	1.82	0.45
24:b:26:DG:H2'	24:b:27:DG:C8	2.52	0.45
26:d:42:DT:H6	26:d:42:DT:H2'	1.59	0.45
1:A:146:VAL:HG13	1:A:187:LEU:CD1	2.46	0.45
1:A:2141:LEU:HD11	1:A:2173:PRO:HB3	1.99	0.45
2:B:305:LEU:HD23	2:B:317:PHE:CD2	2.52	0.45
2:B:577:ILE:HD12	2:B:595:LEU:HD21	1.98	0.45
2:B:773:GLN:NE2	2:B:777:HIS:CE1	2.85	0.45
2:B:994:GLN:HB3	2:B:1027:LEU:HD11	1.97	0.45
3:D:264:PRO:HA	3:D:279:LEU:HB3	1.98	0.45
3:D:621:VAL:O	3:D:625:GLN:NE2	2.48	0.45
3:D:649:LEU:HD11	6:G:205:HIS:O	2.17	0.45
8:I:497:MET:HE2	8:I:505:LEU:HD12	1.98	0.45
8:I:518:ILE:HG22	9:K:452:ILE:O	2.17	0.45
8:I:595:VAL:HG11	8:I:608:VAL:CG2	2.47	0.45
11:P:381:ARG:O	11:P:385:ILE:HG22	2.16	0.45
12:Q:13:TRP:CG	12:Q:23:LEU:HD21	2.53	0.45
14:1:1071:GLU:OE1	14:1:1071:GLU:HA	2.17	0.45
15:2:157:ARG:NH2	15:2:180:ASP:O	2.50	0.45
17:4:18:MET:HE3	17:4:32:GLU:O	2.17	0.45
19:6:96:VAL:HA	19:6:116:VAL:HG23	1.98	0.45
24:b:9:DA:H61	26:d:40:DT:H3	1.64	0.45
1:A:398:HIS:N	1:A:402:ASP:OD2	2.50	0.44
1:A:1162:MET:N	1:A:1162:MET:SD	2.90	0.44
1:A:1166:VAL:HG12	1:A:1170:MET:HE1	1.99	0.44
2:B:135:SER:O	2:B:139:LEU:HG	2.17	0.44
2:B:1088:LEU:HD23	2:B:1088:LEU:C	2.43	0.44
3:D:546:ALA:O	3:D:549:VAL:HG12	2.17	0.44
3:D:678:LEU:HD11	3:D:686:TYR:HD2	1.82	0.44
3:D:686:TYR:OH	3:D:691:ASP:OD2	2.31	0.44
5:F:448:LEU:HD21	5:F:452:VAL:HG11	1.98	0.44
6:G:899:LEU:HD11	6:G:932:GLU:OE2	2.17	0.44
9:K:456:ILE:HD12	9:K:492:LEU:O	2.16	0.44
14:1:359:VAL:HG21	15:2:1106:ARG:CD	2.47	0.44
14:1:604:ARG:NH1	14:1:650:GLY:O	2.50	0.44
14:1:1123:ARG:NH1	14:1:1126:GLU:OE2	2.51	0.44
14:1:1133:LYS:CG	14:1:1133:LYS:O	2.65	0.44
15:2:590:LEU:HD23	15:2:597:ILE:HD13	1.98	0.44
24:b:8:DG:H2''	24:b:9:DA:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:l:22:PHE:HE1	34:l:27:GLU:CA	2.30	0.44
1:A:991:MET:SD	1:A:992:LYS:N	2.90	0.44
1:A:1641:LEU:O	1:A:1657:ARG:NE	2.50	0.44
2:B:466:PHE:HB3	2:B:476:PHE:HZ	1.82	0.44
3:D:822:ALA:HB2	3:D:948:PHE:HE2	1.82	0.44
4:E:782:LEU:HD23	4:E:782:LEU:C	2.43	0.44
5:F:382:MET:HB3	5:F:383:PRO:HD2	1.98	0.44
7:H:419:LEU:HD21	7:H:459:ILE:CD1	2.47	0.44
7:H:766:GLU:HG3	7:H:769:VAL:HG12	1.99	0.44
8:I:101:ILE:HB	8:I:125:ALA:HB2	1.98	0.44
9:K:95:PRO:HB3	9:K:159:LEU:CD2	2.47	0.44
11:P:352:LEU:HD12	11:P:365:LEU:HD11	2.00	0.44
12:Q:236:LEU:HD12	12:Q:237:VAL:N	2.31	0.44
14:1:388:MET:HE1	15:2:1062:ARG:O	2.17	0.44
14:1:599:HIS:C	14:1:600:ILE:HD13	2.41	0.44
14:1:1289:GLU:HA	14:1:1292:MET:HG2	1.99	0.44
15:2:65:ILE:O	15:2:65:ILE:HG23	2.16	0.44
15:2:556:ILE:HG12	15:2:576:ILE:HD11	1.99	0.44
15:2:598:VAL:HG12	15:2:599:SER:N	2.31	0.44
17:4:162:ARG:O	17:4:162:ARG:NH1	2.50	0.44
26:d:7:DA:C6	26:d:8:DG:C6	3.06	0.44
32:j:513:VAL:HG21	32:j:518:LEU:HD21	1.98	0.44
1:A:1253:ILE:HB	1:A:1258:MET:SD	2.56	0.44
2:B:685:ASP:OD1	2:B:686:GLN:N	2.50	0.44
3:D:253:VAL:O	3:D:256:ILE:HG22	2.17	0.44
8:I:147:VAL:O	8:I:147:VAL:HG12	2.15	0.44
11:P:336:ASP:OD1	11:P:337:ALA:N	2.50	0.44
14:1:320:ASN:OD1	14:1:338:SER:N	2.51	0.44
14:1:672:ILE:HG23	14:1:676:ILE:CD1	2.47	0.44
14:1:1171:ALA:O	20:7:59:THR:HG23	2.18	0.44
16:3:187:ASP:OD2	16:3:192:LEU:N	2.40	0.44
16:3:252:LEU:HD23	22:9:98:LEU:HD11	1.99	0.44
17:4:84:ILE:O	17:4:87:ILE:HG12	2.17	0.44
29:g:559:ASN:CA	29:g:562:ILE:HD11	2.48	0.44
3:D:780:LEU:HD23	3:D:780:LEU:C	2.43	0.44
3:D:845:LEU:HD21	3:D:954:VAL:HG21	1.99	0.44
5:F:5:LEU:HD11	5:F:53:VAL:HG23	1.99	0.44
6:G:72:PHE:CD2	6:G:125:MET:HE1	2.52	0.44
7:H:550:VAL:HG21	7:H:571:TYR:CZ	2.53	0.44
11:P:178:THR:HG21	11:P:180:MET:HE2	2.00	0.44
11:P:226:GLU:O	11:P:229:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:P:427:MET:N	11:P:428:PRO:HD2	2.33	0.44
16:3:9:VAL:CG2	22:9:101:LEU:HD11	2.47	0.44
33:k:127:CYS:SG	33:k:129:LYS:NZ	2.84	0.44
1:A:407:SER:O	1:A:410:ILE:HG22	2.17	0.44
1:A:684:ALA:O	1:A:687:GLN:HG2	2.18	0.44
2:B:262:LEU:HD12	2:B:265:ARG:CZ	2.47	0.44
2:B:382:VAL:HG13	2:B:383:VAL:N	2.33	0.44
2:B:922:THR:HA	2:B:925:GLU:OE2	2.16	0.44
3:D:216:ILE:HG21	3:D:251:ALA:HB3	1.98	0.44
3:D:432:ILE:HG21	3:D:466:ALA:HB1	1.99	0.44
3:D:787:LEU:HD21	3:D:798:ILE:HG21	2.00	0.44
11:P:421:LEU:HA	11:P:424:ILE:HG22	1.99	0.44
14:1:734:ARG:HA	14:1:734:ARG:HD3	1.80	0.44
32:j:753:VAL:HG22	32:j:754:GLY:N	2.32	0.44
33:k:107:PHE:O	33:k:160:ILE:HA	2.18	0.44
1:A:1677:ILE:HD12	1:A:1698:LEU:HD13	2.00	0.44
2:B:921:VAL:O	2:B:924:GLU:N	2.51	0.44
3:D:128:ALA:HB1	3:D:169:LYS:HE3	2.00	0.44
3:D:557:THR:OG1	3:D:558:CYS:N	2.50	0.44
3:D:624:LEU:HD12	3:D:627:LEU:CD2	2.47	0.44
3:D:863:VAL:HG22	3:D:913:LEU:CD2	2.48	0.44
6:G:379:LEU:HD12	6:G:382:LEU:HD23	1.99	0.44
7:H:597:LEU:O	7:H:601:THR:HG23	2.18	0.44
14:1:600:ILE:HD11	14:1:660:MET:HE1	2.00	0.44
14:1:651:SER:OG	14:1:652:LEU:N	2.51	0.44
15:2:1095:ILE:HD13	15:2:1103:LEU:HD13	2.00	0.44
16:3:7:PRO:HD2	22:9:100:LEU:HD11	2.00	0.44
20:7:86:CYS:O	20:7:90:GLY:N	2.49	0.44
20:7:86:CYS:SG	20:7:121:HIS:HB3	2.57	0.44
21:8:35:LEU:HD11	21:8:40:LEU:HD22	2.00	0.44
31:i:64:MET:SD	31:i:64:MET:N	2.91	0.44
2:B:524:GLU:OE1	2:B:524:GLU:N	2.51	0.44
2:B:733:ILE:HG22	2:B:734:THR:N	2.33	0.44
3:D:310:GLU:OE1	3:D:310:GLU:N	2.51	0.44
4:E:770:GLN:C	4:E:772:VAL:H	2.26	0.44
4:E:871:LEU:HD12	4:E:878:LEU:HD11	1.98	0.44
5:F:88:LEU:HB3	5:F:134:LEU:HD11	1.99	0.44
5:F:392:LEU:O	5:F:408:TRP:NE1	2.48	0.44
6:G:38:LEU:C	6:G:38:LEU:HD12	2.43	0.44
6:G:632:SER:O	6:G:635:ILE:HG22	2.18	0.44
9:K:83:MET:SD	9:K:125:MET:HE1	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:47:THR:OG1	14:1:52:PRO:HA	2.17	0.44
14:1:94:VAL:O	14:1:250:VAL:HG22	2.18	0.44
14:1:286:ILE:O	14:1:290:LEU:HD23	2.17	0.44
14:1:781:ILE:O	14:1:784:VAL:HG12	2.18	0.44
14:1:1010:VAL:O	14:1:1013:VAL:HG12	2.18	0.44
15:2:296:GLU:O	15:2:299:GLU:HG2	2.18	0.44
19:6:66:GLU:OE1	19:6:66:GLU:N	2.45	0.44
19:6:96:VAL:HA	19:6:116:VAL:HA	2.00	0.44
32:j:710:VAL:CG2	32:j:750:LEU:HD12	2.48	0.44
33:k:5:ILE:HB	34:l:29:ALA:CB	2.47	0.44
1:A:343:ILE:HD12	15:2:582:GLN:NE2	2.33	0.44
1:A:849:ILE:O	1:A:853:VAL:HG23	2.18	0.44
2:B:476:PHE:HA	2:B:479:MET:HB3	1.99	0.44
4:E:607:LEU:HD12	4:E:608:SER:N	2.33	0.44
6:G:218:LEU:HD22	6:G:238:PHE:HD2	1.83	0.44
6:G:692:SER:OG	6:G:693:PHE:N	2.50	0.44
6:G:693:PHE:O	6:G:693:PHE:CG	2.70	0.44
7:H:542:TRP:HA	7:H:572:ILE:HD11	2.00	0.44
8:I:4:TYR:HE1	8:I:504:VAL:HG13	1.83	0.44
9:K:159:LEU:C	9:K:159:LEU:HD23	2.43	0.44
12:Q:52:VAL:HG22	12:Q:53:THR:N	2.33	0.44
14:1:359:VAL:HG21	15:2:1106:ARG:HD3	1.98	0.44
14:1:1863:UNK:O	14:1:1864:UNK:C	2.65	0.44
15:2:348:LEU:O	15:2:351:VAL:HG22	2.17	0.44
15:2:635:LEU:CD1	15:2:661:VAL:HG21	2.48	0.44
15:2:954:MET:HE1	15:2:966:ILE:CG1	2.48	0.44
19:6:96:VAL:CA	19:6:116:VAL:HG23	2.48	0.44
32:j:624:LEU:HD23	32:j:636:PHE:CE2	2.53	0.44
1:A:1751:ASP:OD1	1:A:1751:ASP:N	2.51	0.44
2:B:143:LEU:C	2:B:143:LEU:HD23	2.43	0.44
2:B:1188:CYS:O	2:B:1192:THR:HG23	2.18	0.44
3:D:414:ASP:HA	3:D:417:VAL:HG12	1.99	0.44
3:D:561:MET:H	3:D:562:PRO:HD2	1.83	0.44
3:D:687:LEU:HD23	3:D:687:LEU:H	1.83	0.44
4:E:637:GLU:OE1	4:E:639:LEU:N	2.51	0.44
4:E:841:VAL:HG13	4:E:842:GLU:N	2.33	0.44
4:E:940:ARG:HD3	4:E:941:LEU:HD22	2.00	0.44
6:G:293:GLN:O	6:G:297:GLU:HG2	2.17	0.44
6:G:386:ALA:O	6:G:390:LEU:HG	2.18	0.44
6:G:594:LEU:HD11	6:G:628:LEU:CB	2.48	0.44
8:I:294:ASN:OD1	8:I:390:PRO:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:226:HIS:O	9:K:229:VAL:HG22	2.18	0.44
12:Q:185:ARG:HA	12:Q:195:MET:HE1	1.99	0.44
12:Q:277:GLU:OE2	12:Q:287:LEU:HD11	2.18	0.44
14:1:978:VAL:C	14:1:979:LEU:HD22	2.42	0.44
15:2:383:ASP:OD2	15:2:390:ASN:ND2	2.51	0.44
15:2:403:LEU:CD2	15:2:444:LEU:HD23	2.48	0.44
24:b:25:DC:N4	26:d:23:DC:N4	2.66	0.44
27:e:144:LEU:HD13	27:e:149:LEU:N	2.32	0.44
29:g:538:LEU:HD13	29:g:574:PRO:HB2	2.00	0.44
31:i:23:LYS:HB2	31:i:28:PHE:CE1	2.52	0.44
1:A:2102:LEU:O	1:A:2106:LEU:HD23	2.18	0.43
2:B:28:LYS:O	2:B:29:VAL:HG12	2.18	0.43
3:D:769:LEU:N	3:D:770:PRO:HD2	2.33	0.43
3:D:915:LEU:HB2	3:D:948:PHE:CD1	2.53	0.43
5:F:584:ILE:HG22	5:F:585:ALA:N	2.32	0.43
6:G:552:GLN:C	6:G:553:VAL:HG22	2.43	0.43
8:I:375:HIS:O	8:I:375:HIS:ND1	2.51	0.43
11:P:459:ARG:CZ	11:P:496:LEU:HD21	2.48	0.43
14:1:26:LEU:HD22	15:2:1168:ALA:HB2	1.98	0.43
14:1:538:VAL:HG12	14:1:539:GLN:N	2.33	0.43
14:1:1339:ASP:OD1	14:1:1340:GLY:N	2.51	0.43
14:1:1344:MET:SD	14:1:1344:MET:O	2.76	0.43
15:2:47:PHE:CB	15:2:155:MET:HE3	2.48	0.43
15:2:972:ILE:N	15:2:973:PRO:HD2	2.33	0.43
24:b:35:DA:H2"	24:b:36:DG:C8	2.52	0.43
27:e:79:ILE:HD13	27:e:98:LYS:HA	2.00	0.43
29:g:263:GLN:O	29:g:266:GLN:NE2	2.51	0.43
29:g:410:GLU:O	29:g:414:LEU:HD23	2.19	0.43
29:g:531:ARG:HG3	29:g:565:THR:HG22	1.99	0.43
1:A:259:THR:OG1	1:A:356:SER:O	2.34	0.43
1:A:1793:SER:O	1:A:1797:ARG:HG2	2.18	0.43
3:D:257:TRP:CD2	3:D:305:LEU:HD12	2.54	0.43
3:D:521:LEU:N	3:D:521:LEU:HD12	2.33	0.43
3:D:634:GLU:OE1	3:D:634:GLU:HA	2.18	0.43
4:E:473:PHE:CE2	4:E:477:LEU:HD11	2.54	0.43
5:F:238:ALA:HB3	5:F:309:PHE:C	2.44	0.43
6:G:203:HIS:O	6:G:204:MET:HE2	2.18	0.43
7:H:253:CYS:SG	7:H:277:LYS:O	2.76	0.43
7:H:892:ASN:OD1	7:H:894:HIS:CE1	2.71	0.43
8:I:58:LYS:N	8:I:58:LYS:HD2	2.33	0.43
8:I:645:VAL:HG12	8:I:648:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:67:SER:OG	9:K:68:HIS:N	2.51	0.43
14:1:362:SER:OG	15:2:1084:LEU:HB3	2.18	0.43
14:1:857:THR:HG23	14:1:858:GLY:N	2.33	0.43
15:2:404:PHE:HA	15:2:407:MET:SD	2.58	0.43
15:2:635:LEU:CD1	15:2:661:VAL:HG11	2.48	0.43
20:7:70:ALA:HB1	20:7:120:GLY:HA2	2.00	0.43
32:j:474:MET:HA	32:j:492:ILE:HD11	2.00	0.43
1:A:1625:LEU:C	1:A:1625:LEU:HD12	2.42	0.43
2:B:746:THR:O	2:B:747:ASN:C	2.61	0.43
3:D:545:ILE:HG23	3:D:576:LEU:HD11	2.00	0.43
3:D:710:MET:HE2	3:D:948:PHE:HB3	2.00	0.43
6:G:367:LEU:HD22	6:G:382:LEU:HD11	2.01	0.43
7:H:748:THR:HG21	7:H:753:TYR:CD1	2.53	0.43
9:K:416:GLU:HG2	9:K:417:ALA:N	2.32	0.43
11:P:204:GLU:O	11:P:208:MET:HG2	2.18	0.43
11:P:408:ILE:HG23	11:P:409:VAL:N	2.33	0.43
14:1:979:LEU:HD11	14:1:1040:LEU:HD23	2.00	0.43
14:1:1007:ILE:HG23	14:1:1008:LYS:HD3	2.00	0.43
14:1:1152:GLU:O	14:1:1155:LYS:HG2	2.19	0.43
14:1:1212:LEU:HD21	14:1:1214:VAL:HG13	1.99	0.43
14:1:1343:LEU:O	14:1:1344:MET:HB3	2.17	0.43
16:3:8:THR:OG1	16:3:24:GLU:HB2	2.18	0.43
27:e:156:LEU:HD23	27:e:156:LEU:H	1.83	0.43
1:A:549:MET:SD	1:A:582:ILE:HD12	2.59	0.43
1:A:891:LEU:HD21	1:A:912:GLU:HG3	2.00	0.43
1:A:982:SER:O	1:A:987:ARG:NH1	2.47	0.43
1:A:1722:GLU:HG2	1:A:1723:LEU:N	2.32	0.43
2:B:542:SER:O	2:B:543:ASN:OD1	2.37	0.43
2:B:1131:VAL:HG23	7:H:924:ALA:H	1.84	0.43
2:B:1182:ASP:OD1	2:B:1182:ASP:C	2.62	0.43
3:D:492:ASN:C	3:D:492:ASN:HD22	2.24	0.43
3:D:908:GLN:HE22	3:D:955:TYR:HE1	1.57	0.43
5:F:123:ALA:HB3	5:F:166:GLN:HG3	1.99	0.43
6:G:70:ASP:OD1	6:G:106:ARG:NE	2.52	0.43
6:G:441:ALA:HB2	6:G:449:MET:HE1	1.99	0.43
7:H:893:CYS:HB3	7:H:896:GLN:OE1	2.18	0.43
8:I:246:HIS:N	8:I:247:PRO:CD	2.82	0.43
8:I:584:LEU:HD23	8:I:584:LEU:H	1.82	0.43
11:P:135:LEU:HD12	11:P:143:SER:HB2	2.00	0.43
11:P:284:VAL:HG12	11:P:288:GLN:NE2	2.34	0.43
11:P:470:VAL:HG23	11:P:478:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:141:LEU:HA	14:1:144:VAL:HG12	2.00	0.43
14:1:868:MET:O	14:1:868:MET:HG2	2.18	0.43
15:2:912:ASN:OD1	15:2:915:GLY:N	2.51	0.43
29:g:334:LEU:O	29:g:338:MET:HG2	2.18	0.43
3:D:161:ASP:OD1	3:D:162:THR:N	2.51	0.43
3:D:391:ARG:NH1	3:D:422:ASP:OD1	2.51	0.43
4:E:770:GLN:C	4:E:771:GLU:OE1	2.61	0.43
4:E:924:LEU:O	4:E:927:MET:HB3	2.19	0.43
6:G:22:ALA:HA	6:G:55:TYR:CE2	2.53	0.43
6:G:572:GLU:O	6:G:576:THR:HG23	2.19	0.43
7:H:95:ASP:O	7:H:99:LEU:HD12	2.18	0.43
12:Q:113:ILE:HG23	12:Q:153:LEU:HD22	2.00	0.43
14:1:1192:TRP:HA	14:1:1195:VAL:HG12	2.00	0.43
15:2:1076:GLU:OE1	15:2:1076:GLU:N	2.52	0.43
24:b:25:DC:H42	26:d:24:DG:H1	1.67	0.43
27:e:111:GLU:HA	27:e:118:GLN:OE1	2.17	0.43
29:g:557:LEU:HD13	29:g:578:PHE:CD2	2.53	0.43
32:j:563:MET:HE3	32:j:618:PHE:CD2	2.54	0.43
33:k:83:GLU:O	33:k:147:ILE:N	2.51	0.43
1:A:2146:GLU:O	1:A:2150:LEU:HD23	2.19	0.43
2:B:1045:LEU:HG	2:B:1057:ALA:HB2	2.01	0.43
4:E:483:GLU:O	4:E:487:GLU:HG2	2.18	0.43
5:F:5:LEU:HD23	5:F:125:ILE:HG12	1.99	0.43
5:F:383:PRO:CG	5:F:389:LEU:HD23	2.49	0.43
6:G:514:LYS:O	6:G:515:GLN:C	2.61	0.43
6:G:601:ILE:CD1	6:G:621:VAL:HG13	2.48	0.43
6:G:771:TYR:CD2	6:G:772:MET:HG2	2.54	0.43
7:H:469:LEU:HD11	7:H:473:GLU:HB2	2.00	0.43
7:H:479:ASP:HA	7:H:482:ARG:HG2	2.01	0.43
14:1:48:GLU:HB2	14:1:51:ARG:O	2.18	0.43
14:1:458:PHE:CE2	14:1:501:MET:SD	3.12	0.43
15:2:744:MET:HE3	15:2:908:MET:HE3	1.99	0.43
19:6:10:PHE:HB2	19:6:56:PHE:CE2	2.54	0.43
19:6:90:TYR:CE2	19:6:92:MET:HE3	2.53	0.43
1:A:2094:SER:OG	1:A:2095:ALA:N	2.50	0.43
6:G:488:GLU:O	6:G:491:VAL:HG12	2.19	0.43
8:I:41:LEU:HD11	8:I:81:PRO:HD2	2.01	0.43
9:K:3:GLU:OE1	9:K:3:GLU:N	2.52	0.43
12:Q:189:VAL:HG13	12:Q:189:VAL:O	2.17	0.43
14:1:672:ILE:CG2	14:1:676:ILE:HD12	2.49	0.43
24:b:26:DG:H2"	24:b:27:DG:OP1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:i:24:THR:OG1	31:i:27:GLN:OE1	2.37	0.43
1:A:228:LYS:HG2	1:A:328:TYR:CE2	2.53	0.43
1:A:533:PHE:HB3	1:A:536:ARG:HB3	2.00	0.43
2:B:254:CYS:SG	2:B:255:LYS:N	2.92	0.43
2:B:1084:MET:HE2	2:B:1107:LEU:HD21	2.00	0.43
4:E:568:PRO:HG2	4:E:569:PRO:HD3	2.00	0.43
5:F:154:GLY:CA	5:F:459:LEU:HD21	2.49	0.43
5:F:219:CYS:O	5:F:223:LEU:HG	2.19	0.43
5:F:458:LYS:HG2	5:F:462:GLN:HE22	1.83	0.43
6:G:546:TYR:O	6:G:550:LEU:HG	2.18	0.43
9:K:321:VAL:HG12	9:K:322:PHE:O	2.18	0.43
9:K:421:GLU:HA	9:K:437:MET:CE	2.49	0.43
11:P:424:ILE:HD13	11:P:450:TRP:CE3	2.54	0.43
14:1:492:TYR:CD2	14:1:501:MET:SD	3.12	0.43
14:1:691:ASP:OD2	14:1:765:ASN:ND2	2.46	0.43
14:1:866:LYS:NZ	15:2:1088:GLU:OE2	2.49	0.43
14:1:1305:SER:OG	14:1:1306:LYS:N	2.51	0.43
15:2:333:GLU:C	15:2:335:ARG:H	2.27	0.43
24:b:25:DC:N3	26:d:24:DG:N2	2.51	0.43
1:A:1762:LEU:HG	1:A:1766:LEU:HD23	2.01	0.43
2:B:137:ARG:O	2:B:141:LEU:HD13	2.19	0.43
2:B:456:LEU:O	2:B:460:ILE:HG23	2.18	0.43
2:B:771:VAL:HG12	2:B:775:ILE:HD13	2.01	0.43
6:G:612:ASN:O	6:G:614:LEU:HD12	2.19	0.43
7:H:471:ASP:OD1	7:H:471:ASP:C	2.61	0.43
7:H:526:ARG:HG3	7:H:569:LEU:HD21	2.01	0.43
8:I:357:LEU:O	8:I:358:PRO:C	2.62	0.43
8:I:655:LEU:C	8:I:655:LEU:HD12	2.44	0.43
9:K:82:GLU:HB3	9:K:125:MET:HE2	2.01	0.43
9:K:519:ASP:OD2	9:K:529:ARG:NH1	2.52	0.43
11:P:209:PHE:HZ	11:P:228:CYS:HB2	1.82	0.43
11:P:412:ALA:HB1	11:P:450:TRP:CZ2	2.53	0.43
14:1:1022:ILE:HD11	14:1:1076:PHE:CE1	2.54	0.43
14:1:1224:ARG:O	14:1:1226:LEU:HD22	2.19	0.43
14:1:1473:LEU:HD13	18:5:106:ILE:HD12	2.01	0.43
15:2:907:VAL:HG12	15:2:921:ILE:HG23	2.01	0.43
16:3:252:LEU:O	16:3:256:LEU:HD23	2.18	0.43
16:3:253:LYS:HB2	22:9:98:LEU:HD22	2.00	0.43
19:6:94:GLY:HA3	19:6:118:TYR:HA	2.01	0.43
20:7:17:CYS:SG	20:7:44:TYR:HB3	2.59	0.43
23:a:27:GLU:OE1	23:a:37:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:b:32:DA:H2"	24:b:33:DG:H8	1.84	0.43
29:g:445:THR:HG23	29:g:446:ASP:N	2.33	0.43
32:j:261:THR:O	32:j:265:LYS:HG2	2.19	0.43
33:k:34:VAL:HG22	33:k:45:VAL:HG11	2.01	0.43
1:A:751:ASN:OD1	1:A:751:ASN:N	2.51	0.43
2:B:805:VAL:O	2:B:805:VAL:HG23	2.19	0.43
3:D:206:ASP:O	3:D:212:ARG:NH2	2.51	0.43
3:D:458:ASP:CG	3:D:459:SER:H	2.26	0.43
5:F:95:ALA:O	5:F:99:LEU:HD23	2.19	0.43
5:F:350:VAL:HG22	5:F:366:GLY:O	2.19	0.43
5:F:384:TYR:HB3	5:F:419:MET:SD	2.59	0.43
7:H:676:LEU:O	7:H:695:GLN:NE2	2.52	0.43
14:1:1128:ILE:HG22	14:1:1414:ILE:HB	2.01	0.43
15:2:483:ARG:NH2	15:2:528:LEU:HA	2.34	0.43
15:2:985:LEU:CD1	15:2:1015:LEU:HD11	2.44	0.43
15:2:1035:ARG:NH1	15:2:1036:LYS:O	2.51	0.43
15:2:1072:ARG:O	15:2:1112:ASP:HB3	2.19	0.43
29:g:509:VAL:HG13	29:g:510:LEU:N	2.34	0.43
1:A:1071:SER:HB3	1:A:1123:ILE:HD11	2.00	0.42
3:D:200:ILE:HD12	3:D:219:MET:SD	2.59	0.42
4:E:694:GLU:HA	4:E:694:GLU:OE2	2.19	0.42
5:F:268:ILE:HD13	5:F:379:LEU:HD21	2.01	0.42
6:G:811:SER:O	6:G:819:ILE:HD13	2.18	0.42
7:H:516:LEU:HB2	7:H:528:ILE:HG21	2.00	0.42
8:I:453:ASN:O	8:I:457:VAL:HG23	2.19	0.42
8:I:651:VAL:HG13	8:I:652:LEU:HD22	2.01	0.42
9:K:70:HIS:CE1	9:K:157:HIS:HE2	2.33	0.42
11:P:86:VAL:O	11:P:90:LEU:HG	2.19	0.42
14:1:319:ASP:HB3	14:1:340:LYS:HD3	2.01	0.42
14:1:331:LYS:HE2	26:d:35:DG:C2	2.54	0.42
14:1:466:LYS:N	14:1:1093:GLN:HE21	2.16	0.42
15:2:1084:LEU:HD23	15:2:1085:ARG:O	2.19	0.42
16:3:58:VAL:O	16:3:58:VAL:HG22	2.19	0.42
28:f:152:ASP:O	28:f:156:LEU:N	2.52	0.42
32:j:340:PHE:HZ	32:j:359:LEU:HD22	1.84	0.42
32:j:535:GLU:OE1	32:j:535:GLU:N	2.50	0.42
1:A:1742:GLU:O	1:A:1745:THR:HG23	2.18	0.42
1:A:2163:PHE:HE2	1:A:2167:MET:HE3	1.84	0.42
4:E:689:LEU:O	4:E:693:VAL:HG22	2.19	0.42
4:E:878:LEU:HD13	4:E:914:MET:SD	2.58	0.42
5:F:379:LEU:HD12	5:F:379:LEU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:384:GLN:HA	6:G:387:VAL:HG12	2.02	0.42
7:H:445:ASN:HA	7:H:448:LEU:HD12	2.01	0.42
7:H:757:LEU:O	7:H:761:ILE:HG12	2.18	0.42
8:I:277:MET:SD	8:I:447:PRO:O	2.77	0.42
8:I:298:PRO:HB2	8:I:398:PRO:HA	2.01	0.42
12:Q:38:ILE:HD11	12:Q:108:ARG:CG	2.40	0.42
12:Q:185:ARG:O	12:Q:187:GLN:N	2.51	0.42
13:U:507:UNK:O	13:U:510:UNK:N	2.52	0.42
14:1:1366:PHE:HA	14:1:1374:VAL:CG1	2.48	0.42
15:2:584:MET:HE2	15:2:588:ARG:HH12	1.80	0.42
16:3:78:ILE:HG12	16:3:82:LEU:CD1	2.48	0.42
32:j:255:VAL:HG12	32:j:259:GLU:HB3	2.01	0.42
32:j:612:GLY:O	32:j:624:LEU:HD11	2.19	0.42
1:A:224:GLU:O	1:A:228:LYS:HG3	2.19	0.42
1:A:328:TYR:CZ	1:A:332:MET:HE1	2.55	0.42
1:A:1293:GLN:HE22	1:A:1296:ARG:NH1	2.17	0.42
2:B:52:MET:SD	6:G:643:THR:HA	2.60	0.42
3:D:701:MET:O	3:D:704:THR:OG1	2.31	0.42
4:E:991:VAL:HG22	7:H:160:PRO:HG2	2.01	0.42
5:F:389:LEU:HB2	5:F:415:TYR:CZ	2.54	0.42
8:I:112:TYR:OH	8:I:180:ARG:O	2.36	0.42
14:1:264:VAL:HG23	14:1:272:ASN:HB2	2.01	0.42
14:1:798:ILE:HD13	14:1:838:PHE:CD1	2.54	0.42
15:2:286:GLU:HG2	15:2:558:PRO:HB2	2.02	0.42
17:4:103:LEU:HD23	17:4:104:ILE:N	2.35	0.42
25:c:38:G:H2'	25:c:39:A:C8	2.54	0.42
1:A:1703:HIS:O	1:A:1704:VAL:C	2.60	0.42
2:B:433:PHE:CD2	2:B:479:MET:HE1	2.44	0.42
2:B:532:THR:CG2	2:B:571:VAL:HG21	2.50	0.42
2:B:604:LEU:HD21	2:B:658:TYR:HE1	1.85	0.42
2:B:689:ILE:HG23	2:B:690:LYS:N	2.35	0.42
4:E:455:GLY:O	4:E:459:GLU:N	2.47	0.42
4:E:859:GLU:OE1	4:E:859:GLU:N	2.47	0.42
7:H:849:TYR:CE2	7:H:890:LEU:HD13	2.54	0.42
7:H:932:ILE:HD11	7:H:937:ILE:HB	2.00	0.42
8:I:296:LEU:HD21	8:I:405:VAL:HG23	2.01	0.42
8:I:641:GLU:O	8:I:645:VAL:HG13	2.20	0.42
11:P:240:LEU:HD12	11:P:245:MET:HE3	2.00	0.42
11:P:574:ASP:OD1	11:P:578:PHE:CE2	2.73	0.42
14:1:517:GLU:OE2	14:1:523:ARG:NH2	2.52	0.42
15:2:848:LEU:HA	15:2:854:ILE:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:4:170:LEU:HD23	17:4:208:LEU:HB2	2.01	0.42
31:i:52:CYS:SG	31:i:97:ILE:HD13	2.60	0.42
1:A:404:ASP:O	1:A:408:HIS:ND1	2.41	0.42
3:D:253:VAL:HG11	3:D:290:MET:CE	2.49	0.42
6:G:601:ILE:HD11	6:G:621:VAL:HG22	2.01	0.42
9:K:222:LEU:HD11	9:K:251:LEU:HD11	2.02	0.42
11:P:89:LEU:O	11:P:92:PRO:HG2	2.19	0.42
11:P:177:ASP:OD1	11:P:178:THR:N	2.53	0.42
11:P:222:LEU:O	11:P:225:VAL:HG22	2.19	0.42
11:P:271:GLN:HA	11:P:274:VAL:HG22	2.00	0.42
12:Q:64:ASP:OD1	12:Q:291:PRO:HB3	2.19	0.42
14:1:24:GLY:C	15:2:1168:ALA:HB3	2.45	0.42
14:1:833:PRO:HG3	15:2:677:MET:CE	2.49	0.42
15:2:263:ILE:HG22	15:2:265:GLN:H	1.85	0.42
15:2:552:ASN:HB2	15:2:555:GLU:OE1	2.19	0.42
17:4:162:ARG:O	17:4:164:LYS:NZ	2.33	0.42
34:l:39:MET:SD	34:l:40:LEU:N	2.92	0.42
1:A:487:ASN:OD1	1:A:488:LYS:N	2.52	0.42
1:A:706:LEU:HD13	1:A:838:PRO:HG3	2.01	0.42
2:B:67:ASP:O	2:B:71:ILE:HG12	2.20	0.42
3:D:458:ASP:OD1	3:D:459:SER:N	2.52	0.42
3:D:837:PHE:O	3:D:958:PRO:HA	2.20	0.42
6:G:413:LEU:HD13	6:G:452:CYS:HB2	2.02	0.42
7:H:693:LEU:O	7:H:697:LEU:HD23	2.19	0.42
8:I:67:GLU:OE2	8:I:155:LEU:N	2.48	0.42
8:I:77:VAL:HG22	8:I:78:ASP:H	1.84	0.42
9:K:323:ALA:HB1	9:K:333:SER:HB3	2.01	0.42
11:P:18:ASP:OD1	11:P:19:GLU:N	2.53	0.42
11:P:400:LEU:C	11:P:400:LEU:HD12	2.44	0.42
14:1:86:GLY:C	14:1:255:VAL:HG12	2.45	0.42
14:1:384:ILE:HD11	15:2:1059:ILE:CD1	2.46	0.42
19:6:25:VAL:HG21	19:6:121:LEU:HD11	2.01	0.42
33:k:89:VAL:HG13	33:k:97:LEU:HD11	2.01	0.42
33:k:117:MET:SD	33:k:128:TYR:HB3	2.59	0.42
1:A:343:ILE:HD12	15:2:582:GLN:HE21	1.83	0.42
1:A:1536:VAL:O	1:A:1540:LEU:N	2.49	0.42
2:B:523:GLN:HB2	2:B:524:GLU:OE1	2.19	0.42
2:B:558:TYR:OH	2:B:562:ARG:NH2	2.52	0.42
2:B:645:ILE:HG23	2:B:646:THR:H	1.85	0.42
3:D:387:MET:O	3:D:390:VAL:HG22	2.20	0.42
5:F:321:LYS:C	5:F:434:MET:HE1	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:370:ILE:HG13	6:G:371:THR:N	2.34	0.42
6:G:804:ILE:HD13	6:G:835:VAL:HG23	2.00	0.42
7:H:137:PRO:O	7:H:141:MET:HE3	2.20	0.42
7:H:650:LEU:HB2	7:H:651:PRO:HD3	2.02	0.42
7:H:726:SER:OG	7:H:749:LEU:HD21	2.20	0.42
8:I:127:GLU:O	8:I:130:VAL:HG12	2.20	0.42
9:K:8:PRO:HG2	9:K:438:PRO:HB2	2.01	0.42
9:K:519:ASP:OD2	9:K:529:ARG:NH2	2.50	0.42
9:K:558:LEU:HB3	9:K:572:LEU:HD11	2.02	0.42
12:Q:4:LYS:HB3	12:Q:8:LYS:NZ	2.34	0.42
14:1:459:ASN:ND2	14:1:469:MET:HE1	2.33	0.42
14:1:734:ARG:O	14:1:737:PHE:N	2.51	0.42
14:1:811:ILE:HD11	20:7:79:PRO:HA	2.02	0.42
14:1:865:ILE:O	14:1:869:GLU:HG3	2.19	0.42
16:3:58:VAL:HG21	21:8:59:LEU:HB3	2.01	0.42
22:9:24:ASP:HB3	22:9:30:ALA:HB3	2.00	0.42
24:b:40:DG:H2''	24:b:41:DC:H5'	2.02	0.42
29:g:295:ALA:HB1	29:g:309:ASP:OD1	2.19	0.42
32:j:433:LEU:HB3	32:j:436:LEU:HD12	2.02	0.42
34:l:31:THR:HB	34:l:94:LYS:HD3	2.02	0.42
2:B:457:SER:O	2:B:460:ILE:HG12	2.20	0.42
3:D:555:ALA:HA	3:D:561:MET:SD	2.59	0.42
6:G:52:PHE:CE2	6:G:65:PHE:HE1	2.37	0.42
6:G:370:ILE:HD11	6:G:382:LEU:HD21	2.01	0.42
6:G:382:LEU:HD12	6:G:385:ASP:HB2	2.02	0.42
6:G:493:LEU:O	6:G:497:ILE:HG22	2.20	0.42
7:H:897:VAL:HG13	7:H:898:ALA:N	2.33	0.42
8:I:137:MET:HG2	8:I:182:TYR:OH	2.20	0.42
8:I:285:LEU:HD13	8:I:295:VAL:HG11	2.01	0.42
9:K:240:PHE:CE2	25:c:25:A:OP1	2.73	0.42
11:P:29:LEU:O	11:P:29:LEU:HD23	2.20	0.42
14:1:26:LEU:HG	14:1:31:LEU:HD21	2.02	0.42
14:1:225:PHE:HA	14:1:228:ILE:HG12	2.00	0.42
14:1:721:HIS:O	20:7:110:LEU:HD23	2.20	0.42
14:1:1148:ALA:HB3	14:1:1333:GLU:OE2	2.19	0.42
14:1:1292:MET:HA	14:1:1296:MET:HG2	2.02	0.42
15:2:155:MET:HB3	15:2:185:PHE:CE1	2.54	0.42
16:3:127:VAL:O	16:3:128:ILE:HG23	2.19	0.42
29:g:185:GLN:CB	29:g:207:THR:HG21	2.50	0.42
29:g:470:LEU:O	29:g:474:VAL:HG22	2.20	0.42
2:B:411:LEU:O	2:B:415:MET:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:791:GLU:O	2:B:795:SER:OG	2.27	0.42
3:D:839:SER:N	3:D:959:LYS:O	2.53	0.42
4:E:940:ARG:HH12	4:E:944:LEU:HD13	1.84	0.42
7:H:478:VAL:HG12	7:H:482:ARG:HE	1.83	0.42
7:H:856:TYR:CE1	7:H:880:VAL:HG13	2.55	0.42
7:H:970:ASN:HB3	7:H:971:PRO:HD2	2.02	0.42
8:I:266:LEU:HD12	8:I:475:TYR:CD2	2.55	0.42
8:I:497:MET:HE1	8:I:505:LEU:HD12	2.02	0.42
11:P:319:GLU:O	11:P:323:MET:CE	2.68	0.42
14:1:99:PHE:N	14:1:1440:MET:HE2	2.35	0.42
14:1:833:PRO:HB2	15:2:506:TRP:HH2	1.85	0.42
14:1:896:LEU:HD13	14:1:980:PRO:HB3	2.02	0.42
15:2:404:PHE:CE1	15:2:440:ILE:HD11	2.55	0.42
15:2:753:TYR:O	15:2:776:ILE:HG12	2.19	0.42
15:2:961:ILE:HD11	21:8:42:ARG:HG2	2.02	0.42
17:4:151:MET:HE1	17:4:155:GLU:HG2	2.01	0.42
18:5:56:TYR:CE1	18:5:124:ILE:HD11	2.54	0.42
1:A:761:PRO:O	1:A:765:MET:HE3	2.18	0.42
1:A:1774:GLU:OE1	1:A:1774:GLU:N	2.49	0.42
1:A:2071:ASP:OD2	1:A:2109:ARG:NH2	2.52	0.42
2:B:272:CYS:SG	2:B:312:LYS:NZ	2.87	0.42
2:B:593:LEU:HB2	2:B:594:PRO:HD3	2.01	0.42
6:G:186:GLY:O	6:G:187:LEU:HB3	2.18	0.42
6:G:280:ALA:HB1	6:G:318:LEU:CD2	2.50	0.42
6:G:435:LEU:CD1	6:G:467:MET:HG3	2.50	0.42
6:G:641:LEU:C	6:G:641:LEU:HD23	2.45	0.42
6:G:824:ASN:OD1	6:G:824:ASN:C	2.63	0.42
7:H:856:TYR:CD2	7:H:884:MET:CE	3.02	0.42
9:K:71:LEU:C	9:K:73:HIS:N	2.77	0.42
9:K:252:LEU:HD23	9:K:252:LEU:HA	1.93	0.42
14:1:104:MET:HE1	14:1:193:ARG:HB3	2.02	0.42
14:1:386:ALA:O	14:1:449:HIS:CD2	2.73	0.42
14:1:681:LEU:HD21	15:2:1030:ASN:ND2	2.35	0.42
14:1:725:LEU:HD23	14:1:725:LEU:C	2.45	0.42
15:2:37:LYS:O	15:2:41:ARG:HD3	2.20	0.42
15:2:797:ASN:OD1	15:2:797:ASN:C	2.63	0.42
18:5:57:MET:C	18:5:57:MET:SD	3.03	0.42
21:8:2:ILE:HD11	21:8:56:ILE:HD13	2.02	0.42
33:k:166:ASP:OD1	33:k:167:TYR:N	2.53	0.42
1:A:146:VAL:HG13	1:A:187:LEU:HD11	2.02	0.41
1:A:1657:ARG:N	1:A:1658:PRO:HD2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:603:ILE:O	2:B:615:THR:HG23	2.20	0.41
2:B:876:ILE:HG22	2:B:880:MET:HE2	2.02	0.41
3:D:903:TRP:CZ3	3:D:907:CYS:HB2	2.55	0.41
5:F:156:GLU:OE1	5:F:156:GLU:N	2.51	0.41
6:G:176:ILE:O	6:G:177:CYS:C	2.63	0.41
6:G:623:LEU:HB3	6:G:685:TYR:HE1	1.84	0.41
7:H:422:CYS:O	7:H:426:VAL:HG12	2.20	0.41
7:H:860:GLY:HA3	7:H:876:TYR:OH	2.20	0.41
7:H:908:ASP:CG	7:H:911:THR:HG22	2.44	0.41
8:I:26:LEU:HD13	8:I:236:TYR:CD2	2.54	0.41
8:I:242:LEU:HD21	8:I:456:GLN:CD	2.45	0.41
8:I:400:LEU:HD12	8:I:409:MET:HE1	2.02	0.41
11:P:53:PRO:O	11:P:56:THR:OG1	2.32	0.41
12:Q:82:PHE:CE2	12:Q:111:ILE:HD11	2.55	0.41
14:1:1218:ARG:NH2	14:1:1250:ASP:OD1	2.53	0.41
15:2:836:THR:O	15:2:888:THR:OG1	2.28	0.41
15:2:1068:GLN:OE1	15:2:1073:GLN:O	2.38	0.41
18:5:125:ILE:HG22	18:5:127:ASP:H	1.84	0.41
19:6:71:ASP:OD1	19:6:71:ASP:N	2.52	0.41
21:8:66:GLU:OE1	21:8:66:GLU:HA	2.20	0.41
1:A:1280:ILE:HG21	1:A:1283:LYS:HG2	2.02	0.41
1:A:2071:ASP:HA	1:A:2074:SER:OG	2.20	0.41
1:A:2181:LEU:HD11	2:B:1197:ILE:CD1	2.50	0.41
4:E:515:GLY:N	4:E:516:PRO:HD2	2.35	0.41
4:E:565:THR:CG2	4:E:566:LEU:H	2.31	0.41
5:F:329:LEU:HD11	5:F:379:LEU:HD23	2.01	0.41
7:H:853:LEU:O	7:H:857:LEU:HD13	2.20	0.41
9:K:228:THR:HG21	9:K:235:VAL:HG22	2.02	0.41
9:K:240:PHE:CB	25:c:26:U:OP1	2.68	0.41
14:1:706:ILE:HG13	14:1:707:LYS:N	2.36	0.41
14:1:892:GLY:C	14:1:893:GLU:HG2	2.45	0.41
14:1:918:LYS:O	14:1:1052:ARG:NH2	2.53	0.41
15:2:369:VAL:O	15:2:373:LEU:HD23	2.20	0.41
15:2:796:MET:HE1	15:2:935:PHE:CE2	2.55	0.41
17:4:92:GLN:O	17:4:96:GLU:OE1	2.37	0.41
19:6:36:LYS:HD2	27:e:16:LYS:HD2	2.02	0.41
19:6:39:LEU:HG	19:6:123:MET:CE	2.49	0.41
32:j:305:LEU:O	32:j:307:MET:HE1	2.21	0.41
1:A:630:TRP:CG	1:A:631:PRO:HA	2.55	0.41
1:A:1722:GLU:O	1:A:1723:LEU:HD12	2.20	0.41
2:B:542:SER:O	2:B:543:ASN:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1074:LEU:HA	2:B:1114:PHE:CE2	2.56	0.41
3:D:744:LEU:HD12	3:D:745:ASP:N	2.35	0.41
3:D:851:LEU:HD13	3:D:861:VAL:HG21	2.02	0.41
6:G:536:MET:CA	6:G:536:MET:HE3	2.50	0.41
7:H:760:PHE:O	7:H:764:LEU:HD23	2.19	0.41
9:K:94:HIS:NE2	9:K:135:ALA:HB1	2.34	0.41
11:P:176:ASP:OD1	11:P:177:ASP:N	2.53	0.41
11:P:463:THR:HG22	11:P:507:VAL:HG21	2.02	0.41
12:Q:94:VAL:HG13	12:Q:95:GLU:N	2.35	0.41
14:1:724:GLU:OE1	14:1:724:GLU:N	2.52	0.41
14:1:1163:HIS:ND1	14:1:1301:ILE:O	2.51	0.41
14:1:1224:ARG:CB	14:1:1226:LEU:HD23	2.49	0.41
15:2:93:LEU:HD13	15:2:160:TYR:CD2	2.54	0.41
15:2:721:ARG:HD2	15:2:975:ARG:HB3	2.02	0.41
18:5:110:LEU:HD23	18:5:112:ASP:H	1.84	0.41
22:9:21:ILE:HD13	22:9:33:PHE:CE2	2.54	0.41
29:g:462:HIS:HB2	29:g:465:LEU:HD12	2.02	0.41
1:A:1276:LEU:HD21	1:A:1304:PHE:CE1	2.55	0.41
1:A:1713:GLN:O	1:A:1714:ARG:C	2.64	0.41
2:B:276:GLY:HA2	2:B:335:VAL:HG21	2.03	0.41
2:B:600:ILE:HD11	2:B:658:TYR:CD1	2.55	0.41
2:B:855:ILE:HD11	2:B:891:TYR:CE2	2.55	0.41
3:D:176:ASN:OD1	3:D:176:ASN:C	2.63	0.41
3:D:515:PRO:HG3	3:D:557:THR:HG21	2.03	0.41
4:E:586:GLN:NE2	4:E:631:ILE:O	2.48	0.41
5:F:67:LYS:NZ	5:F:68:GLU:OE2	2.48	0.41
6:G:826:GLN:OE1	6:G:894:LEU:O	2.37	0.41
7:H:346:ILE:HG12	7:H:424:ARG:HD3	2.03	0.41
7:H:346:ILE:HD13	7:H:421:VAL:HG13	2.03	0.41
8:I:266:LEU:CD2	8:I:457:VAL:HG21	2.51	0.41
14:1:92:LYS:HD2	14:1:307:VAL:HG21	2.02	0.41
14:1:553:VAL:HG13	14:1:588:GLY:H	1.86	0.41
14:1:784:VAL:HG23	15:2:978:ILE:HD13	2.03	0.41
15:2:727:ALA:C	15:2:728:MET:HE2	2.46	0.41
15:2:809:VAL:HG22	15:2:810:PHE:N	2.34	0.41
15:2:995:GLU:OE1	15:2:995:GLU:N	2.54	0.41
15:2:1145:GLN:HG2	15:2:1145:GLN:O	2.20	0.41
18:5:64:ARG:O	18:5:68:THR:HG22	2.21	0.41
19:6:42:ASP:HB2	19:6:121:LEU:HD12	2.02	0.41
19:6:72:ASP:OD1	19:6:72:ASP:N	2.52	0.41
24:b:13:DG:H1	26:d:36:DC:H42	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:k:164:MET:N	33:k:164:MET:SD	2.93	0.41
1:A:1630:VAL:HG12	1:A:1637:GLN:HB3	2.02	0.41
2:B:180:VAL:O	2:B:184:LEU:HD13	2.20	0.41
2:B:534:HIS:O	2:B:537:ARG:HG2	2.20	0.41
3:D:915:LEU:HD23	3:D:915:LEU:C	2.46	0.41
4:E:568:PRO:N	4:E:569:PRO:HD2	2.34	0.41
4:E:844:ASP:OD1	4:E:880:GLY:HA2	2.19	0.41
5:F:386:TYR:N	5:F:387:PRO:CD	2.84	0.41
6:G:714:SER:O	6:G:717:ILE:HG22	2.21	0.41
6:G:821:VAL:HG12	6:G:823:ASN:H	1.84	0.41
8:I:194:ILE:CG2	8:I:195:GLN:N	2.83	0.41
8:I:246:HIS:CG	8:I:247:PRO:HD3	2.55	0.41
8:I:529:MET:O	8:I:537:LEU:N	2.48	0.41
8:I:603:PHE:CB	8:I:606:ILE:HD11	2.46	0.41
9:K:94:HIS:CD2	9:K:135:ALA:HB1	2.55	0.41
11:P:52:LEU:HB3	11:P:53:PRO:HD3	2.01	0.41
14:1:18:ILE:HD12	15:2:1172:MET:O	2.20	0.41
14:1:367:ILE:HG21	14:1:501:MET:HE3	2.01	0.41
14:1:560:VAL:O	14:1:564:LEU:HD13	2.20	0.41
14:1:779:ILE:O	14:1:783:GLN:OE1	2.38	0.41
14:1:845:GLU:O	14:1:848:ILE:HG22	2.21	0.41
15:2:236:TRP:HB2	15:2:259:THR:HB	2.03	0.41
15:2:593:GLN:C	15:2:594:MET:SD	3.04	0.41
15:2:1105:GLU:HA	15:2:1109:GLU:CD	2.45	0.41
15:2:1145:GLN:OE1	15:2:1145:GLN:N	2.53	0.41
16:3:103:LEU:C	16:3:103:LEU:HD23	2.45	0.41
19:6:116:VAL:HG13	19:6:123:MET:HB3	2.02	0.41
23:a:24:THR:HG21	23:a:38:GLU:OE2	2.21	0.41
29:g:310:ILE:HD11	29:g:337:PHE:HE1	1.86	0.41
1:A:408:HIS:O	1:A:412:ILE:HG13	2.21	0.41
2:B:578:TYR:CE1	2:B:627:ILE:HD11	2.54	0.41
2:B:1090:VAL:O	2:B:1091:LEU:HB2	2.20	0.41
2:B:1090:VAL:HG22	7:H:950:GLU:OE2	2.19	0.41
2:B:1182:ASP:OD1	2:B:1183:VAL:HG23	2.21	0.41
3:D:399:CYS:HB3	3:D:434:THR:OG1	2.19	0.41
3:D:549:VAL:HG22	3:D:553:ASN:ND2	2.34	0.41
5:F:197:THR:HB	5:F:198:PRO:HD3	2.03	0.41
8:I:138:GLU:OE1	8:I:184:MET:SD	2.79	0.41
14:1:85:PHE:CZ	14:1:254:PRO:HB3	2.56	0.41
15:2:185:PHE:CE2	15:2:194:LEU:HD23	2.55	0.41
15:2:197:GLN:HE21	15:2:466:VAL:HG13	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2:285:LEU:O	15:2:288:ILE:HG22	2.19	0.41
15:2:288:ILE:HD12	15:2:369:VAL:HG23	2.03	0.41
15:2:348:LEU:HD23	15:2:364:PHE:HD2	1.84	0.41
15:2:589:LYS:HG3	15:2:590:LEU:N	2.36	0.41
16:3:42:VAL:HG23	16:3:42:VAL:O	2.21	0.41
16:3:57:SER:HB3	16:3:153:LEU:HD21	2.03	0.41
18:5:59:LYS:O	18:5:62:ARG:HG2	2.20	0.41
26:d:17:DT:H2''	26:d:18:DG:H8	1.79	0.41
32:j:505:ASP:OD1	32:j:505:ASP:N	2.54	0.41
1:A:486:THR:HG23	1:A:537:PHE:CE1	2.56	0.41
2:B:578:TYR:CZ	2:B:623:GLU:HG3	2.55	0.41
3:D:102:THR:O	3:D:103:ALA:HB3	2.20	0.41
3:D:560:THR:O	3:D:561:MET:HB3	2.20	0.41
4:E:1005:ARG:NH2	7:H:326:TYR:OH	2.54	0.41
5:F:486:VAL:O	5:F:487:ARG:NH1	2.53	0.41
6:G:224:SER:C	6:G:226:PRO:HD3	2.46	0.41
6:G:472:MET:HE1	6:G:512:VAL:HG23	2.03	0.41
6:G:685:TYR:HD2	6:G:707:GLN:HA	1.86	0.41
7:H:897:VAL:HG11	7:H:915:SER:HB2	2.03	0.41
11:P:20:LEU:HD12	11:P:21:ARG:N	2.35	0.41
11:P:384:ILE:HG23	11:P:385:ILE:N	2.36	0.41
14:1:388:MET:HG3	14:1:450:MET:HE1	2.03	0.41
16:3:187:ASP:OD1	16:3:190:ASN:N	2.54	0.41
17:4:183:PHE:HB3	17:4:185:ILE:HD11	2.03	0.41
29:g:396:LEU:O	29:g:399:ASN:OD1	2.38	0.41
1:A:615:VAL:HG13	1:A:616:LEU:HD22	2.02	0.41
1:A:778:PRO:O	1:A:788:ARG:NH2	2.54	0.41
1:A:1051:GLN:HE21	1:A:1085:LEU:HD13	1.86	0.41
1:A:1221:LEU:HA	1:A:1224:ILE:HD12	2.02	0.41
3:D:169:LYS:O	3:D:172:GLN:NE2	2.54	0.41
3:D:300:VAL:O	3:D:304:LYS:HG3	2.21	0.41
3:D:460:SER:O	3:D:461:ARG:C	2.63	0.41
3:D:659:PHE:CZ	3:D:811:LEU:HD21	2.56	0.41
5:F:154:GLY:HA3	5:F:459:LEU:HD21	2.03	0.41
6:G:798:LYS:NZ	6:G:801:SER:OG	2.54	0.41
6:G:854:VAL:HG11	6:G:892:PHE:CD2	2.56	0.41
7:H:456:VAL:O	7:H:459:ILE:HG22	2.20	0.41
7:H:541:PHE:O	7:H:544:VAL:HG13	2.21	0.41
7:H:932:ILE:HG23	7:H:938:LEU:HD11	2.03	0.41
8:I:608:VAL:HG22	8:I:617:VAL:HG23	2.03	0.41
9:K:398:ILE:HD12	9:K:398:ILE:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:553:VAL:HG12	9:K:583:LEU:HD21	2.03	0.41
11:P:28:ARG:HB3	11:P:65:VAL:HG11	2.03	0.41
11:P:448:MET:CE	11:P:485:LYS:HB2	2.50	0.41
11:P:475:LYS:HD3	11:P:516:ILE:HD12	2.03	0.41
14:1:239:GLU:OE1	14:1:242:TYR:N	2.41	0.41
14:1:359:VAL:HG22	14:1:360:ASP:N	2.35	0.41
14:1:1359:SER:OG	14:1:1360:ASN:N	2.54	0.41
15:2:184:TYR:CE1	15:2:191:GLU:OE2	2.74	0.41
19:6:99:ILE:HG12	19:6:137:VAL:HG22	2.03	0.41
22:9:7:PHE:CD2	22:9:11:LEU:HD12	2.56	0.41
33:k:29:LYS:O	33:k:32:THR:OG1	2.31	0.41
33:k:97:LEU:HD23	33:k:108:ILE:HD12	2.03	0.41
34:l:37:VAL:O	34:l:41:LEU:HD13	2.21	0.41
1:A:1096:ARG:HG2	2:B:131:GLU:OE2	2.20	0.41
1:A:1630:VAL:O	1:A:1630:VAL:HG23	2.21	0.41
1:A:1712:ASP:OD1	1:A:1713:GLN:N	2.54	0.41
1:A:1761:ARG:O	1:A:1764:LEU:HG	2.20	0.41
2:B:153:VAL:HG21	2:B:200:ALA:HA	2.02	0.41
2:B:682:SER:O	2:B:686:GLN:NE2	2.48	0.41
2:B:732:GLU:HG2	2:B:733:ILE:N	2.36	0.41
3:D:869:ASP:OD1	3:D:869:ASP:C	2.64	0.41
3:D:894:THR:OG1	3:D:895:GLN:N	2.54	0.41
3:D:899:SER:OG	8:I:44:VAL:HG11	2.20	0.41
4:E:972:ASP:OD1	4:E:975:ARG:NH1	2.54	0.41
5:F:52:LEU:HD22	5:F:77:LEU:HA	2.03	0.41
5:F:210:VAL:HA	5:F:215:MET:HE1	2.01	0.41
6:G:266:LYS:CD	6:G:307:LEU:HD21	2.51	0.41
6:G:330:ILE:HG13	6:G:330:ILE:O	2.21	0.41
6:G:514:LYS:O	6:G:518:GLU:OE1	2.38	0.41
6:G:796:PHE:O	6:G:797:GLN:HB3	2.21	0.41
7:H:442:PHE:O	7:H:446:VAL:HG23	2.21	0.41
7:H:446:VAL:O	7:H:450:LEU:HD23	2.21	0.41
7:H:720:VAL:O	7:H:723:GLN:HG2	2.20	0.41
8:I:103:ASN:OD1	8:I:103:ASN:C	2.64	0.41
8:I:150:ALA:O	8:I:151:GLN:C	2.63	0.41
8:I:161:ILE:O	8:I:165:LEU:HG	2.21	0.41
9:K:157:HIS:CD2	9:K:178:ASP:HB2	2.56	0.41
9:K:417:ALA:O	9:K:420:MET:HB2	2.21	0.41
9:K:538:LEU:CD1	9:K:587:LEU:HD21	2.51	0.41
11:P:86:VAL:HG11	11:P:118:GLU:OE2	2.21	0.41
11:P:499:MET:HE2	11:P:539:ASN:HD22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:85:PHE:CE2	14:1:254:PRO:HB3	2.55	0.41
14:1:223:GLU:O	14:1:227:ARG:HG2	2.21	0.41
14:1:345:GLY:O	14:1:348:GLY:N	2.45	0.41
14:1:412:GLN:O	14:1:413:TYR:C	2.64	0.41
14:1:420:ILE:HB	14:1:445:LYS:HB2	2.02	0.41
14:1:565:MET:HE2	14:1:565:MET:HB3	1.89	0.41
14:1:567:LEU:CD1	14:1:675:VAL:HG11	2.51	0.41
14:1:769:MET:SD	15:2:973:PRO:HG3	2.61	0.41
14:1:1006:PRO:O	14:1:1010:VAL:HG23	2.21	0.41
14:1:1382:LEU:HD22	14:1:1398:LEU:HG	2.01	0.41
14:1:1472:ASP:C	14:1:1473:LEU:HD22	2.46	0.41
15:2:348:LEU:N	15:2:348:LEU:HD12	2.35	0.41
15:2:909:VAL:O	23:a:44:MET:HB3	2.21	0.41
15:2:937:SER:OG	15:2:938:ARG:N	2.54	0.41
16:3:9:VAL:CG1	16:3:10:ARG:N	2.84	0.41
16:3:53:ASP:HB2	16:3:160:ARG:HG2	2.03	0.41
17:4:52:ARG:HG3	17:4:53:PRO:HD3	2.02	0.41
17:4:56:THR:HG22	17:4:56:THR:O	2.21	0.41
18:5:60:TYR:O	18:5:64:ARG:HG2	2.21	0.41
22:9:63:VAL:O	22:9:63:VAL:HG23	2.21	0.41
23:a:52:LEU:C	23:a:52:LEU:HD12	2.45	0.41
27:e:184:GLU:O	27:e:187:GLN:HG3	2.21	0.41
29:g:321:ASP:N	29:g:321:ASP:OD1	2.53	0.41
29:g:344:PRO:O	29:g:347:ARG:NH1	2.45	0.41
29:g:386:THR:O	29:g:390:VAL:HG23	2.21	0.41
29:g:470:LEU:HD22	29:g:508:TYR:CE2	2.51	0.41
32:j:426:VAL:CG1	32:j:440:ILE:HD11	2.51	0.41
33:k:5:ILE:HB	34:l:29:ALA:HB2	2.01	0.41
34:l:83:VAL:HG22	34:l:137:LYS:HD2	2.01	0.41
1:A:1702:ILE:H	1:A:1702:ILE:HD12	1.86	0.41
2:B:764:VAL:HG13	2:B:765:PRO:CD	2.51	0.41
2:B:1091:LEU:CD2	2:B:1096:ARG:HA	2.50	0.41
5:F:77:LEU:HD23	5:F:77:LEU:C	2.46	0.41
8:I:127:GLU:HB3	8:I:128:PRO:HD3	2.03	0.41
11:P:135:LEU:HG	11:P:147:ALA:HB2	2.02	0.41
14:1:22:GLN:NE2	14:1:1446:GLY:O	2.54	0.41
14:1:652:LEU:HA	14:1:655:ILE:HG12	2.03	0.41
14:1:892:GLY:O	14:1:893:GLU:HG2	2.20	0.41
22:9:104:ARG:O	22:9:107:VAL:HG22	2.22	0.41
1:A:773:ASN:HB3	1:A:893:ASP:OD2	2.21	0.40
1:A:1292:VAL:HA	2:B:73:ARG:CZ	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2047:MET:HG2	1:A:2051:MET:HE1	2.03	0.40
1:A:2170:GLN:NE2	7:H:993:LEU:HD21	2.36	0.40
2:B:1103:THR:O	2:B:1106:SER:HB3	2.21	0.40
3:D:309:MET:SD	3:D:310:GLU:N	2.93	0.40
4:E:568:PRO:HG2	4:E:569:PRO:CD	2.51	0.40
4:E:914:MET:HE1	4:E:919:LEU:HD12	2.03	0.40
6:G:793:ARG:O	6:G:794:TYR:C	2.63	0.40
6:G:805:LYS:HE2	6:G:834:VAL:HG12	2.03	0.40
7:H:861:ALA:O	7:H:864:SER:O	2.38	0.40
8:I:93:LEU:HA	8:I:96:VAL:HG23	2.03	0.40
9:K:68:HIS:NE2	9:K:70:HIS:HB2	2.36	0.40
9:K:228:THR:OG1	9:K:347:MET:HG3	2.22	0.40
9:K:412:LEU:HB2	9:K:420:MET:SD	2.62	0.40
9:K:538:LEU:HD21	9:K:586:PHE:CE2	2.56	0.40
12:Q:97:VAL:HG13	12:Q:146:PHE:HE2	1.86	0.40
14:1:361:PHE:HA	14:1:388:MET:SD	2.61	0.40
14:1:502:ASN:OD1	15:2:1084:LEU:HD11	2.21	0.40
14:1:1398:LEU:C	14:1:1398:LEU:HD23	2.46	0.40
15:2:755:GLN:OE1	15:2:777:ASN:ND2	2.53	0.40
15:2:931:ILE:O	15:2:931:ILE:HG13	2.21	0.40
15:2:988:LYS:NZ	15:2:1026:GLU:OE2	2.38	0.40
17:4:14:ARG:HG3	17:4:18:MET:SD	2.61	0.40
17:4:116:GLN:NE2	17:4:120:ASP:OD1	2.54	0.40
26:d:28:DG:H5"	26:d:28:DG:C8	2.53	0.40
29:g:275:ASP:OD1	29:g:275:ASP:N	2.54	0.40
29:g:353:LYS:HA	29:g:356:TYR:HD2	1.86	0.40
1:A:1714:ARG:O	3:D:571:ARG:NH2	2.53	0.40
2:B:177:ALA:O	2:B:180:VAL:HG22	2.21	0.40
2:B:443:VAL:O	2:B:443:VAL:HG13	2.20	0.40
3:D:219:MET:HE1	3:D:229:LEU:HD22	2.03	0.40
3:D:255:LEU:HA	3:D:258:VAL:HG12	2.02	0.40
3:D:449:LEU:O	3:D:453:LEU:HG	2.21	0.40
3:D:762:GLN:HE21	3:D:763:ARG:HD3	1.87	0.40
5:F:193:ASP:OD1	5:F:193:ASP:N	2.54	0.40
6:G:582:ASN:OD1	6:G:584:SER:OG	2.32	0.40
6:G:675:MET:SD	6:G:679:ARG:NH2	2.95	0.40
6:G:825:GLN:HG3	6:G:826:GLN:H	1.87	0.40
7:H:645:TYR:OH	7:H:655:LEU:HD12	2.22	0.40
7:H:894:HIS:CE1	7:H:918:GLU:HG3	2.57	0.40
8:I:77:VAL:HG22	8:I:78:ASP:N	2.36	0.40
8:I:302:SER:C	8:I:305:ILE:HG22	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:537:LEU:HD23	8:I:537:LEU:H	1.86	0.40
8:I:622:ALA:CB	8:I:643:LEU:HD13	2.49	0.40
9:K:79:TYR:HA	9:K:83:MET:HE2	2.02	0.40
9:K:130:MET:O	9:K:133:VAL:HG22	2.21	0.40
9:K:283:ILE:O	9:K:285:TRP:N	2.51	0.40
11:P:155:TYR:CE1	11:P:166:LEU:HD11	2.55	0.40
11:P:209:PHE:HE1	11:P:227:ALA:HB3	1.85	0.40
14:1:814:ASP:OD1	14:1:814:ASP:N	2.50	0.40
15:2:610:ARG:NH2	20:7:71:ASP:OD2	2.55	0.40
15:2:798:ARG:N	15:2:949:TYR:O	2.44	0.40
16:3:9:VAL:HG22	16:3:23:ILE:CD1	2.51	0.40
17:4:30:GLN:O	17:4:34:ASP:OD1	2.40	0.40
17:4:122:ALA:N	17:4:123:PRO:HD2	2.36	0.40
26:d:38:DG:H1'	26:d:39:DC:H5'	2.03	0.40
29:g:291:ARG:NH1	29:g:312:VAL:HG13	2.36	0.40
29:g:414:LEU:O	29:g:418:ILE:HG12	2.21	0.40
1:A:358:CYS:SG	1:A:387:LEU:HD12	2.62	0.40
1:A:2065:GLU:OE2	7:H:743:LYS:HE2	2.22	0.40
2:B:174:LEU:CD1	2:B:210:PHE:HE1	2.34	0.40
3:D:458:ASP:OD1	3:D:458:ASP:N	2.54	0.40
3:D:688:LYS:HA	3:D:691:ASP:OD1	2.20	0.40
4:E:641:PRO:HG3	7:H:862:VAL:HG22	2.02	0.40
6:G:470:ASP:O	6:G:474:LEU:HD23	2.22	0.40
6:G:552:GLN:O	6:G:553:VAL:CG2	2.69	0.40
6:G:640:SER:O	6:G:643:THR:N	2.38	0.40
6:G:908:SER:OG	6:G:909:SER:N	2.54	0.40
7:H:717:LEU:HA	7:H:720:VAL:HG22	2.03	0.40
8:I:308:LEU:HD23	8:I:308:LEU:C	2.46	0.40
8:I:316:ILE:HG23	8:I:317:ASP:N	2.37	0.40
8:I:497:MET:SD	8:I:497:MET:O	2.80	0.40
9:K:412:LEU:C	9:K:420:MET:HE1	2.47	0.40
14:1:451:CYS:SG	14:1:452:ASP:N	2.93	0.40
14:1:466:LYS:HA	15:2:1093:CYS:SG	2.61	0.40
14:1:530:SER:O	14:1:531:ASN:C	2.63	0.40
14:1:848:ILE:CD1	15:2:499:ARG:HG3	2.51	0.40
14:1:1228:MET:SD	14:1:1247:PHE:HB2	2.62	0.40
15:2:55:VAL:HG13	15:2:56:GLN:N	2.36	0.40
15:2:294:ASP:H	15:2:298:MET:HE1	1.87	0.40
15:2:344:GLN:C	15:2:353:VAL:HG13	2.46	0.40
15:2:437:THR:O	15:2:440:ILE:HG22	2.21	0.40
19:6:55:LYS:O	19:6:147:LYS:HD2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:9:100:LEU:HD12	22:9:101:LEU:N	2.36	0.40
29:g:411:LEU:CD1	29:g:454:LEU:HD21	2.51	0.40
33:k:3:TYR:CE1	34:l:94:LYS:NZ	2.89	0.40
1:A:389:MET:SD	1:A:390:SER:N	2.94	0.40
1:A:616:LEU:HD12	1:A:679:LEU:HD13	2.04	0.40
1:A:1076:VAL:HG13	1:A:1082:HIS:CE1	2.55	0.40
2:B:227:ARG:CA	2:B:267:MET:HE1	2.50	0.40
2:B:301:PHE:CE1	2:B:305:LEU:HD11	2.56	0.40
2:B:304:GLY:HA2	6:G:606:ALA:HA	2.04	0.40
2:B:486:TYR:CZ	2:B:494:ALA:HB1	2.57	0.40
3:D:751:CYS:O	3:D:755:LEU:HD23	2.22	0.40
4:E:770:GLN:O	4:E:771:GLU:CD	2.64	0.40
6:G:276:LEU:HD22	6:G:287:TRP:CH2	2.56	0.40
6:G:826:GLN:CG	6:G:893:LEU:HD12	2.52	0.40
6:G:847:ILE:HG22	6:G:910:VAL:HG11	2.02	0.40
7:H:593:PHE:O	7:H:611:MET:HE2	2.21	0.40
14:1:780:ASN:O	15:2:976:MET:HE2	2.22	0.40
15:2:553:LEU:H	15:2:553:LEU:HD23	1.84	0.40
15:2:604:ILE:O	15:2:604:ILE:HG23	2.22	0.40
24:b:39:DA:H2"	24:b:40:DG:C8	2.57	0.40
27:e:122:GLY:O	27:e:126:GLU:OE1	2.39	0.40
1:A:382:ARG:HB2	1:A:383:PRO:HD3	2.03	0.40
1:A:573:GLU:OE1	1:A:573:GLU:N	2.46	0.40
1:A:1669:SER:O	1:A:1672:THR:OG1	2.36	0.40
2:B:764:VAL:N	2:B:765:PRO:HD2	2.37	0.40
2:B:1093:GLN:HG2	2:B:1094:ALA:N	2.37	0.40
5:F:449:SER:OG	5:F:452:VAL:HG23	2.22	0.40
6:G:413:LEU:HD12	6:G:448:LEU:HB3	2.02	0.40
6:G:511:ALA:O	6:G:514:LYS:HG2	2.22	0.40
6:G:640:SER:O	6:G:641:LEU:C	2.64	0.40
6:G:671:MET:HG3	6:G:721:ILE:HG21	2.04	0.40
7:H:248:MET:SD	7:H:248:MET:N	2.94	0.40
7:H:993:LEU:C	7:H:993:LEU:HD23	2.47	0.40
8:I:246:HIS:ND1	8:I:307:ASP:OD1	2.55	0.40
8:I:421:ILE:O	8:I:421:ILE:HG22	2.20	0.40
8:I:625:LEU:HD12	8:I:625:LEU:O	2.21	0.40
9:K:52:THR:HG22	9:K:60:PHE:HB2	2.04	0.40
9:K:538:LEU:HD11	9:K:587:LEU:HD21	2.03	0.40
12:Q:68:LEU:C	12:Q:68:LEU:HD23	2.46	0.40
12:Q:188:GLU:O	12:Q:189:VAL:C	2.65	0.40
14:1:57:LEU:HD11	14:1:281:ALA:CA	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1:1127:LEU:O	14:1:1130:ILE:HD13	2.22	0.40
15:2:38:GLY:C	15:2:39:LEU:HD22	2.47	0.40
15:2:710:ILE:O	15:2:710:ILE:HG22	2.21	0.40
16:3:31:ALA:O	16:3:231:TYR:OH	2.35	0.40
26:d:2:DC:H2"	26:d:3:DT:H72	2.03	0.40
29:g:473:LEU:HB3	29:g:500:MET:HE3	2.02	0.40
32:j:612:GLY:C	32:j:624:LEU:HD11	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1755/2190 (80%)	1671 (95%)	82 (5%)	2 (0%)	48	82
2	B	1045/1204 (87%)	998 (96%)	47 (4%)	0	100	100
3	D	814/963 (84%)	754 (93%)	54 (7%)	6 (1%)	18	55
4	E	794/1019 (78%)	734 (92%)	57 (7%)	3 (0%)	30	66
5	F	554/887 (62%)	541 (98%)	13 (2%)	0	100	100
6	G	904/962 (94%)	830 (92%)	70 (8%)	4 (0%)	30	66
7	H	933/995 (94%)	892 (96%)	41 (4%)	0	100	100
8	I	629/658 (96%)	592 (94%)	37 (6%)	0	100	100
9	K	586/600 (98%)	551 (94%)	33 (6%)	2 (0%)	36	71
11	P	579/589 (98%)	559 (96%)	20 (4%)	0	100	100
12	Q	291/309 (94%)	267 (92%)	24 (8%)	0	100	100
14	1	1425/1970 (72%)	1335 (94%)	86 (6%)	4 (0%)	36	71
15	2	1099/1174 (94%)	995 (90%)	104 (10%)	0	100	100
16	3	255/271 (94%)	239 (94%)	16 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	4	207/210 (99%)	201 (97%)	6 (3%)	0	100	100
18	5	79/127 (62%)	77 (98%)	2 (2%)	0	100	100
19	6	146/150 (97%)	135 (92%)	11 (8%)	0	100	100
20	7	115/125 (92%)	111 (96%)	4 (4%)	0	100	100
21	8	65/67 (97%)	61 (94%)	4 (6%)	0	100	100
22	9	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
23	a	44/58 (76%)	40 (91%)	4 (9%)	0	100	100
27	e	181/528 (34%)	177 (98%)	4 (2%)	0	100	100
28	f	466/580 (80%)	451 (97%)	14 (3%)	1 (0%)	43	77
29	g	530/590 (90%)	501 (94%)	29 (6%)	0	100	100
30	h	20/380 (5%)	20 (100%)	0	0	100	100
31	i	114/121 (94%)	111 (97%)	3 (3%)	0	100	100
32	j	470/1087 (43%)	451 (96%)	19 (4%)	0	100	100
33	k	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
34	l	126/142 (89%)	122 (97%)	4 (3%)	0	100	100
All	All	14510/18245 (80%)	13686 (94%)	802 (6%)	22 (0%)	44	77

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1816	PRO
3	D	63	PRO
3	D	106	SER
3	D	561	MET
4	E	282	ILE
4	E	740	PRO
4	E	742	PRO
6	G	553	VAL
14	1	910	LYS
1	A	904	VAL
3	D	141	LEU
28	f	231	ASN
3	D	688	LYS
9	K	72	ASP
6	G	189	THR
6	G	788	PRO
6	G	797	GLN

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Mol	Chain	Res	Type
9	K	32	ASP
14	1	78	MET
3	D	147	ILE
14	1	1763	SER
14	1	188	GLN

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	A	1253/1907 (66%)	1252 (100%)	1 (0%)	88	88
2	B	946/1072 (88%)	945 (100%)	1 (0%)	88	88
3	D	617/845 (73%)	616 (100%)	1 (0%)	87	86
4	E	395/812 (49%)	394 (100%)	1 (0%)	86	84
5	F	490/796 (62%)	490 (100%)	0	100	100
6	G	744/840 (89%)	741 (100%)	3 (0%)	84	82
7	H	822/896 (92%)	820 (100%)	2 (0%)	87	86
8	I	575/600 (96%)	575 (100%)	0	100	100
9	K	505/520 (97%)	504 (100%)	1 (0%)	87	86
11	P	508/512 (99%)	507 (100%)	1 (0%)	87	86
12	Q	259/274 (94%)	259 (100%)	0	100	100
14	1	1239/1736 (71%)	1234 (100%)	5 (0%)	84	82
15	2	908/1027 (88%)	906 (100%)	2 (0%)	87	86
16	3	227/248 (92%)	227 (100%)	0	100	100
17	4	191/192 (100%)	191 (100%)	0	100	100
18	5	70/111 (63%)	69 (99%)	1 (1%)	59	70
19	6	129/131 (98%)	129 (100%)	0	100	100
20	7	105/112 (94%)	105 (100%)	0	100	100
21	8	56/56 (100%)	56 (100%)	0	100	100
22	9	106/106 (100%)	106 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	a	43/55 (78%)	43 (100%)	0	100	100
27	e	158/451 (35%)	158 (100%)	0	100	100
29	g	339/513 (66%)	338 (100%)	1 (0%)	86	84
31	i	102/105 (97%)	102 (100%)	0	100	100
32	j	425/940 (45%)	424 (100%)	1 (0%)	87	86
33	k	136/153 (89%)	136 (100%)	0	100	100
34	l	104/126 (82%)	104 (100%)	0	100	100
All	All	11452/15136 (76%)	11431 (100%)	21 (0%)	85	86

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	964	ASP
2	B	445	THR
3	D	823	THR
4	E	897	THR
6	G	275	ASP
6	G	823	ASN
6	G	935	TYR
7	H	591	GLN
7	H	713	THR
9	K	246	GLN
11	P	304	HIS
14	1	551	ARG
14	1	695	ASP
14	1	1138	SER
14	1	1770	SER
14	1	1797	TYR
15	2	818	GLU
15	2	1129	ASN
18	5	58	THR
29	g	264	GLU
32	j	728	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	221	ASN

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Mol	Chain	Res	Type
1	A	678	HIS
1	A	839	GLN
1	A	871	ASN
1	A	1102	HIS
1	A	1667	GLN
1	A	2185	HIS
2	B	103	GLN
2	B	132	HIS
2	B	151	ASN
2	B	748	ASN
2	B	773	GLN
2	B	777	HIS
2	B	934	GLN
2	B	1063	HIS
2	B	1130	GLN
3	D	164	HIS
3	D	221	GLN
3	D	289	HIS
3	D	492	ASN
3	D	553	ASN
3	D	611	GLN
3	D	625	GLN
3	D	650	GLN
3	D	699	GLN
3	D	723	HIS
3	D	853	HIS
3	D	908	GLN
4	E	701	ASN
4	E	888	HIS
4	E	903	HIS
5	F	15	ASN
5	F	225	GLN
5	F	282	HIS
5	F	378	ASN
5	F	462	GLN
6	G	205	HIS
6	G	406	GLN
6	G	425	HIS
6	G	439	HIS
6	G	823	ASN
6	G	826	GLN
6	G	902	HIS

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Mol	Chain	Res	Type
7	H	91	HIS
7	H	179	GLN
7	H	402	GLN
7	H	445	ASN
7	H	533	HIS
7	H	858	GLN
7	H	894	HIS
7	H	946	HIS
8	I	341	GLN
9	K	335	GLN
9	K	497	GLN
9	K	518	HIS
9	K	533	HIS
9	K	545	HIS
11	P	288	GLN
11	P	304	HIS
11	P	433	GLN
11	P	465	ASN
11	P	557	GLN
12	Q	12	GLN
12	Q	125	GLN
12	Q	141	ASN
12	Q	229	ASN
14	1	143	HIS
14	1	278	HIS
14	1	432	HIS
14	1	685	HIS
14	1	746	ASN
14	1	780	ASN
14	1	861	GLN
14	1	884	ASN
14	1	926	ASN
14	1	1101	GLN
14	1	1220	HIS
14	1	1310	HIS
15	2	111	ASN
15	2	197	GLN
15	2	725	GLN
15	2	777	ASN
15	2	980	HIS
15	2	1071	ASN
15	2	1094	GLN

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Mol	Chain	Res	Type
15	2	1117	HIS
15	2	1129	ASN
17	4	43	GLN
17	4	65	ASN
17	4	108	GLN
27	e	187	GLN
29	g	278	GLN
29	g	468	GLN
32	j	595	HIS
34	l	43	HIS
34	l	47	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	c	22/23 (95%)	14 (63%)	0

All (14) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	c	25	A
25	c	26	U
25	c	27	A
25	c	28	A
25	c	29	C
25	c	30	C
25	c	31	G
25	c	32	G
25	c	33	A
25	c	34	G
25	c	35	A
25	c	36	G
25	c	37	G
25	c	39	A

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

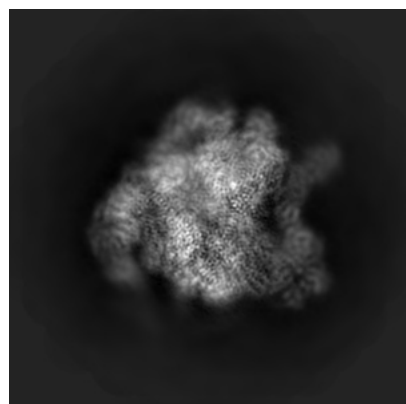
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33741. These allow visual inspection of the internal detail of the map and identification of artifacts.

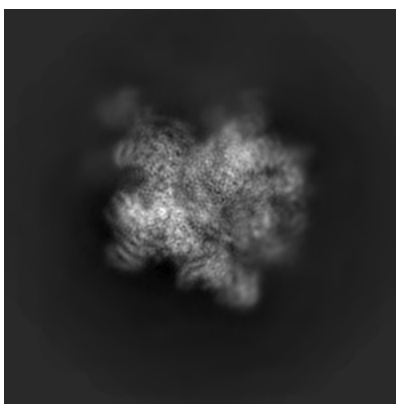
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

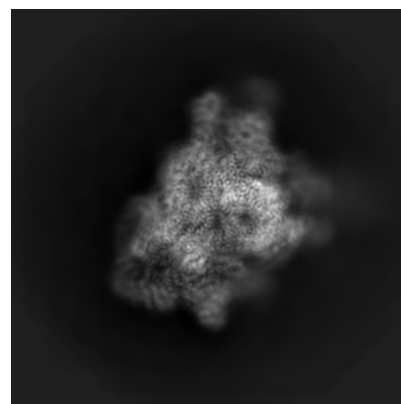
6.1.1 Primary map



X

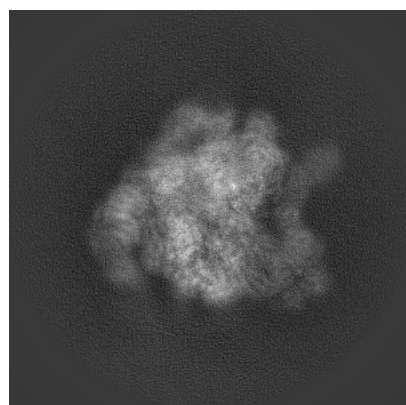


Y

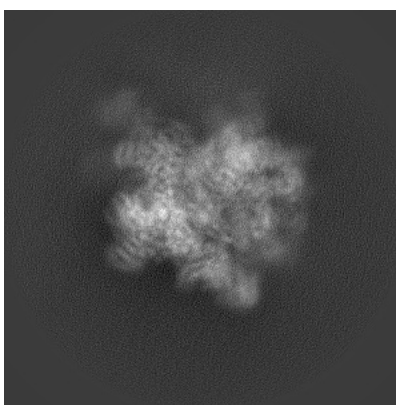


Z

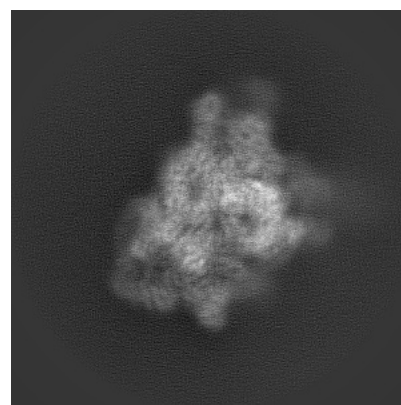
6.1.2 Raw map



X



Y

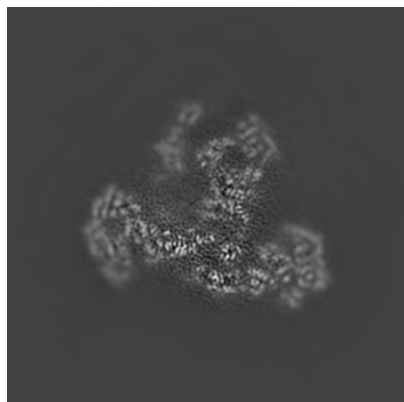


Z

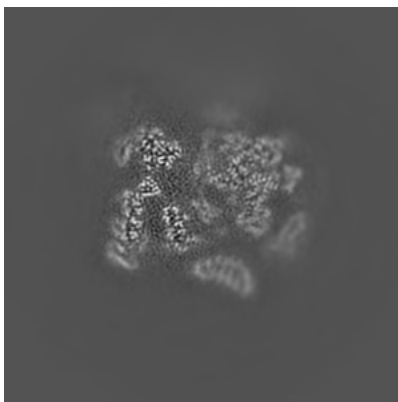
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

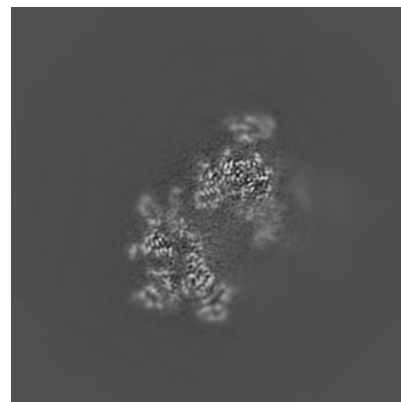
6.2.1 Primary map



X Index: 210

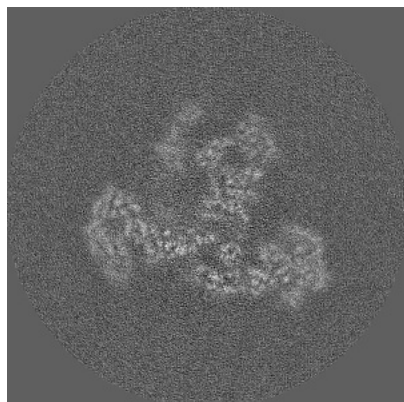


Y Index: 210

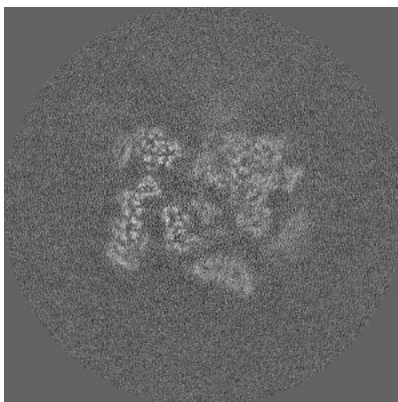


Z Index: 210

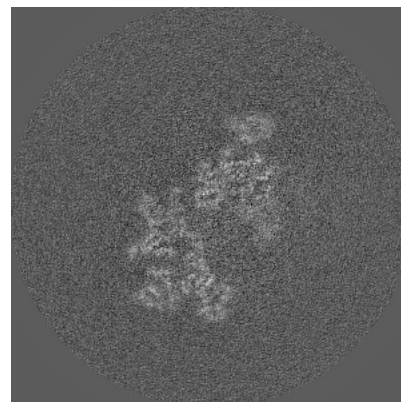
6.2.2 Raw map



X Index: 210



Y Index: 210

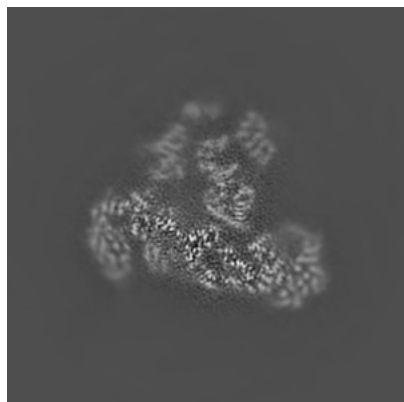


Z Index: 210

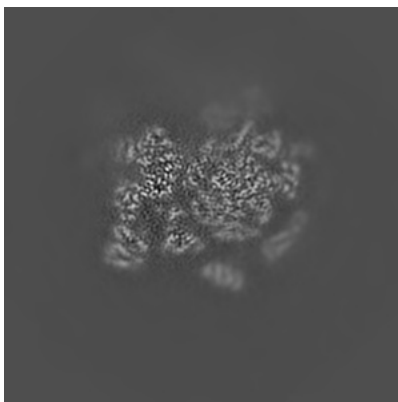
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

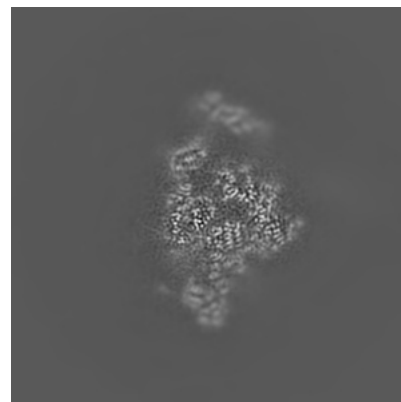
6.3.1 Primary map



X Index: 203

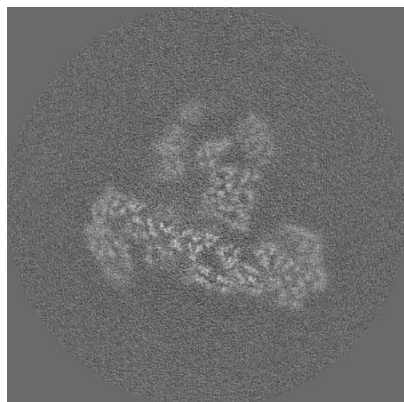


Y Index: 220

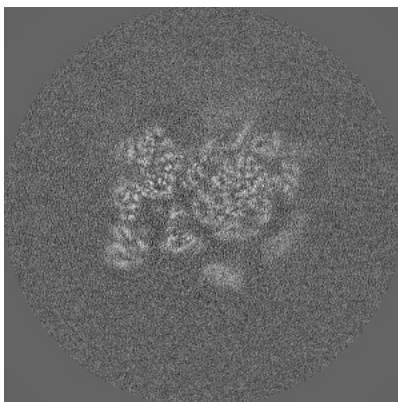


Z Index: 174

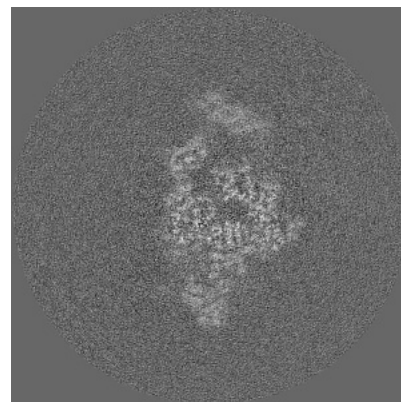
6.3.2 Raw map



X Index: 207



Y Index: 220

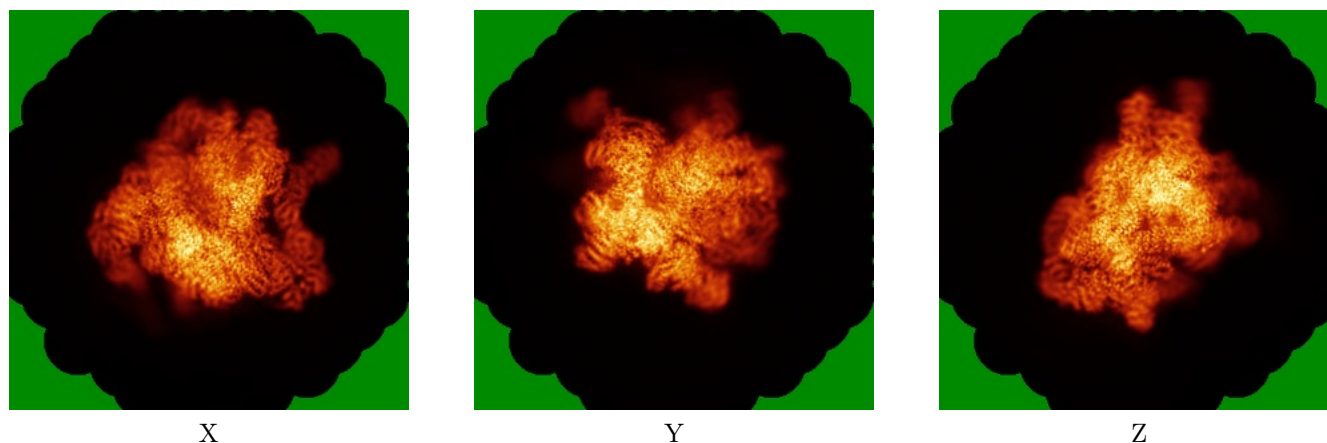


Z Index: 174

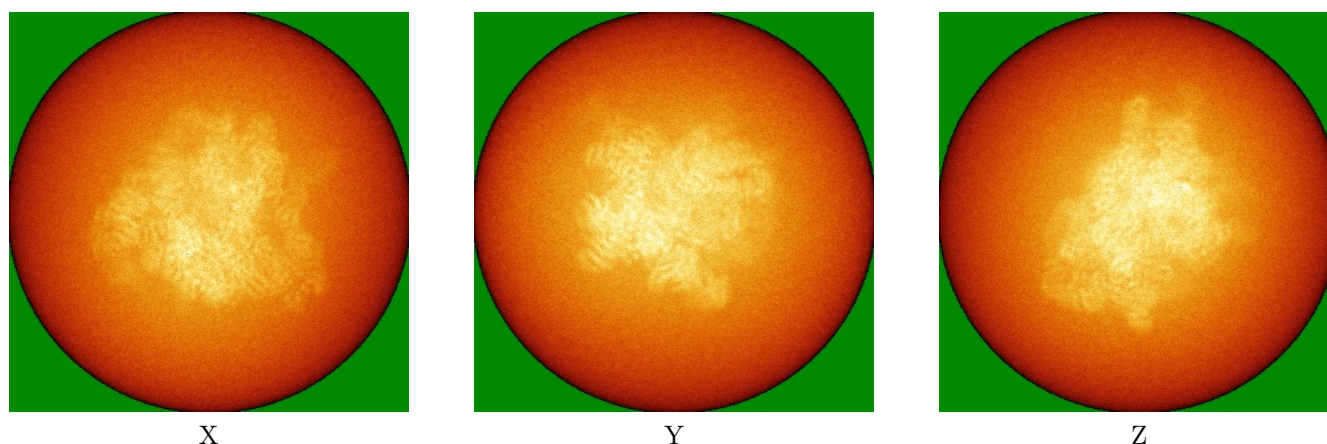
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

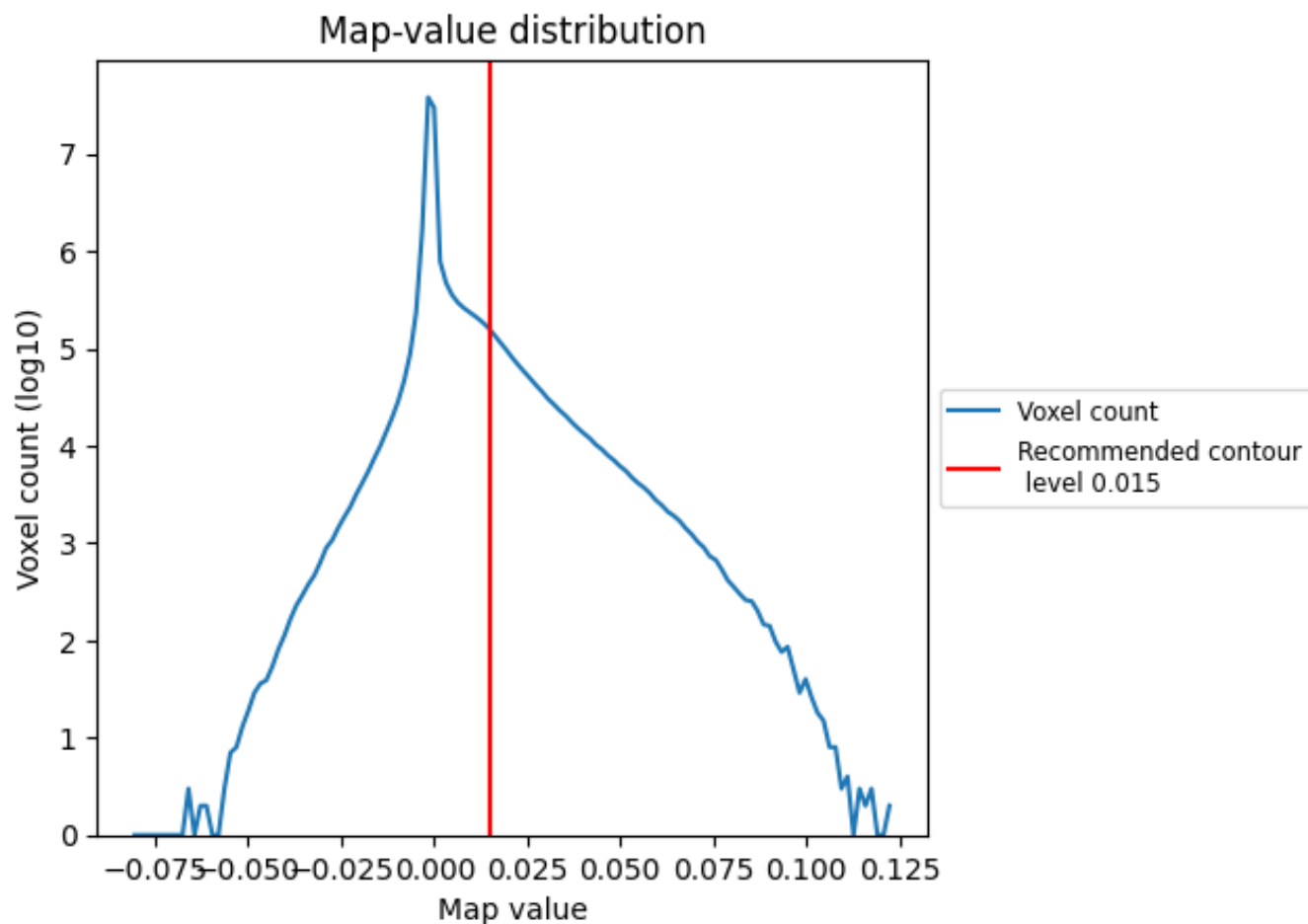
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

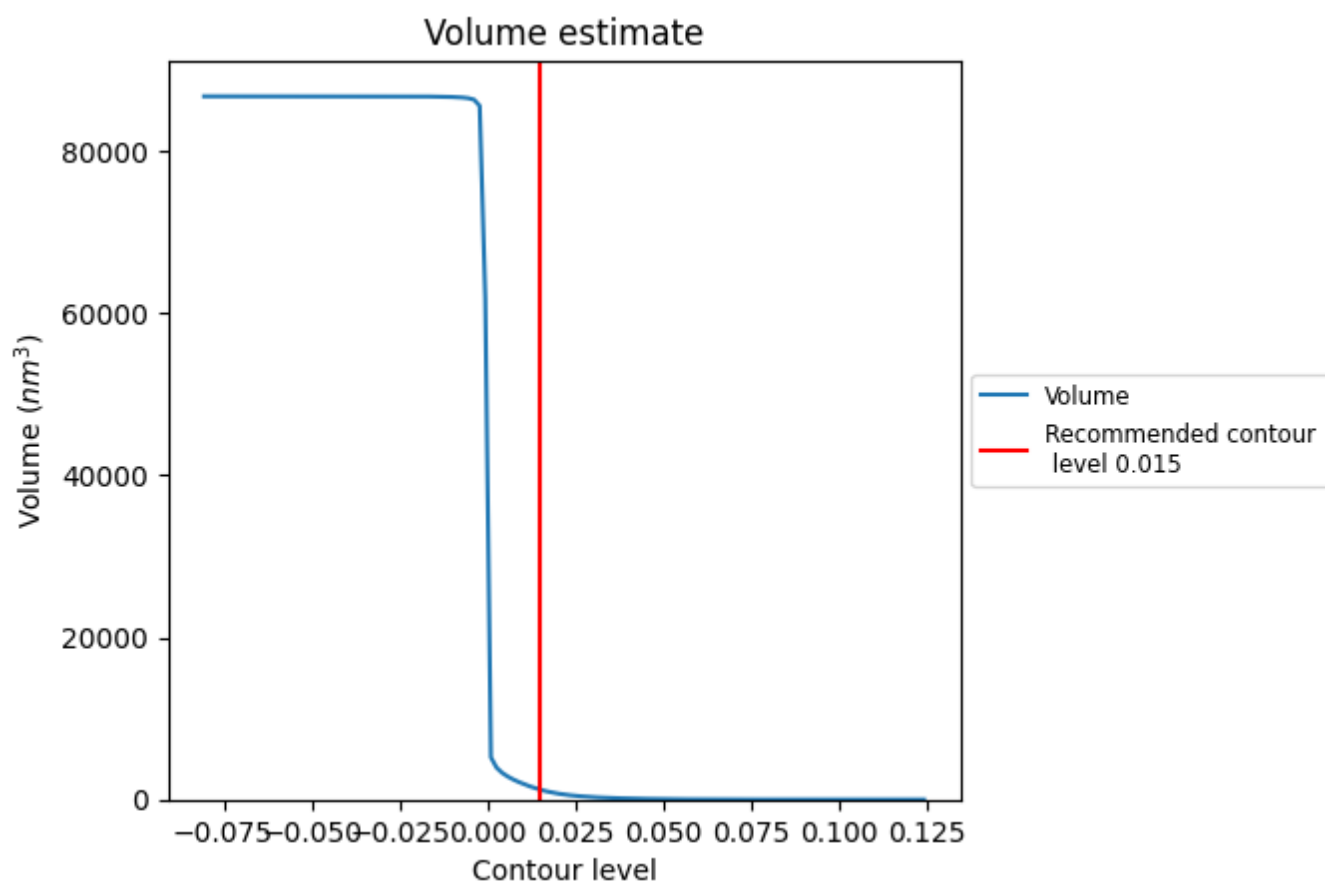
This section contains the results of statistical analysis of the map.

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.

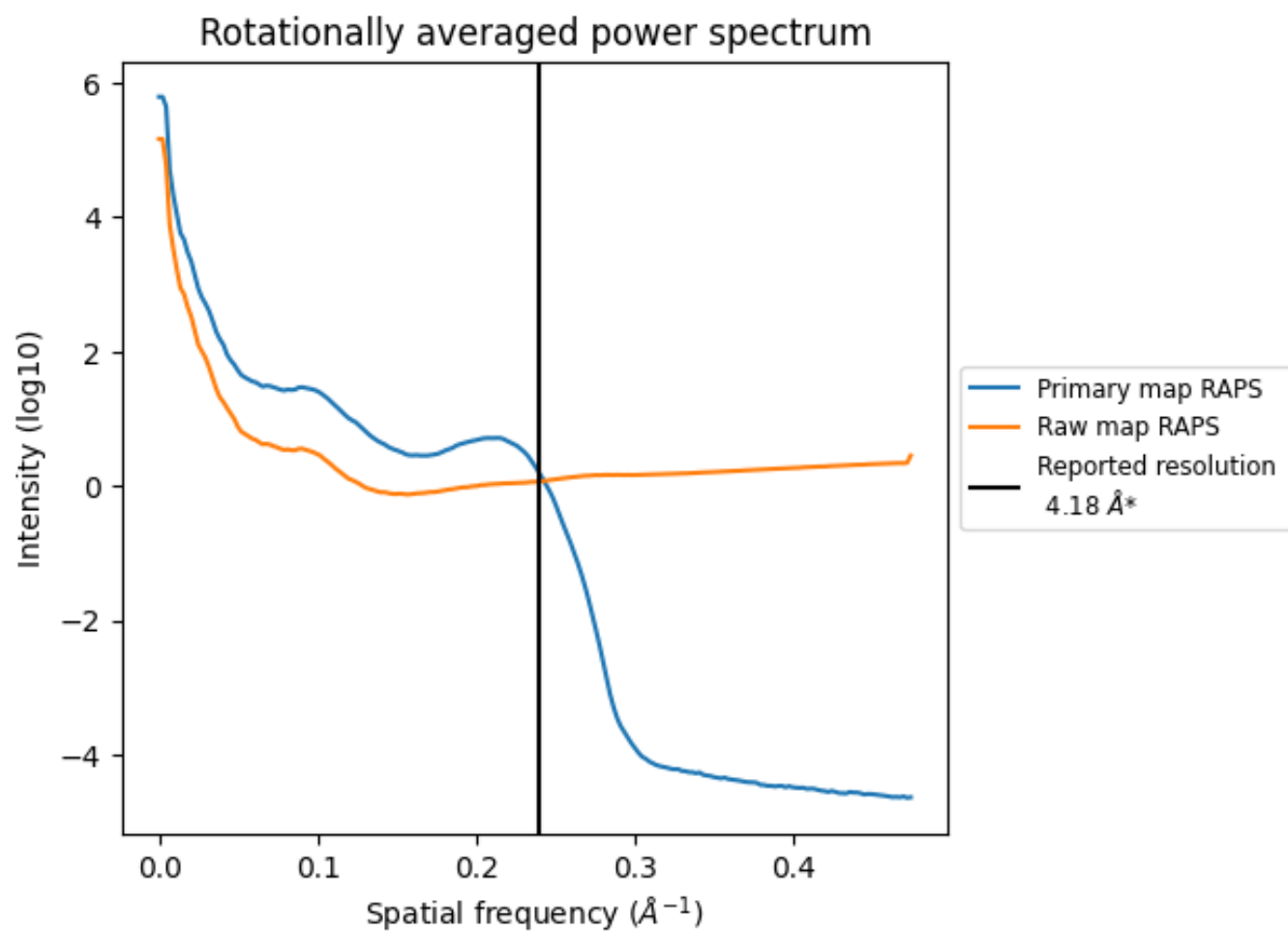
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1216 nm³; this corresponds to an approximate mass of 1099 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

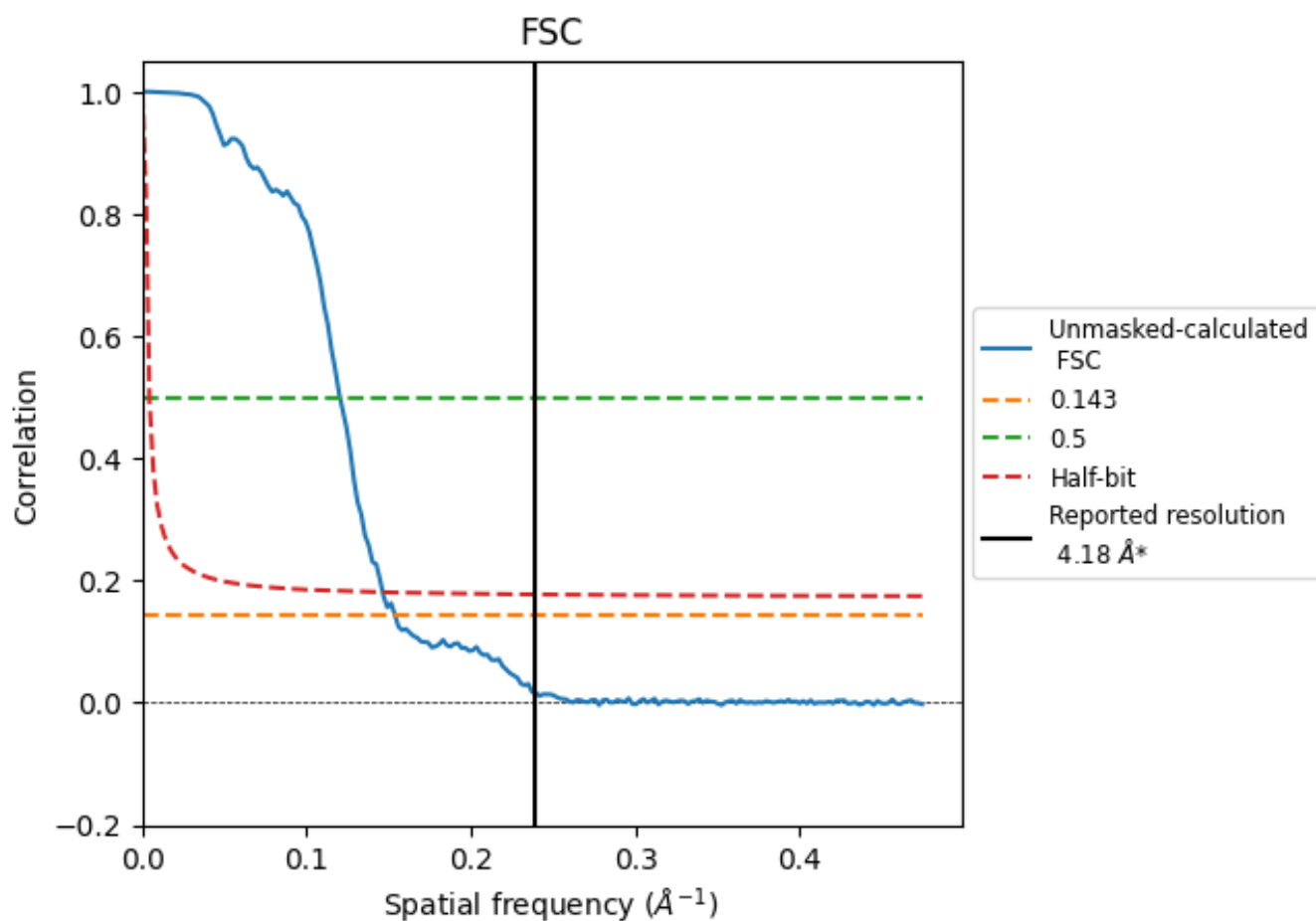


*Reported resolution corresponds to spatial frequency of 0.239 Å⁻¹

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 0.239 $\text{\AA}^{-1}$

8.2 Resolution estimates

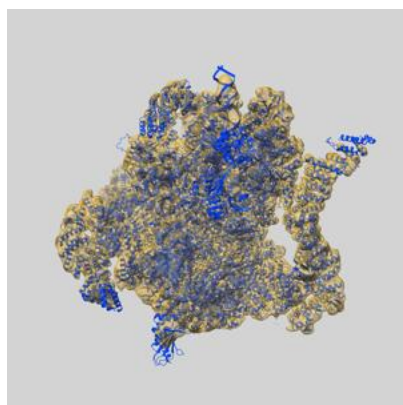
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.18	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.50	8.31	6.84

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.50 differs from the reported value 4.18 by more than 10 %

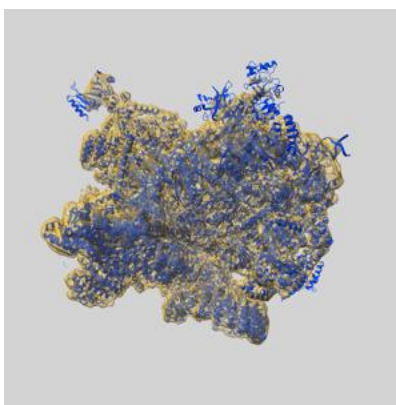
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33741 and PDB model 7YCX. Per-residue inclusion information can be found in section [3](#) on page [11](#).

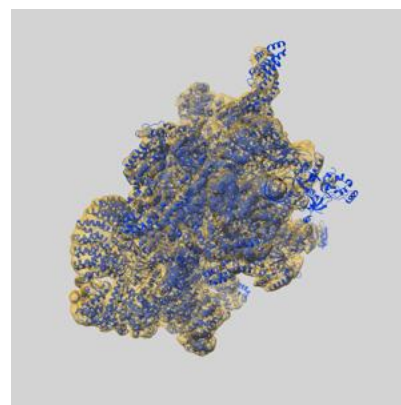
9.1 Map-model overlay [i](#)



X



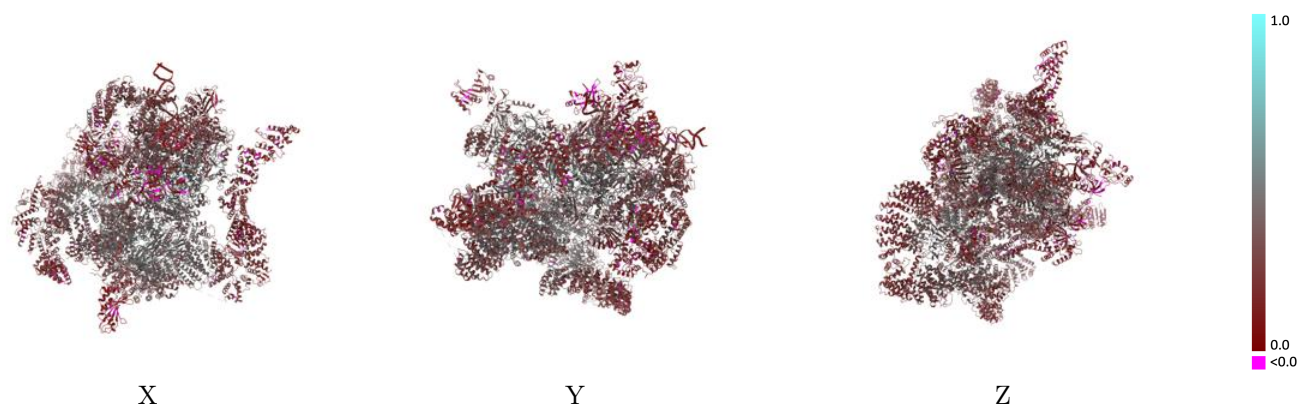
Y



Z

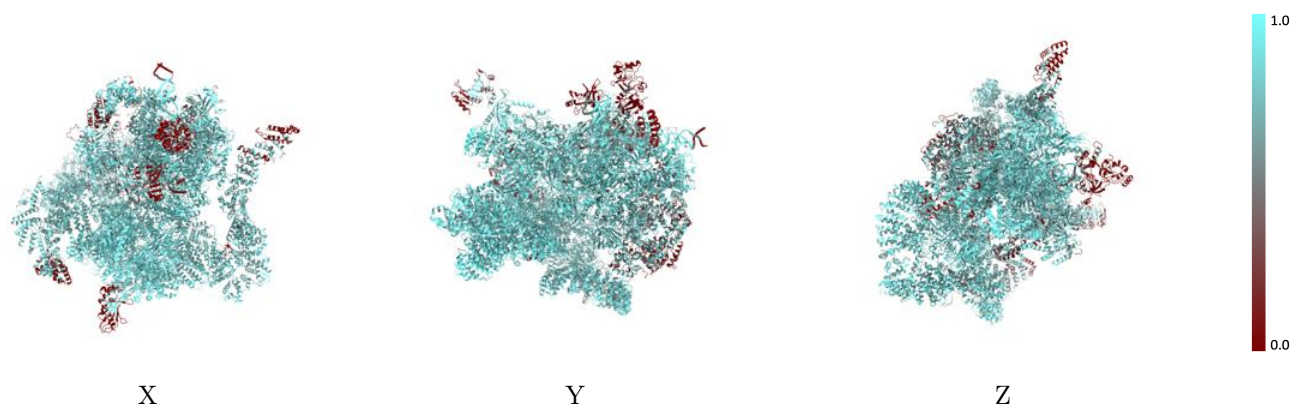
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



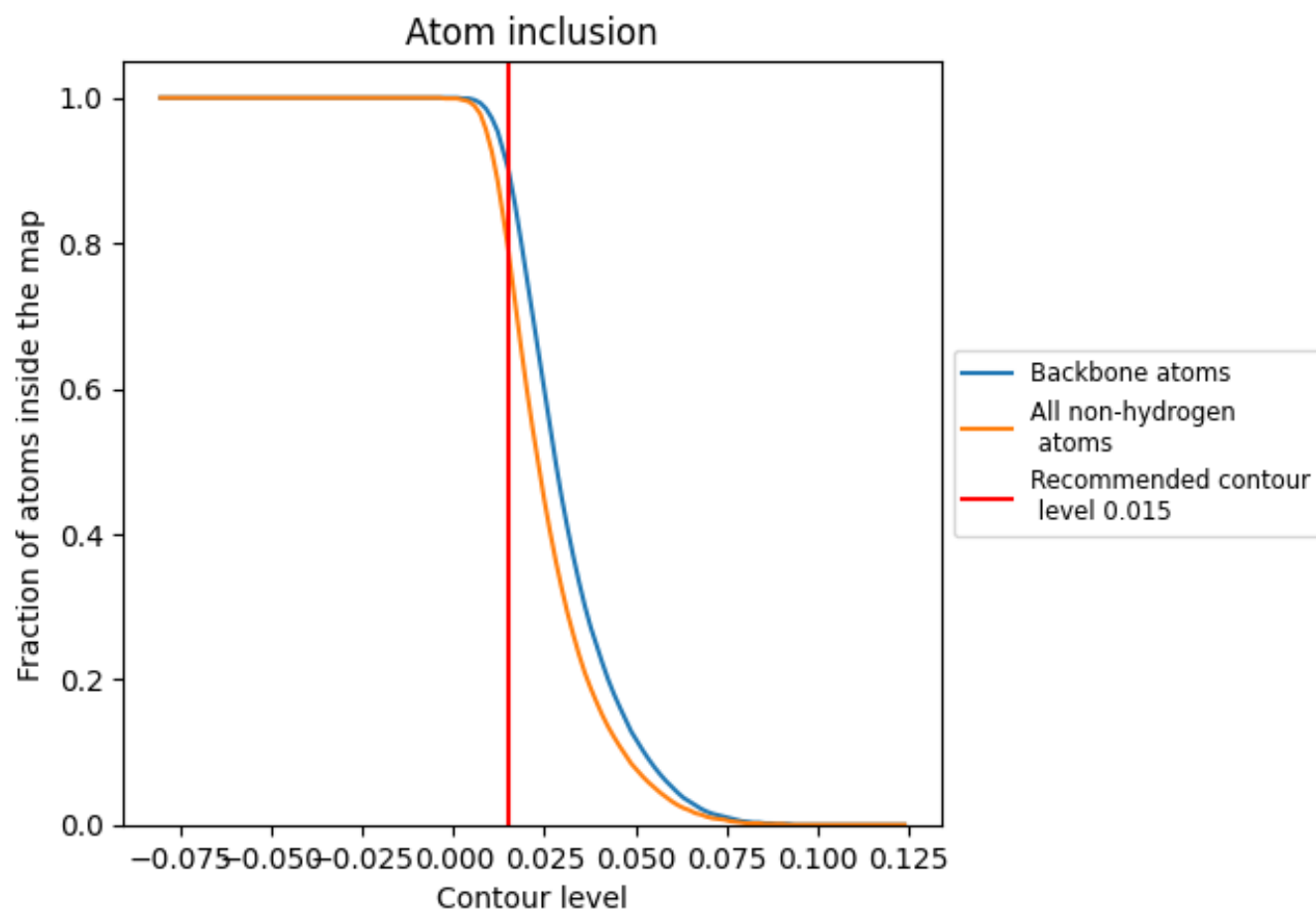
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 90% 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	 0.3110
1	 0.8490	 0.3500
2	 0.8960	 0.4060
3	 0.8970	 0.4240
4	 0.8170	 0.2900
5	 0.7870	 0.3040
6	 0.7760	 0.2510
7	 0.8220	 0.2580
8	 0.9190	 0.4570
9	 0.8390	 0.3640
A	 0.7480	 0.2340
B	 0.8730	 0.3770
D	 0.9070	 0.4000
E	 0.7750	 0.2950
F	 0.7790	 0.2680
G	 0.9070	 0.4090
H	 0.8120	 0.2520
I	 0.8410	 0.3820
K	 0.7610	 0.3240
M	 0.9650	 0.2820
P	 0.8260	 0.2400
Q	 0.8950	 0.3830
U	 0.9410	 0.4100
a	 0.9140	 0.4090
b	 0.7000	 0.1950
c	 0.8100	 0.2900
d	 0.7810	 0.2390
e	 0.5240	 0.1810
f	 0.6490	 0.2700
g	 0.5480	 0.2040
h	 0.5780	 0.2680
i	 0.0210	 0.1200
j	 0.3860	 0.1780
k	 0.7400	 0.2080
l	 0.7450	 0.1850

