



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 12:33 PM UTC

PDB ID : 8BD7 / pdb_00008bd7
EMDB ID : EMD-15977
Title : IFTB1 subcomplex of anterograde Intraflagellar transport trains (Chlamydomonas reinhardtii)
Authors : Lacey, S.E.; Foster, H.E.; Pigino, G.
Deposited on : 2022-10-18
Resolution : 9.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

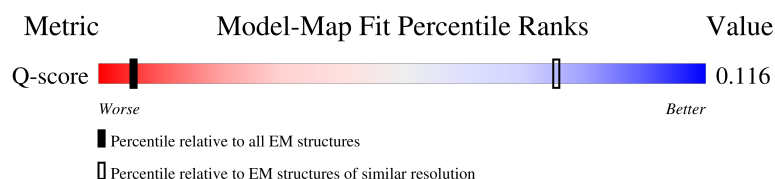
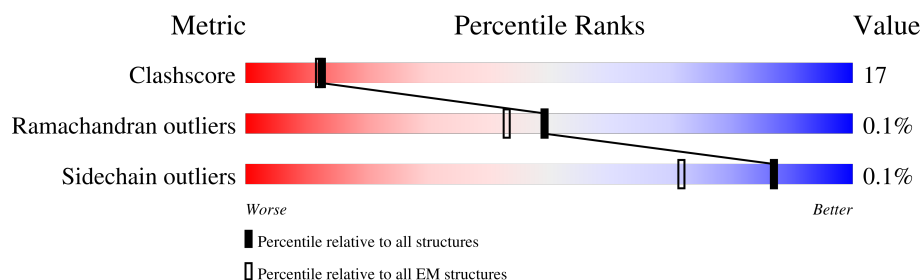
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

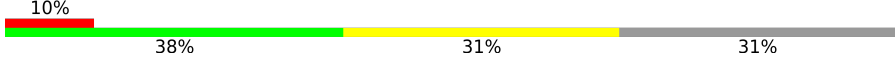
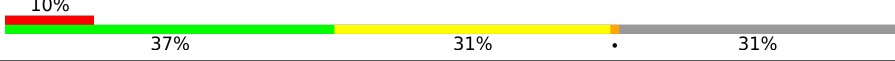
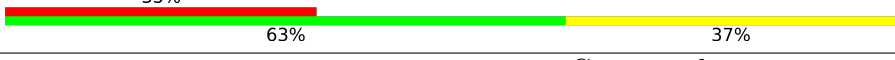
The reported resolution of this entry is 9.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	149 (9.40 - 10.40)

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

Mol	Chain	Length	Quality of chain
1	A	782	
1	H	782	
2	B	454	
2	J	454	

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Mol	Chain	Length	Quality of chain
3	C	647	
3	K	647	
4	D	344	
4	N	344	
5	E	555	
5	O	555	
6	F	683	
6	P	683	
7	G	641	
7	Q	641	
8	I	765	
8	R	765	
9	L	443	
9	T	443	
10	M	469	
10	U	469	
11	W	135	
11	Y	135	
12	X	510	
12	Z	510	
13	S	1755	
13	V	1755	

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 86268 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 IFT88.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	539	Total	C	N	O	S	0	0
			4337	2747	762	795	33		
1	H	539	Total	C	N	O	S	0	0
			4337	2747	762	795	33		

- Molecule 2 is a protein called Osm-6-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	454	Total	C	N	O	S	0	0
			3553	2269	591	680	13		
2	J	454	Total	C	N	O	S	0	0
			3553	2269	591	680	13		

- Molecule 3 is a protein called IFT70.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	619	Total	C	N	O	S	0	0
			4978	3171	826	948	33		
3	K	619	Total	C	N	O	S	0	0
			4978	3171	826	948	33		

- Molecule 4 is a protein called Intraflagellar transport protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	133	Total	C	N	O	S	0	0
			1045	666	172	197	10		
4	N	133	Total	C	N	O	S	0	0
			1045	666	172	197	10		

- Molecule 5 is a protein called Intraflagellar transport protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	555	Total	C	N	O	S	0	0
			4465	2855	763	820	27		
5	O	555	Total	C	N	O	S	0	0
			4465	2855	763	820	27		

- Molecule 6 is a protein called Intraflagellar transport protein 81.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	335	Total	C	N	O	S	0	0
			2701	1692	476	526	7		
6	P	335	Total	C	N	O	S	0	0
			2701	1692	476	526	7		

- Molecule 7 is a protein called Intraflagellar transport protein 74.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	205	Total	C	N	O	S	0	0
			1674	1023	302	342	7		
7	Q	205	Total	C	N	O	S	0	0
			1674	1023	302	342	7		

- Molecule 8 is a protein called Intraflagellar transport protein 80.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	765	Total	C	N	O	S	0	0
			6025	3807	1053	1132	33		
8	R	765	Total	C	N	O	S	0	0
			6025	3807	1053	1132	33		

- Molecule 9 is a protein called Clusterin-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	303	Total	C	N	O	S	0	0
			2472	1547	439	476	10		
9	T	303	Total	C	N	O	S	0	0
			2472	1547	439	476	10		

- Molecule 10 is a protein called Intraflagellar transport protein 57.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	164	Total	C	N	O	S	0	0
			1328	812	247	264	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	U	164	Total	C	N	O	S	0	0
			1328	812	247	264	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	356	ALA	PHE	conflict	UNP Q2XQY7
U	356	ALA	PHE	conflict	UNP Q2XQY7

- Molecule 11 is a protein called Intraflagellar transport particle protein IFT20.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	W	114	Total	C	N	O	S	0	0
			919	562	166	187	4		
11	Y	114	Total	C	N	O	S	0	0
			919	562	166	187	4		

- Molecule 12 is a protein called IFT54.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	X	106	Total	C	N	O	S	0	0
			849	524	155	164	6		
12	Z	106	Total	C	N	O	S	0	0
			849	524	155	164	6		

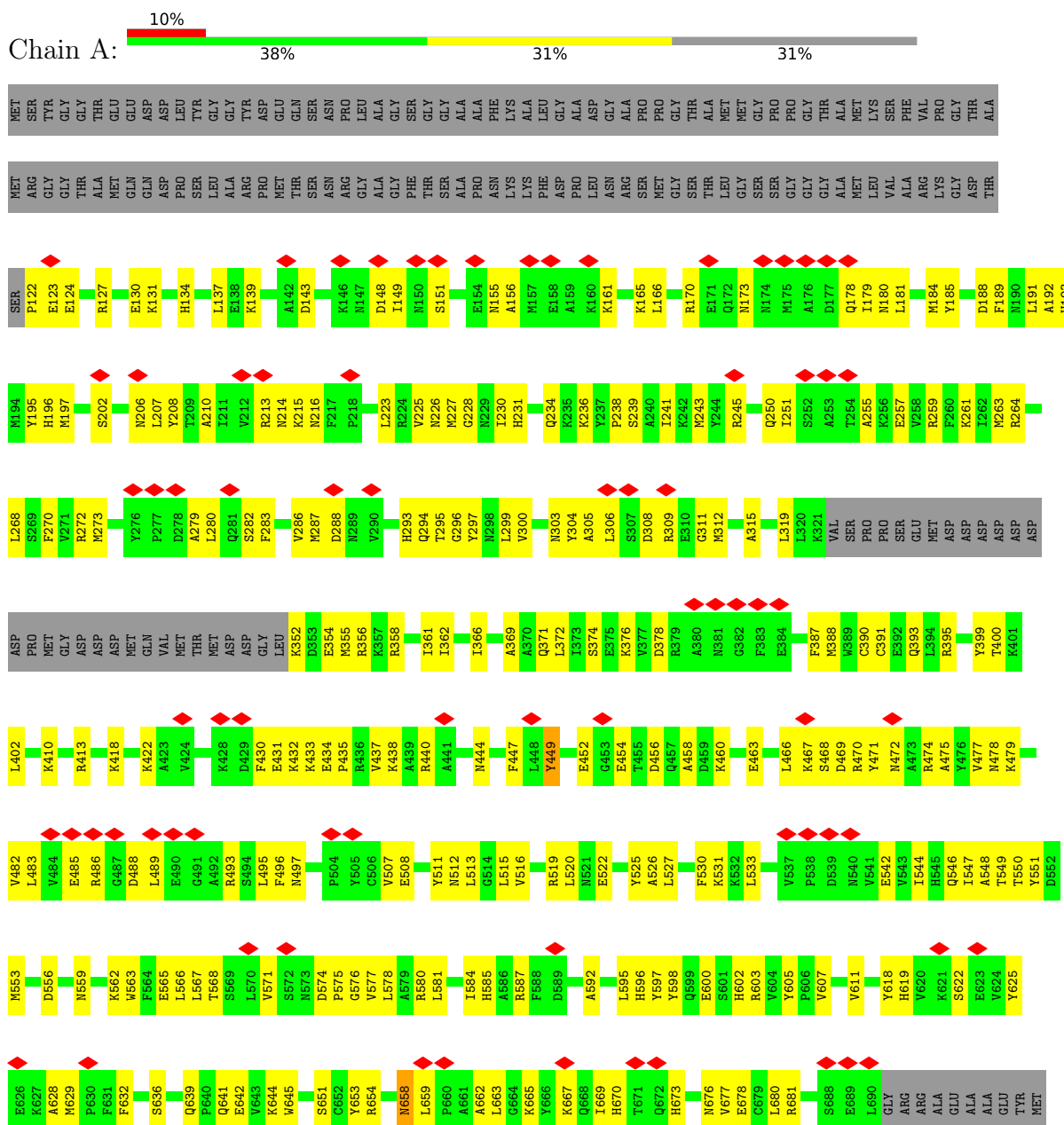
- Molecule 13 is a protein called Intraflagellar transport protein 172.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	1104	Total	C	N	O	S	0	0
			8788	5556	1532	1656	44		
13	V	1104	Total	C	N	O	S	0	0
			8788	5556	1532	1656	44		

3 Residue-property plots

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

• Molecule 1: IFT88



[illegible]

- Molecule 1: IFT88

[illegible][illegible][illegible][illegible]

PRO	PRO	GLU	MET	ASP	ASP	ASP	ASP	ASP	PRO	MET	GLY	ASP	ASP	GLN	VAL	THR	THR	ASP	ASP	GLY	LEU	K352	K353	K354	K355	K356	K357	K358	I361	I362	I366	K369	K370	K371	K372	I373	S374	D378	K379	A380	N381	G382	F383	E384	M388	W389	C391	T362	M263	R264	S265	M266	G267	L268	A269	F270	V271	A272	Y276	P277	D278	A279	L280	Q281	S282	F283	A284	T285	M287	D288	N289	V290	P291	D292	H293	Q294	T295	G296	Y297	W298	L299	V300	M301	C302	N303	Y304	A305	L306	S307	D308	R309	E310	G311	M312	K313	N314	A315	F316	I317	K318	L319	L320	K321	VAL	SFR
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E392	E393	E394	E395	E399	T400	K401	A402	A403	N404	K410	A411	T412	R413	F414	M415	K418	Q419	F420	D421	K422	K428	D429	F430	K432	K433	E434	P435	K436	V437	K438	A439	R440	N444	F447	L448	Y449	E452	G453	T454	T455	D456	Q457	A458	D459	K460	M464	A465	L466	A467
PRO	PRO	GLU	MET	ASP	ASP	ASP	ASP	ASP	ASP	PRO	MET	GLY	ASP	ASP	ASP	MET	VAL	MET	THR	MET	ASP	GLY	LEU	K352	E354	K355	K356	K357	K358	T361	L362	L366	K369	A370	Q371	L372	L373	S374	D378	A379	A380	N381	K382	F383	E384	K388	K389	C390	C391

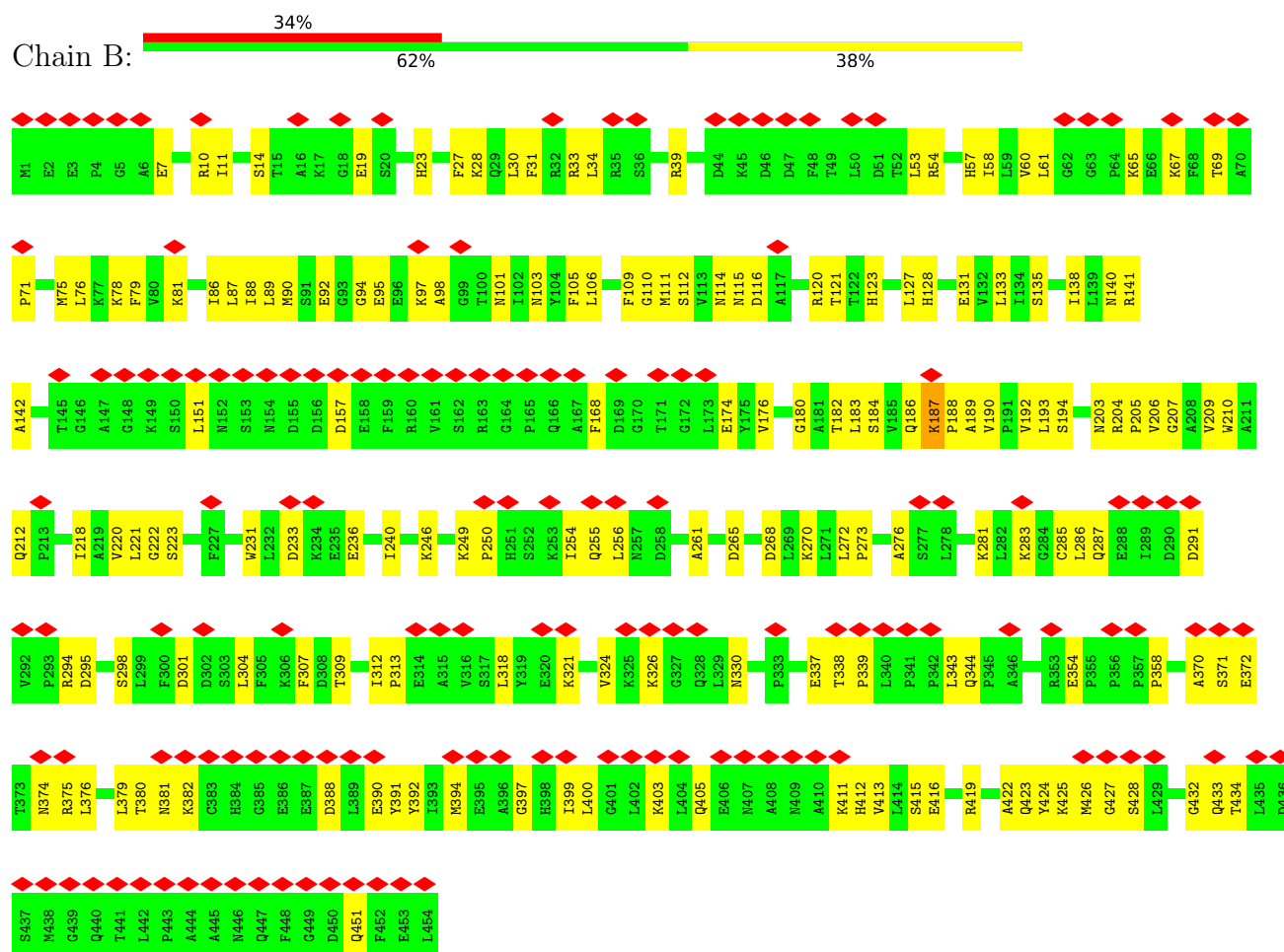
R470	Y471	N472	A473	A474	A475	Y476	V477	N478	K479	V482	L483	V484	E485	A486	G487	D488	L489	E490	G491	A492	A493	S494	L495	F496	N497	E498	G501	L502	D503	P504	Y505	C506	V507	E508	Y511	N512	L513	G514	L515	V516	R519	E522	A526	L527	F530	K532	L533	Y536	V537	P538	R470	Y471	N472	A473	A474	A475	Y476	V477	N478	K479	V482	L483	V484	E485	A486	G487	D488	L489	E490	G491	A492	A493	S494	L495	F496	N497	E498	G501	L502	D503	P504	Y505	C506	V507	E508	Y511	N512	L513	G514	L515	V516	R519	E522	A526	L527	F530	K532	L533	Y536	V537	P538	R470	Y471	N472	A473	A474	A475	Y476	V477	N478	K479	V482	L483	V484	E485	A486	G487	D488	L489	E490	G491	A492	A493	S494	L495	F496	N497	E498	G501	L502	D503	P504	Y505	C506	V507	E508	Y511	N512	L513	G514	L515	V516	R519	E522	A526	L527	F530	K532	L533	Y536	V537	P538
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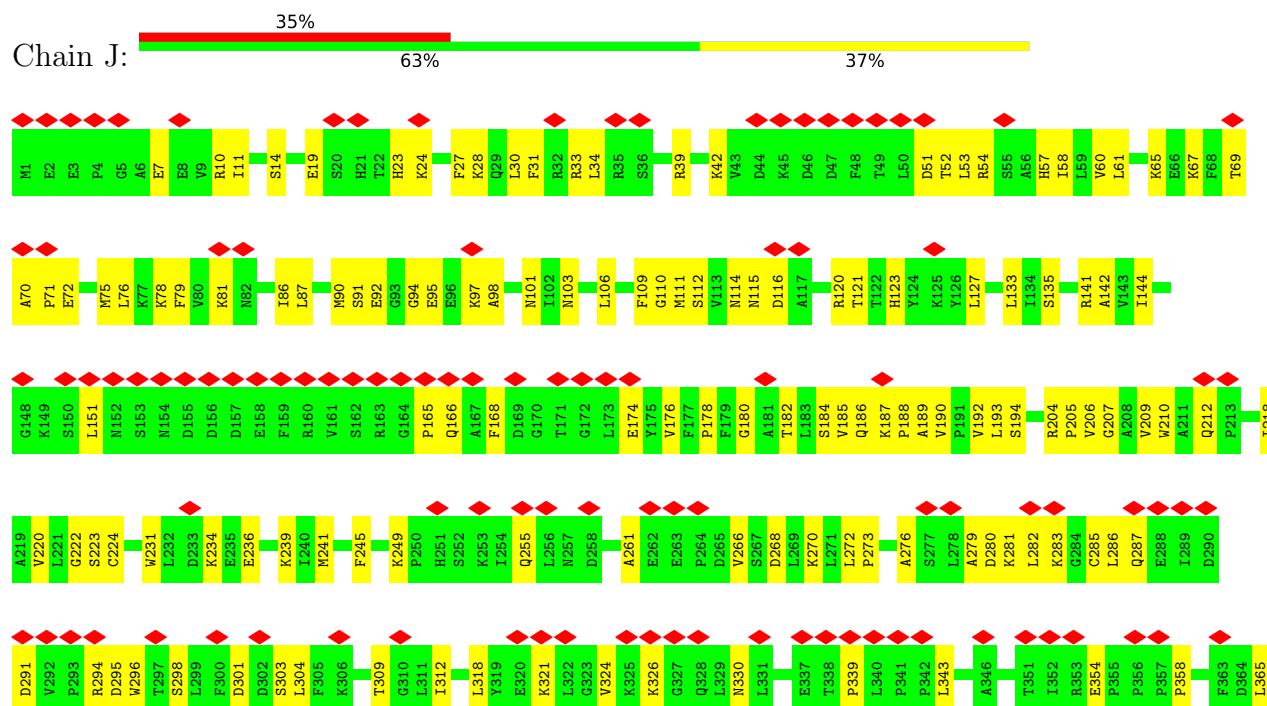
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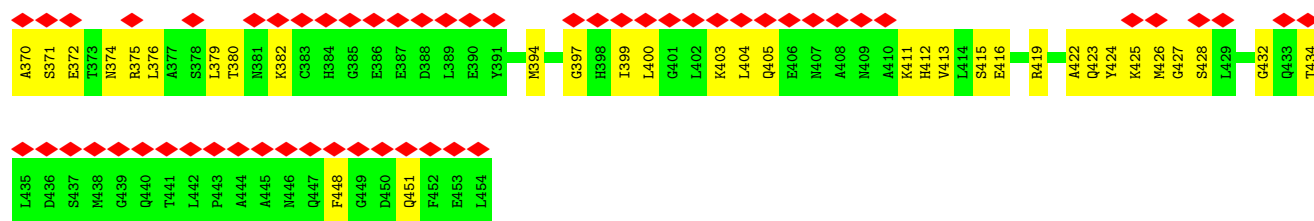
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- Molecule 2: Osm-6-like protein



• Molecule 2: Osm-6-like protein

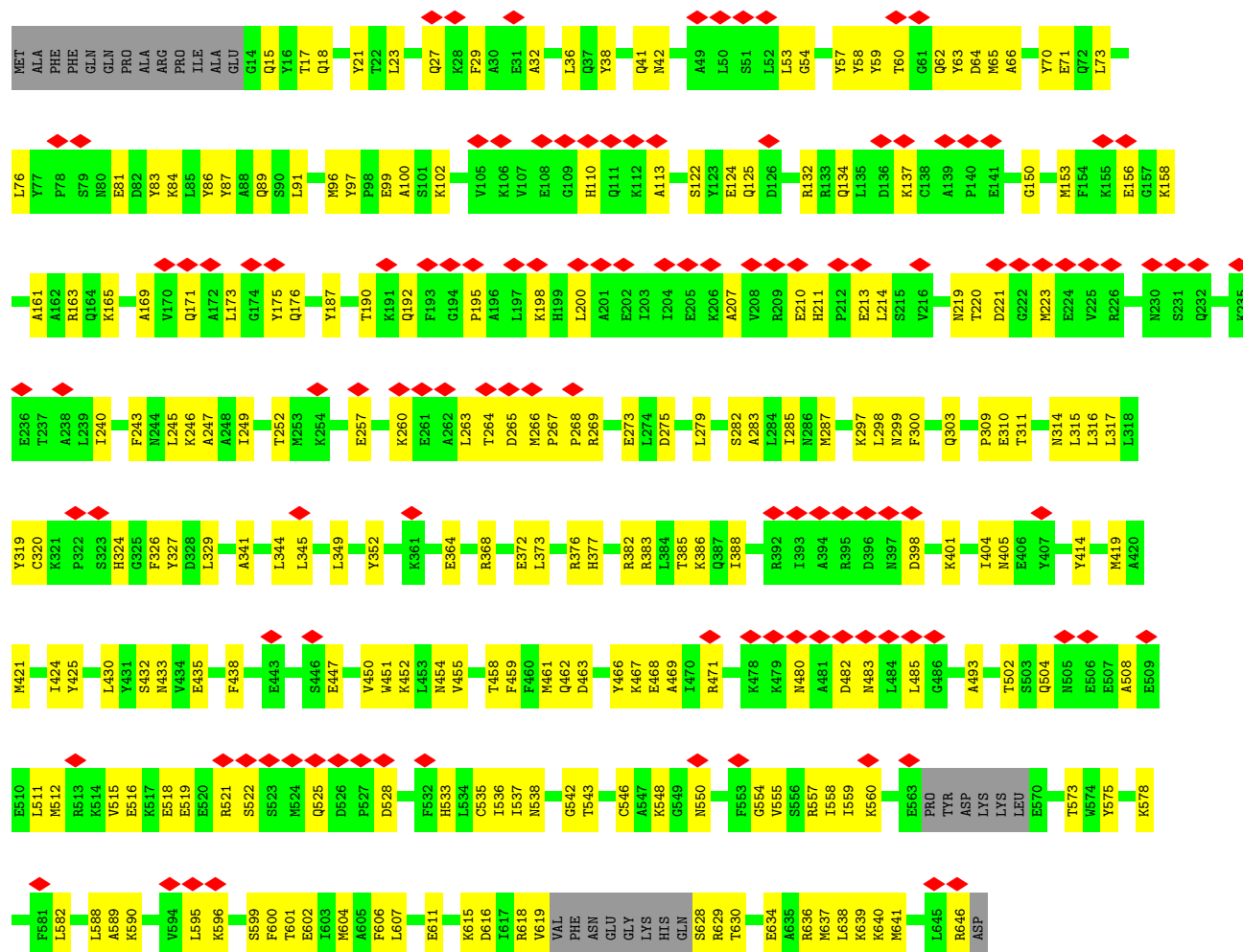




• Molecule 3: IFT70



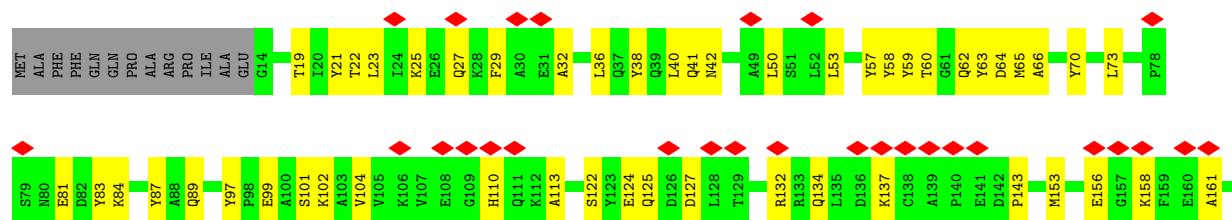
Chain C:



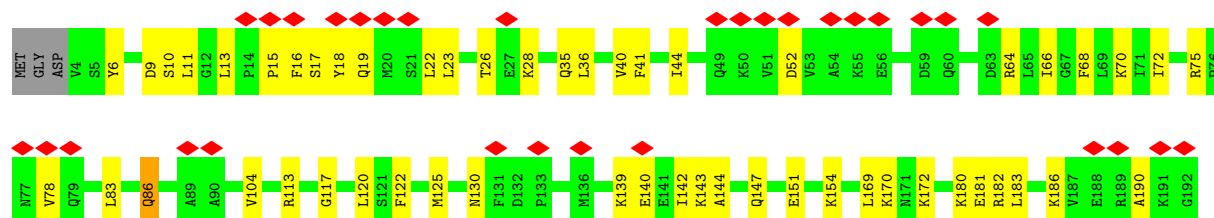
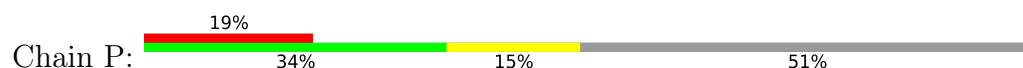
• Molecule 3: IFT70

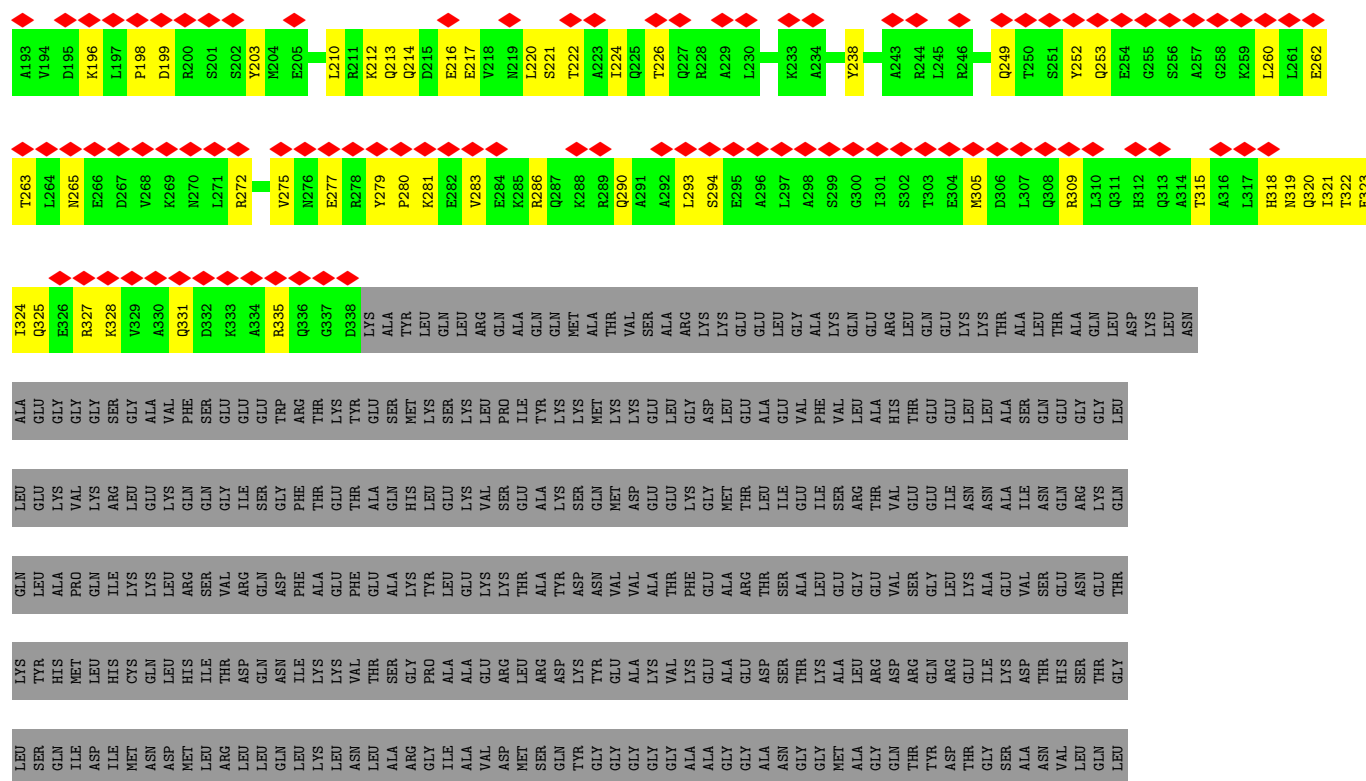


Chain K:

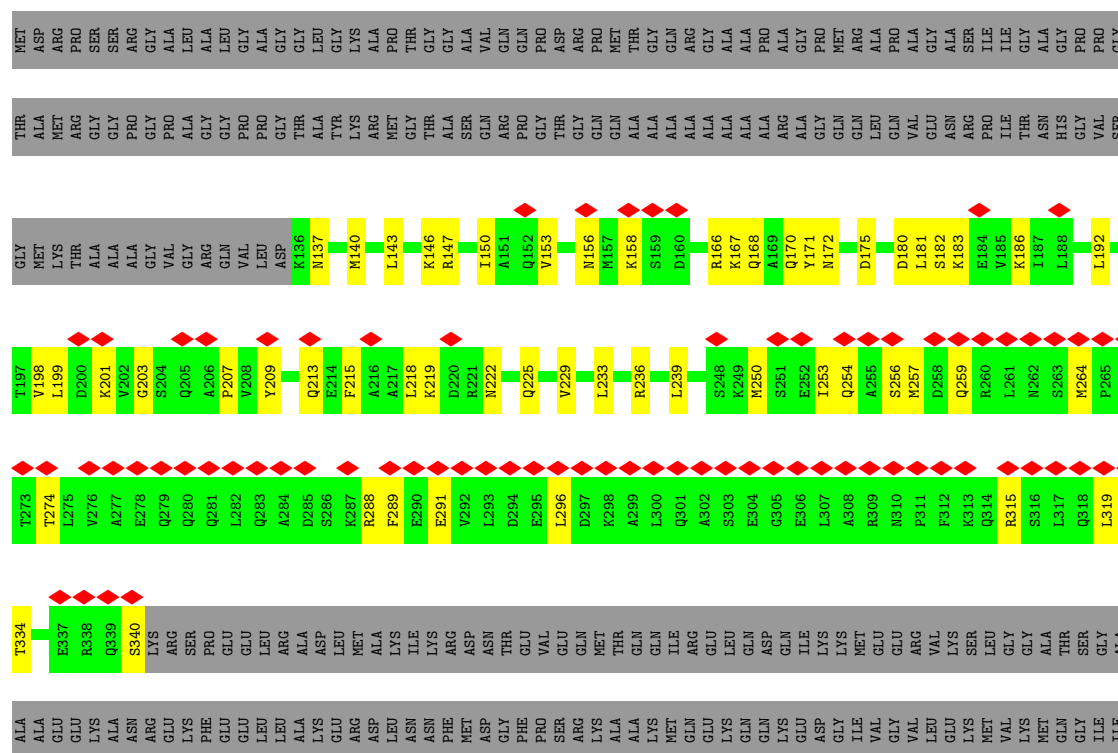


Chain F: 18% 35% 14% 51%

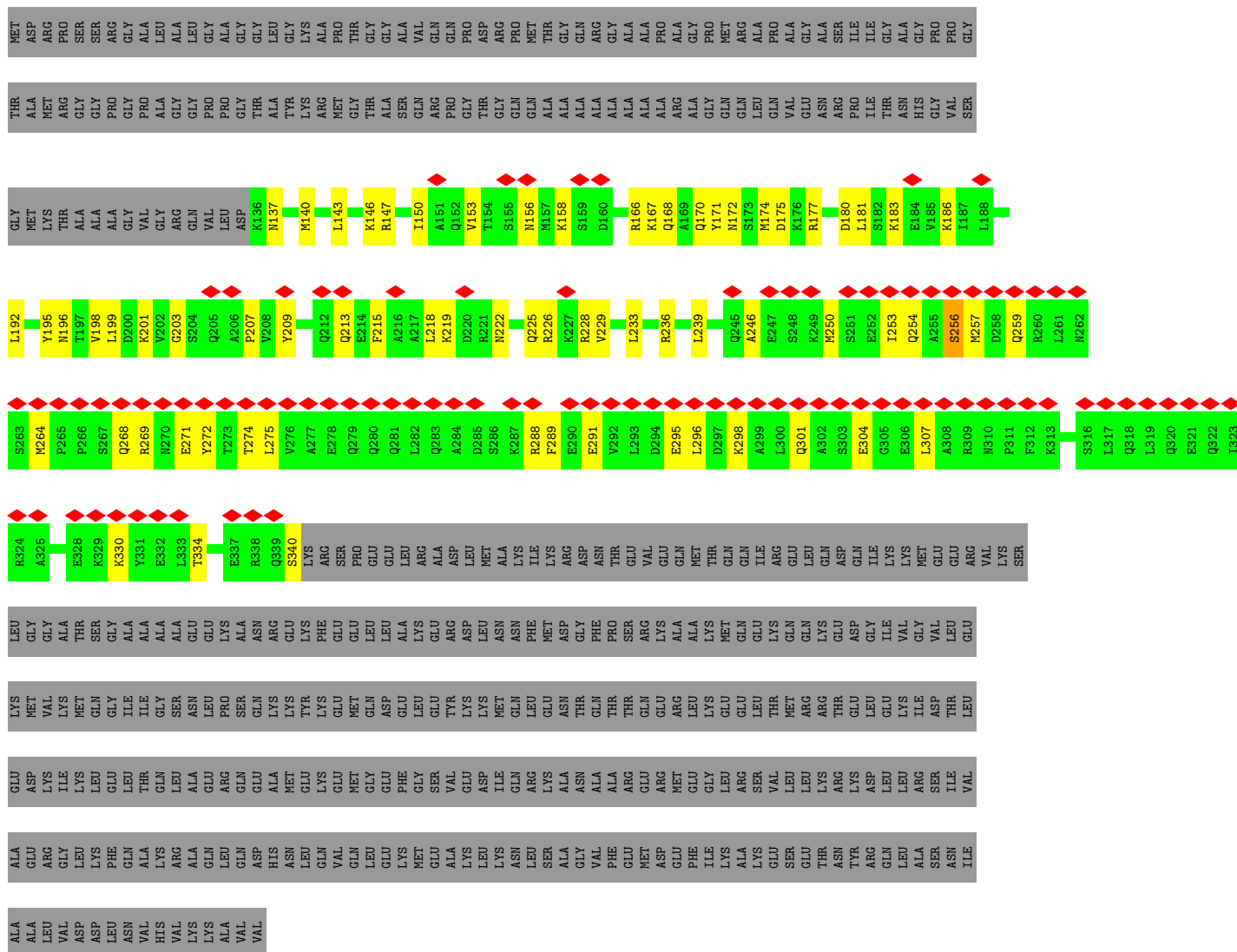




• Molecule 7: Intraflagellar transport protein 74

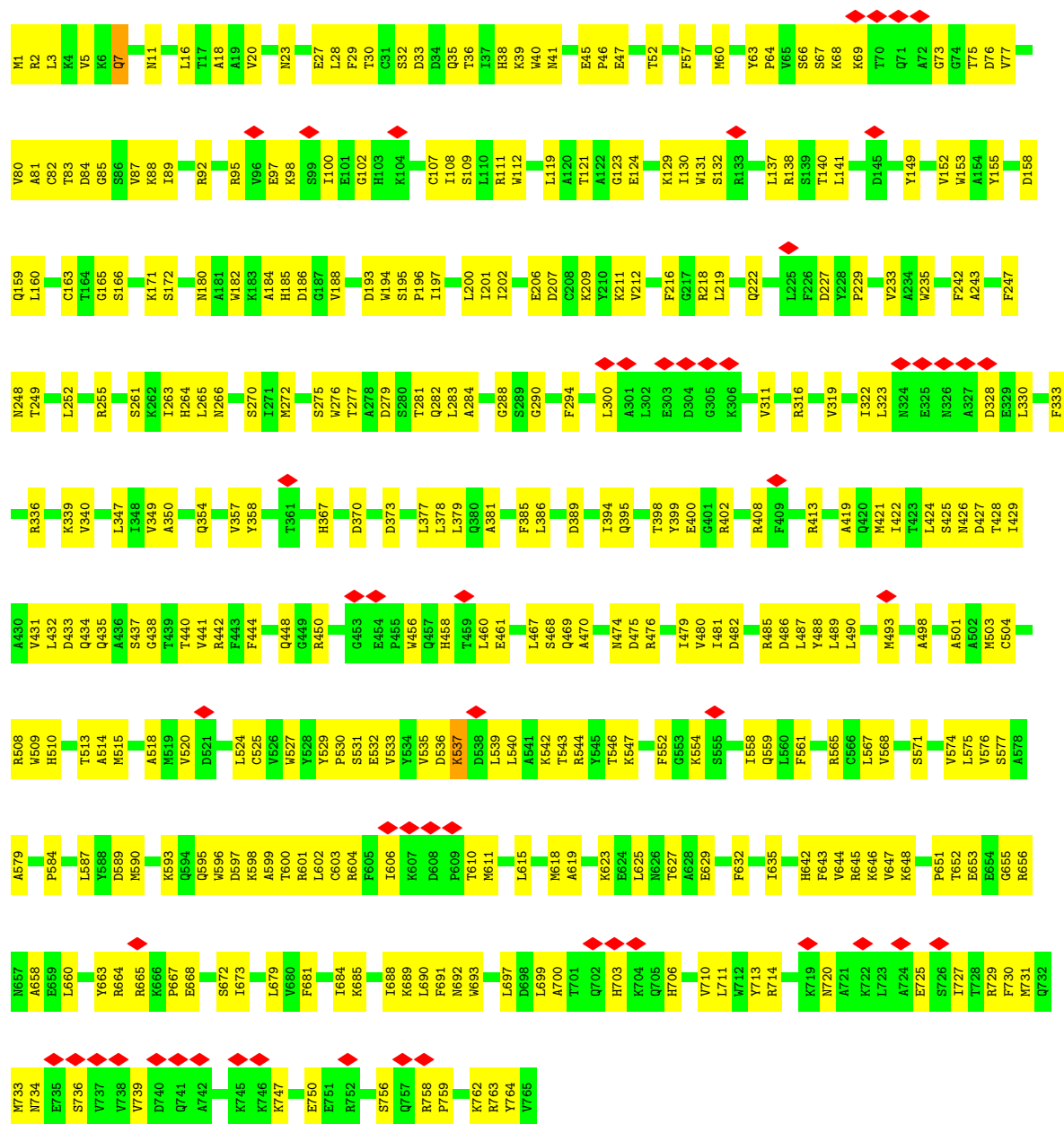


- Molecule 7: Intraflagellar transport protein 74

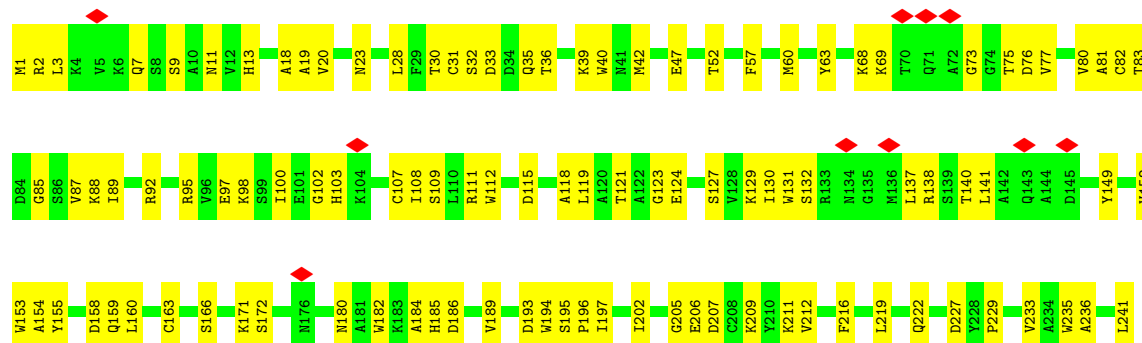


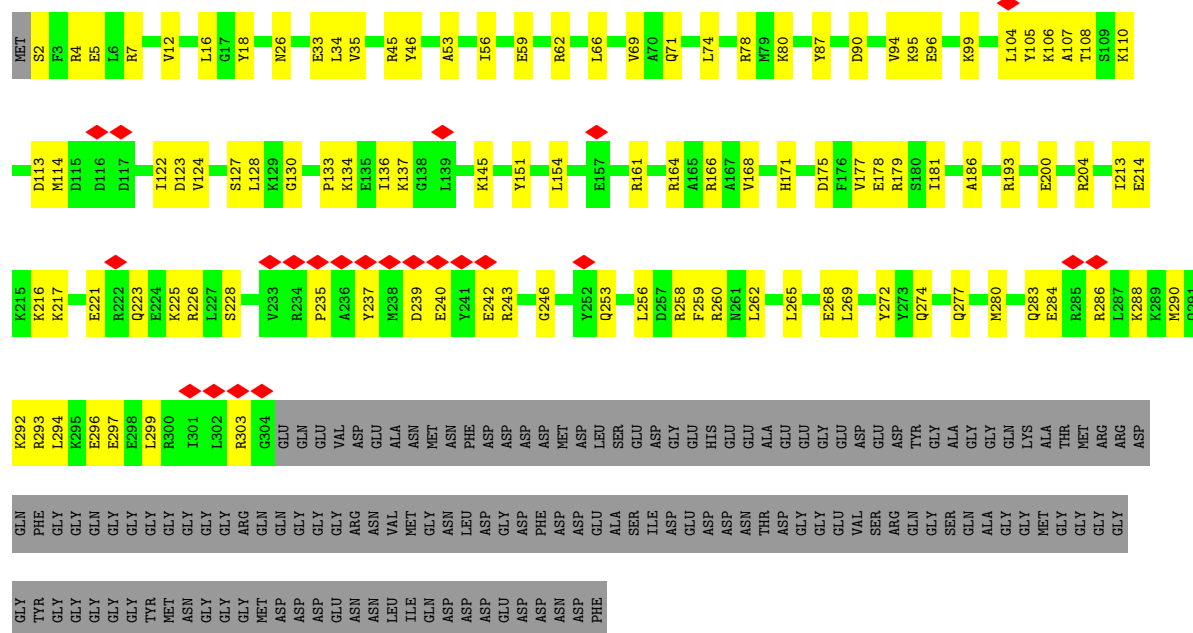
- Molecule 8: Intraflagellar transport protein 80



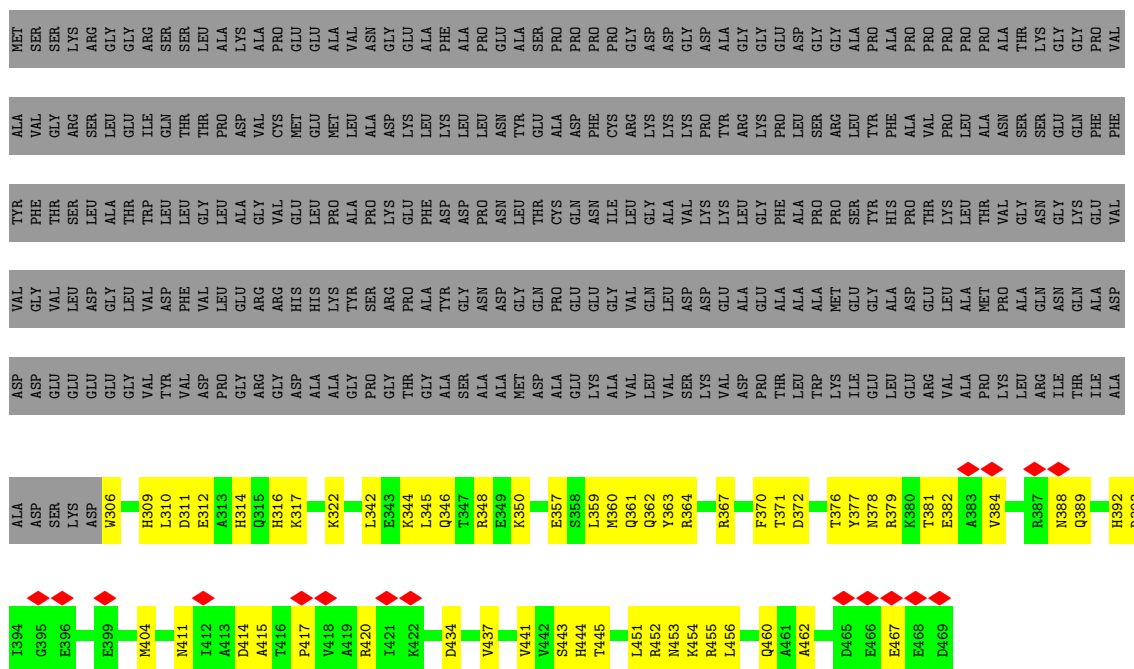


● Molecule 8: Intraflagellar transport protein 80

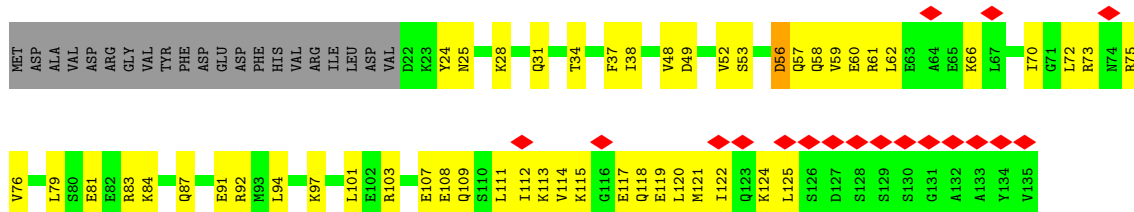




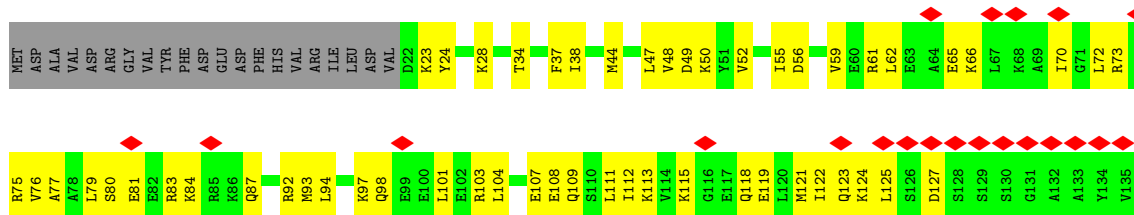




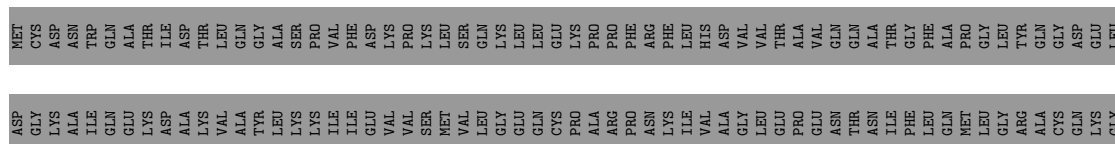
• Molecule 11: Intraflagellar transport particle protein IFT20



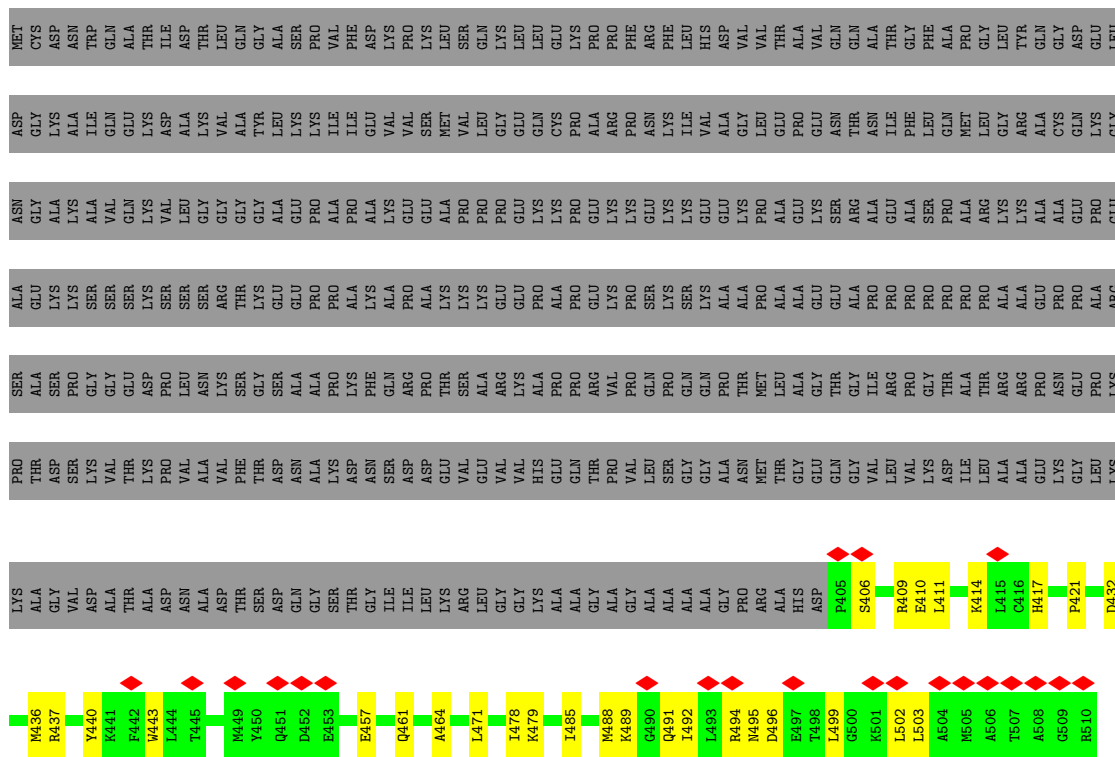
• Molecule 11: Intraflagellar transport particle protein IFT20



• Molecule 12: IFT54

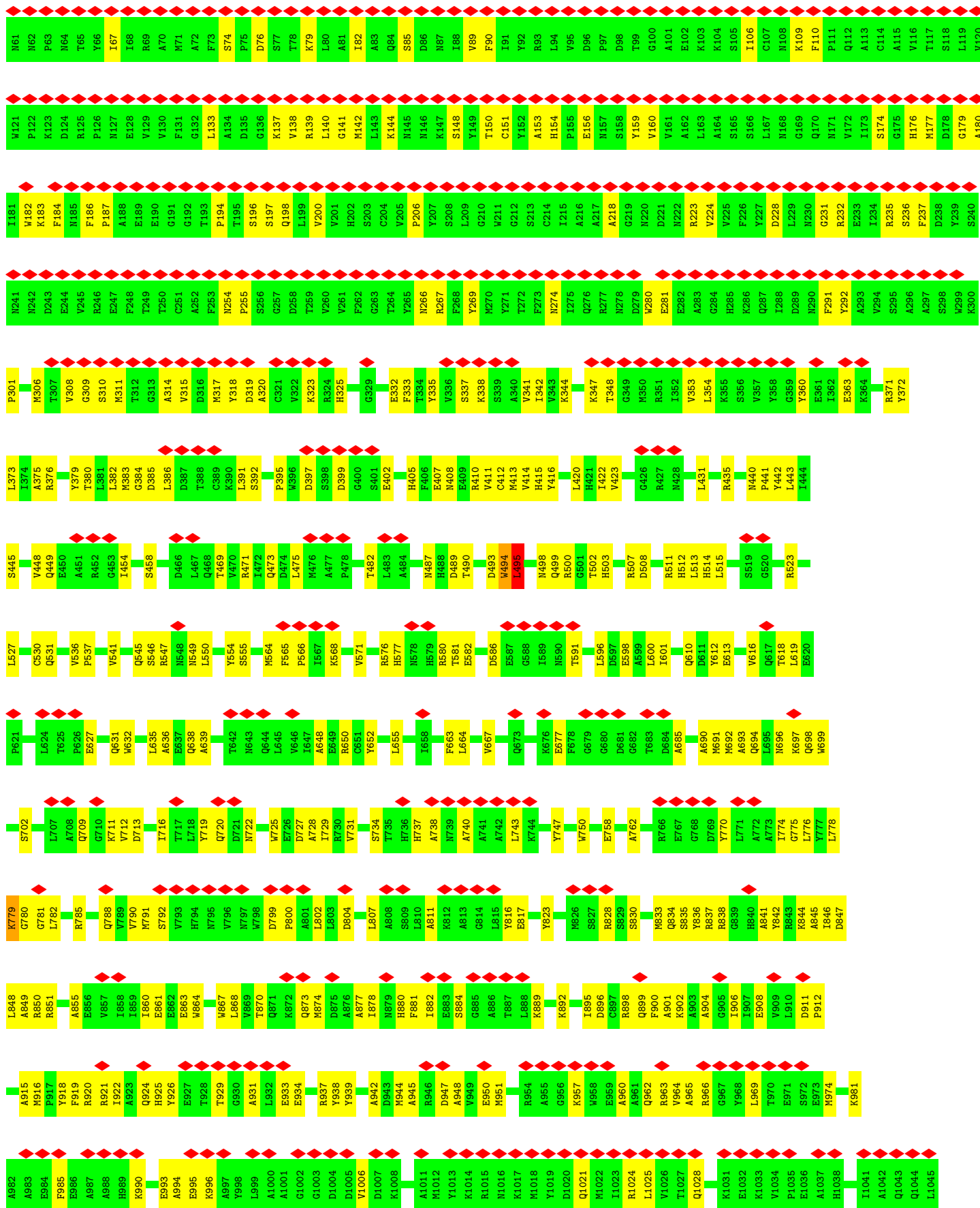


- Molecule 12: IFT54



- Molecule 13: Intraflagellar transport protein 172







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4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	18216	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Warp/Relion/M - CTF Refinement in M	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	104	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.372	Depositor
Minimum map value	-0.388	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.466	Depositor
Map size ($\text{\AA}$)	775.68, 775.68, 775.68	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.03, 3.03, 3.03	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.23	0/4423	0.60	2/5956 (0.0%)
1	H	0.30	2/4423 (0.0%)	0.62	3/5956 (0.1%)
2	B	0.20	0/3635	0.47	0/4918
2	J	0.19	0/3635	0.49	0/4918
3	C	0.18	0/5080	0.49	0/6863
3	K	0.17	0/5080	0.48	0/6863
4	D	0.19	0/1068	0.53	0/1441
4	N	0.23	0/1068	0.55	0/1441
5	E	0.15	0/4570	0.41	0/6180
5	O	0.15	0/4570	0.40	0/6180
6	F	0.21	0/2740	0.53	0/3688
6	P	0.22	0/2740	0.56	0/3688
7	G	0.24	0/1687	0.59	0/2257
7	Q	0.31	1/1687 (0.1%)	0.62	1/2257 (0.0%)
8	I	0.18	0/6147	0.43	0/8333
8	R	0.17	0/6147	0.44	0/8333
9	L	0.21	0/2504	0.53	0/3356
9	T	0.39	3/2504 (0.1%)	0.58	2/3356 (0.1%)
10	M	0.19	0/1343	0.49	0/1804
10	U	0.23	0/1343	0.53	0/1804
11	W	0.56	1/922 (0.1%)	0.71	3/1226 (0.2%)
11	Y	0.27	0/922	0.64	0/1226
12	X	0.35	0/857	0.66	0/1144
12	Z	0.34	0/857	0.65	0/1144
13	S	0.19	2/8979 (0.0%)	0.43	0/12160
13	V	0.21	3/8979 (0.0%)	0.45	1/12160 (0.0%)
All	All	0.22	12/87910 (0.0%)	0.50	12/118652 (0.0%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	W	56	ASP	C-N	14.86	1.53	1.33
9	T	72	VAL	C-N	10.39	1.49	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	262	ILE	C-N	9.30	1.45	1.33
9	T	269	LEU	C-N	8.65	1.45	1.34
9	T	268	GLU	C-N	-8.11	1.22	1.33
13	S	494	TRP	C-N	7.26	1.43	1.33
7	Q	256	SER	C-N	6.99	1.44	1.33
13	S	495	LEU	C-N	6.73	1.43	1.33
13	V	494	TRP	C-N	6.30	1.42	1.33
13	V	495	LEU	C-N	6.01	1.42	1.33
13	V	846	ILE	C-N	-5.33	1.25	1.33
1	H	263	MET	C-N	-5.16	1.26	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	658	ASN	CA-C-N	7.67	129.67	120.09
1	H	658	ASN	C-N-CA	7.67	129.67	120.09
1	A	658	ASN	CA-C-N	7.42	128.90	120.06
1	A	658	ASN	C-N-CA	7.42	128.90	120.06
11	W	56	ASP	CA-C-N	-7.23	110.48	120.38
11	W	56	ASP	C-N-CA	-7.23	110.48	120.38
9	T	72	VAL	O-C-N	6.96	129.07	121.97
1	H	262	ILE	O-C-N	6.88	129.57	121.80
7	Q	256	SER	O-C-N	6.66	130.42	123.62
11	W	56	ASP	O-C-N	5.82	128.37	122.09
13	V	847	ASP	N-CA-C	-5.74	104.47	112.45
9	T	269	LEU	N-CA-C	-5.26	105.22	111.69

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4337	0	4306	196	0
1	H	4337	0	4306	207	0
2	B	3553	0	3523	158	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	3553	0	3523	150	0
3	C	4978	0	4912	171	0
3	K	4978	0	4912	161	0
4	D	1045	0	1039	48	0
4	N	1045	0	1039	48	0
5	E	4465	0	4396	110	0
5	O	4465	0	4396	98	0
6	F	2701	0	2731	81	0
6	P	2701	0	2731	80	0
7	G	1674	0	1673	49	0
7	Q	1674	0	1673	56	0
8	I	6025	0	5988	287	0
8	R	6025	0	5988	257	0
9	L	2472	0	2484	112	0
9	T	2472	0	2484	107	0
10	M	1328	0	1322	51	0
10	U	1328	0	1322	52	0
11	W	919	0	936	68	0
11	Y	919	0	936	56	0
12	X	849	0	863	51	0
12	Z	849	0	863	45	0
13	S	8788	0	8605	252	0
13	V	8788	0	8605	298	0
All	All	86268	0	85556	2893	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 17.

All (2893) 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)
9:L:136:ILE:HG21	12:X:410:GLU:CD	1.18	1.50
9:L:136:ILE:CG2	12:X:410:GLU:CD	1.98	1.33
9:L:136:ILE:HG21	12:X:410:GLU:OE2	1.21	1.27
9:L:136:ILE:CG2	12:X:410:GLU:OE1	2.02	1.07
9:T:133:PRO:HA	9:T:136:ILE:HG22	1.32	1.06
2:J:110:GLY:HA3	2:J:188:PRO:HG3	1.39	1.03
2:B:110:GLY:HA3	2:B:188:PRO:HG3	1.43	1.00
11:W:117:GLU:HA	13:V:781:GLY:HA3	1.45	0.98
1:H:240:ALA:HA	1:H:243:MET:HE2	1.44	0.98
9:L:136:ILE:HG23	12:X:410:GLU:OE1	1.60	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L:136:ILE:CG2	12:X:410:GLU:OE2	2.04	0.91
2:J:189:ALA:HB2	2:J:210:TRP:HD1	1.35	0.89
9:L:106:LYS:HA	11:W:56:ASP:CB	2.04	0.87
2:J:189:ALA:HB2	2:J:210:TRP:CD1	2.09	0.85
13:V:756:GLN:HA	13:V:780:GLY:HA2	1.58	0.84
1:A:449:TYR:CD1	1:A:458:ALA:HB2	2.12	0.84
8:I:688:ILE:HD12	13:V:662:ARG:HH22	1.41	0.83
2:B:189:ALA:HB2	2:B:210:TRP:HD1	1.41	0.83
13:V:847:ASP:HB2	13:V:860:ILE:HA	1.59	0.82
2:J:106:LEU:HB3	2:J:111:MET:HB2	1.62	0.81
11:W:117:GLU:CA	13:V:781:GLY:HA3	2.10	0.80
2:B:428:SER:H	4:D:254:PRO:HD2	1.45	0.80
13:V:668:VAL:O	13:V:672:GLN:HB2	1.81	0.80
2:B:106:LEU:HB3	2:B:111:MET:HB2	1.64	0.80
2:J:428:SER:H	4:N:254:PRO:HD2	1.46	0.80
2:B:189:ALA:HB2	2:B:210:TRP:CD1	2.16	0.80
6:P:199:ASP:HB2	6:P:203:TYR:HB2	1.63	0.79
2:J:273:PRO:HA	9:T:269:LEU:HD13	1.65	0.79
1:H:449:TYR:CD1	1:H:458:ALA:HB2	2.18	0.78
11:W:120:LEU:HB3	13:V:781:GLY:HA2	1.64	0.78
13:V:758:GLU:CD	13:V:782:LEU:HB2	2.09	0.78
9:L:106:LYS:HA	11:W:56:ASP:HB3	1.64	0.78
11:W:56:ASP:HA	11:W:59:VAL:HG22	1.63	0.77
5:E:1:MET:HB3	5:E:194:LEU:HD22	1.65	0.77
6:F:199:ASP:HB2	6:F:203:TYR:HB2	1.65	0.77
1:A:449:TYR:CE2	1:A:454:GLU:HG3	2.19	0.77
8:I:651:PRO:HB2	8:I:764:TYR:H	1.50	0.77
12:Z:406:SER:HB2	12:Z:409:ARG:HH21	1.50	0.76
1:H:449:TYR:CE2	1:H:454:GLU:HG3	2.20	0.76
10:M:360:MET:SD	10:M:364:ARG:NH1	2.58	0.76
5:E:224:ASN:HD21	5:E:259:LEU:HD11	1.50	0.76
5:O:224:ASN:HD21	5:O:259:LEU:HD11	1.51	0.76
9:L:106:LYS:HA	11:W:56:ASP:HB2	1.68	0.75
9:T:136:ILE:CG1	12:Z:410:GLU:HG3	2.16	0.75
1:A:388:MET:SD	1:A:410:LYS:NZ	2.60	0.75
10:U:360:MET:SD	10:U:364:ARG:NH1	2.60	0.75
13:V:787:ALA:O	13:V:791:MET:HB2	1.87	0.75
11:W:124:LYS:HD3	13:V:779:LYS:HG2	1.68	0.75
9:T:133:PRO:CA	9:T:136:ILE:HG22	2.16	0.75
9:T:136:ILE:HG12	12:Z:410:GLU:HG3	1.69	0.74
8:I:3:LEU:HB2	8:I:263:ILE:HG13	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:R:651:PRO:HG2	8:R:763:ARG:HE	1.52	0.74
1:A:263:MET:HG2	1:A:286:VAL:HG21	1.67	0.74
1:H:449:TYR:CE1	1:H:458:ALA:HB2	2.23	0.74
5:O:277:LEU:HD11	5:O:280:LEU:HB2	1.68	0.74
8:R:688:ILE:HG12	8:R:710:VAL:HA	1.70	0.74
11:W:117:GLU:HA	13:V:781:GLY:CA	2.16	0.73
8:I:629:GLU:O	13:V:724:ARG:NH1	2.20	0.73
13:V:332:GLU:HG3	13:V:344:LYS:HB2	1.71	0.73
8:I:651:PRO:HG2	8:I:763:ARG:HE	1.52	0.73
3:K:23:LEU:HB3	3:K:29:PHE:HB3	1.71	0.72
13:S:413:MET:HB3	13:S:420:LEU:HD11	1.72	0.72
13:S:440:ASN:HB3	13:S:443:LEU:HD23	1.71	0.72
3:K:459:PHE:HA	3:K:462:GLN:HB2	1.71	0.72
6:P:286:ARG:HD2	7:Q:296:LEU:HB2	1.70	0.72
3:C:23:LEU:HB3	3:C:29:PHE:HB3	1.69	0.72
13:V:413:MET:HB3	13:V:420:LEU:HD11	1.72	0.72
4:D:242:ARG:HH22	4:D:246:ILE:HG12	1.52	0.72
6:P:249:GLN:O	6:P:253:GLN:HB2	1.89	0.72
8:I:688:ILE:O	13:V:665:HIS:NE2	2.23	0.72
10:M:452:ARG:HH22	10:M:455:ARG:HH11	1.35	0.72
13:V:990:LYS:HD3	13:V:993:GLU:HB2	1.72	0.71
13:S:990:LYS:HD3	13:S:993:GLU:HB2	1.72	0.71
5:E:80:TYR:O	5:E:84:LEU:HB2	1.90	0.71
13:S:413:MET:HG3	13:S:422:ILE:HG22	1.72	0.71
3:C:171:GLN:HG2	5:E:303:GLU:HB3	1.72	0.71
13:S:179:GLY:HA2	13:S:206:PRO:HD3	1.73	0.71
3:C:29:PHE:HB2	3:C:32:ALA:HB3	1.73	0.71
8:I:354:GLN:HA	8:I:370:ASP:HA	1.73	0.71
11:W:124:LYS:HG2	13:V:779:LYS:HA	1.73	0.71
3:C:163:ARG:NH2	3:C:190:THR:OG1	2.19	0.71
1:H:418:LYS:HG2	9:T:274:GLN:HE21	1.55	0.70
2:J:270:LYS:NZ	9:T:268:GLU:OE1	2.20	0.70
8:I:759:PRO:HA	8:I:762:LYS:HB2	1.74	0.70
1:A:581:LEU:O	1:A:585:HIS:ND1	2.25	0.70
13:S:410:ARG:HE	13:S:448:VAL:HB	1.56	0.69
13:V:413:MET:HG3	13:V:422:ILE:HG22	1.73	0.69
8:R:433:ASP:HB3	8:R:440:THR:HB	1.74	0.69
13:V:841:ALA:HB1	13:V:844:LYS:HB3	1.74	0.69
8:I:645:ARG:HG2	13:V:722:ASN:HA	1.73	0.69
8:R:152:VAL:HG21	8:R:193:ASP:HA	1.73	0.69
3:C:459:PHE:HA	3:C:462:GLN:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:ASP:OD1	1:A:460:LYS:NZ	2.24	0.69
11:W:81:GLU:HA	11:W:84:LYS:HE2	1.74	0.69
8:I:152:VAL:HG21	8:I:193:ASP:HA	1.73	0.69
11:W:94:LEU:HD13	12:X:471:LEU:HG	1.75	0.69
8:R:354:GLN:HA	8:R:370:ASP:HA	1.75	0.69
8:R:759:PRO:HA	8:R:762:LYS:HB2	1.75	0.69
1:H:472:ASN:O	1:H:474:ARG:NH1	2.26	0.69
5:O:275:GLN:HG3	5:O:276:VAL:HG23	1.74	0.69
1:A:449:TYR:CE1	1:A:458:ALA:HB2	2.28	0.69
9:L:18:TYR:HB3	9:L:45:ARG:HH11	1.58	0.69
1:H:581:LEU:O	1:H:585:HIS:ND1	2.26	0.68
7:Q:295:GLU:HA	7:Q:298:LYS:HZ2	1.56	0.68
8:R:235:TRP:HA	8:R:242:PHE:HA	1.75	0.68
2:B:273:PRO:O	9:L:269:LEU:HD13	1.94	0.68
8:I:642:HIS:HB3	13:V:694:GLN:HA	1.76	0.68
11:W:117:GLU:HB3	13:V:780:GLY:O	1.93	0.68
8:R:155:TYR:OH	8:R:413:ARG:NH2	2.26	0.68
8:R:651:PRO:HB2	8:R:764:TYR:H	1.58	0.68
13:S:412:CYS:HB3	13:S:423:VAL:HB	1.76	0.68
13:S:847:ASP:OD2	13:S:864:TRP:NE1	2.26	0.68
8:I:85:GLY:HA2	8:I:107:CYS:HB2	1.74	0.68
13:V:440:ASN:HB3	13:V:443:LEU:HD23	1.74	0.68
9:T:204:ARG:HE	10:U:378:ASN:HB3	1.58	0.68
13:V:6:PHE:HB3	13:V:317:MET:HG3	1.74	0.68
3:K:81:GLU:HA	3:K:84:LYS:HE2	1.76	0.68
13:V:503:HIS:HB3	13:V:515:LEU:HD11	1.76	0.68
1:H:642:GLU:HB3	1:H:645:TRP:HB3	1.76	0.68
6:P:305:MET:O	6:P:309:ARG:NH1	2.27	0.68
12:X:419:SER:HA	12:X:422:LEU:HD12	1.74	0.67
8:R:536:ASP:HA	8:R:665:ARG:HB2	1.76	0.67
13:V:410:ARG:HE	13:V:448:VAL:HB	1.60	0.67
2:B:381:ASN:HD21	4:D:234:ALA:H	1.40	0.67
3:K:616:ASP:HA	3:K:630:THR:HA	1.75	0.67
3:C:96:MET:HB3	3:C:99:GLU:HB2	1.75	0.67
13:V:224:VAL:HB	13:V:237:PHE:HB2	1.76	0.67
1:H:512:ASN:HA	1:H:515:LEU:HD12	1.76	0.67
8:I:235:TRP:HA	8:I:242:PHE:HA	1.75	0.67
8:I:679:LEU:HB2	8:I:758:ARG:HH22	1.60	0.67
13:V:412:CYS:HB3	13:V:423:VAL:HB	1.77	0.67
8:I:111:ARG:NH1	8:I:112:TRP:O	2.27	0.67
3:C:81:GLU:HA	3:C:84:LYS:HE2	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:29:PHE:HB2	3:K:32:ALA:HB3	1.75	0.67
13:V:443:LEU:HA	13:V:495:LEU:HD21	1.75	0.67
3:K:542:GLY:O	3:K:546:CYS:N	2.27	0.67
5:E:183:ASP:H	5:E:186:ARG:HB2	1.60	0.67
8:I:589:ASP:O	8:I:593:LYS:NZ	2.26	0.67
12:X:406:SER:HB2	12:X:409:ARG:HH21	1.59	0.67
4:N:221:TRP:O	4:N:225:ILE:HB	1.95	0.67
9:T:18:TYR:HB3	9:T:45:ARG:HH11	1.59	0.67
5:O:261:ARG:HE	5:O:264:LEU:HD21	1.60	0.67
10:U:411:ASN:HA	10:U:415:ALA:HB3	1.77	0.66
8:I:155:TYR:OH	8:I:413:ARG:NH2	2.28	0.66
8:I:386:LEU:HB2	8:I:424:LEU:HD22	1.76	0.66
13:S:841:ALA:HB1	13:S:844:LYS:HB3	1.77	0.66
1:H:279:ALA:HB3	1:H:302:CYS:SG	2.34	0.66
8:I:632:PHE:HB2	13:V:724:ARG:HH12	1.60	0.66
13:S:948:ALA:HA	13:S:951:MET:HE2	1.77	0.66
8:R:155:TYR:HB2	8:R:196:PRO:HB2	1.77	0.66
6:F:70:LYS:HG3	6:F:75:ARG:HH21	1.61	0.66
8:I:1:MET:O	8:I:261:SER:OG	2.14	0.66
13:V:757:GLU:HG3	13:V:779:LYS:HE2	1.76	0.66
1:A:544:ILE:HG21	1:A:566:LEU:HD22	1.76	0.66
8:R:85:GLY:HA2	8:R:107:CYS:HB2	1.76	0.66
4:D:249:LEU:HD23	4:D:251:GLN:HE21	1.61	0.66
13:S:874:MET:HA	13:S:877:ALA:HB3	1.77	0.66
9:T:193:ARG:HD3	10:U:371:THR:HA	1.77	0.66
12:Z:433:ILE:HG22	12:Z:437:ARG:HE	1.60	0.66
13:V:823:TYR:HB3	13:V:828:ARG:HB3	1.77	0.66
1:A:418:LYS:HG2	9:L:274:GLN:HE21	1.60	0.66
3:C:616:ASP:HA	3:C:630:THR:HA	1.76	0.66
5:O:114:ALA:O	5:O:123:GLN:NE2	2.29	0.66
1:A:508:GLU:HG2	2:B:283:LYS:HB3	1.76	0.66
1:A:294:GLN:NE2	2:B:301:ASP:OD1	2.29	0.66
2:B:390:GLU:HG3	2:B:391:TYR:HD1	1.60	0.66
8:I:697:LEU:HD11	8:I:729:ARG:HB3	1.78	0.66
8:R:3:LEU:HB2	8:R:263:ILE:HG13	1.77	0.66
13:V:652:TYR:HB3	13:V:663:PHE:HB3	1.77	0.66
1:A:202:SER:O	1:A:206:ASN:ND2	2.29	0.66
1:A:642:GLU:HB3	1:A:645:TRP:HB3	1.77	0.66
3:C:383:ARG:NH2	3:K:25:LYS:O	2.28	0.66
8:I:731:MET:HA	8:I:734:ASN:HB2	1.76	0.66
13:S:990:LYS:HB3	13:S:994:ALA:HB2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:90:MET:HE1	2:B:220:VAL:HB	1.76	0.65
1:H:508:GLU:HG2	2:J:283:LYS:HB3	1.76	0.65
5:O:36:LYS:NZ	5:O:38:ASP:O	2.27	0.65
13:V:179:GLY:HA2	13:V:206:PRO:HD3	1.76	0.65
1:A:472:ASN:O	1:A:474:ARG:NH1	2.29	0.65
4:D:341:VAL:HB	4:D:344:LEU:HD12	1.79	0.65
11:W:61:ARG:HB3	12:X:440:TYR:HE2	1.61	0.65
2:J:133:LEU:HD22	2:J:176:VAL:HA	1.79	0.65
4:N:341:VAL:HB	4:N:344:LEU:HD12	1.78	0.65
11:Y:125:LEU:HD22	12:Z:502:LEU:HD13	1.79	0.65
1:A:463:GLU:HB3	1:A:467:LYS:HZ3	1.61	0.65
1:H:456:ASP:OD1	1:H:460:LYS:NZ	2.29	0.65
13:V:990:LYS:HB3	13:V:994:ALA:HB2	1.79	0.65
8:I:524:LEU:HB3	8:I:547:LYS:HB3	1.79	0.65
1:H:170:ARG:HE	1:H:173:ASN:HB2	1.61	0.65
1:H:294:GLN:NE2	2:J:301:ASP:OD1	2.30	0.65
6:P:72:ILE:O	6:P:113:ARG:NH1	2.30	0.65
8:R:558:ILE:HA	8:R:568:VAL:HG12	1.79	0.65
2:B:65:LYS:HA	2:B:98:ALA:HB1	1.78	0.65
5:E:277:LEU:HD11	5:E:280:LEU:HB2	1.78	0.65
8:I:433:ASP:HB3	8:I:440:THR:HB	1.77	0.65
12:X:413:GLN:HB3	10:U:348:ARG:HD3	1.77	0.65
9:T:33:GLU:HB3	9:T:56:ILE:HG21	1.79	0.65
1:A:565:GLU:OE1	9:T:231:GLN:NE2	2.30	0.65
7:G:167:LYS:O	7:G:171:TYR:HB3	1.97	0.65
5:O:152:GLU:HA	5:O:155:LEU:HB2	1.79	0.65
8:R:111:ARG:NH1	8:R:112:TRP:O	2.29	0.65
1:A:641:GLN:NE2	1:A:642:GLU:OE2	2.30	0.64
5:E:94:PHE:HD1	5:E:113:GLN:HE21	1.43	0.64
8:I:601:ARG:NH2	13:V:754:THR:OG1	2.30	0.64
1:H:202:SER:O	1:H:206:ASN:ND2	2.29	0.64
11:Y:124:LYS:HG3	11:Y:125:LEU:HD12	1.77	0.64
5:E:114:ALA:O	5:E:123:GLN:NE2	2.30	0.64
8:I:693:TRP:HE3	13:V:662:ARG:HG3	1.63	0.64
8:R:282:GLN:HB2	8:R:336:ARG:HH22	1.63	0.64
10:U:309:HIS:HE1	11:Y:38:ILE:HG12	1.62	0.64
13:V:690:ALA:O	13:V:722:ASN:ND2	2.30	0.64
6:F:72:ILE:O	6:F:113:ARG:NH1	2.29	0.64
9:L:130:GLY:O	9:L:134:LYS:N	2.30	0.64
13:S:405:HIS:HB2	13:S:413:MET:HB2	1.79	0.64
6:P:210:LEU:HG	6:P:214:GLN:HE22	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:238:TYR:HE2	7:G:239:LEU:HB3	1.62	0.64
13:V:266:ASN:HA	13:V:291:PHE:HB3	1.80	0.64
8:R:576:VAL:HG22	11:Y:92:ARG:HH12	1.62	0.64
5:E:125:ARG:NE	5:E:152:GLU:OE1	2.30	0.64
8:I:711:LEU:HD12	8:I:733:MET:HG3	1.78	0.64
1:H:227:MET:SD	1:H:243:MET:SD	2.95	0.64
8:R:219:LEU:HD21	8:R:222:GLN:HB2	1.80	0.64
8:R:688:ILE:HG21	8:R:706:HIS:HE1	1.61	0.64
1:A:184:MET:HG2	1:A:216:ASN:HD21	1.63	0.64
3:C:299:ASN:O	3:C:303:GLN:NE2	2.31	0.64
6:F:181:GLU:OE2	6:F:182:ARG:NH1	2.31	0.64
9:L:193:ARG:HD3	10:M:371:THR:HA	1.80	0.64
9:L:293:ARG:HH22	9:L:294:LEU:HG	1.62	0.64
13:S:847:ASP:HB2	13:S:860:ILE:HA	1.79	0.64
13:S:995:GLU:HB2	13:S:1006:VAL:HG13	1.80	0.64
1:H:537:VAL:HG21	10:U:460:GLN:HG2	1.80	0.64
13:V:133:LEU:HB2	13:V:139:ARG:HH12	1.62	0.64
3:C:383:ARG:NH2	3:K:27:GLN:OE1	2.31	0.63
13:V:667:VAL:HG12	13:V:691:MET:HG2	1.80	0.63
1:A:512:ASN:HA	1:A:515:LEU:HD12	1.79	0.63
9:L:290:MET:HG2	9:L:293:ARG:HH21	1.64	0.63
13:S:1052:ARG:HH22	10:U:359:LEU:HG	1.63	0.63
4:N:273:LEU:HB3	4:N:277:THR:HB	1.81	0.63
8:I:713:TYR:HB3	13:V:665:HIS:HD2	1.62	0.63
1:H:231:HIS:CD2	1:H:243:MET:SD	2.91	0.63
8:R:357:VAL:HB	8:R:367:HIS:HB2	1.80	0.63
8:I:689:LYS:HG3	13:V:666:LYS:HD3	1.81	0.63
2:J:419:ARG:HH11	4:N:344:LEU:HB3	1.63	0.63
6:P:315:THR:HA	6:P:318:HIS:CD2	2.33	0.63
8:R:679:LEU:HB2	8:R:758:ARG:HH22	1.62	0.63
9:T:130:GLY:O	9:T:134:LYS:N	2.32	0.63
9:T:133:PRO:HA	9:T:136:ILE:CG2	2.21	0.63
6:F:285:LYS:HD2	6:F:286:ARG:HH21	1.63	0.63
3:K:171:GLN:HG2	5:O:303:GLU:HB3	1.79	0.63
4:N:252:GLU:HG2	4:N:254:PRO:HD3	1.81	0.63
8:R:598:LYS:HE2	12:Z:496:ASP:HB3	1.79	0.63
8:I:598:LYS:HB2	12:X:499:LEU:HD23	1.81	0.63
13:S:811:ALA:O	13:S:838:ARG:NH1	2.31	0.63
1:H:447:PHE:CE2	2:J:286:LEU:HB2	2.33	0.63
2:J:343:LEU:HD21	3:K:317:LEU:HD21	1.80	0.63
6:P:70:LYS:HG3	6:P:75:ARG:HH21	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:V:403:LYS:HG2	13:V:439:MET:HE1	1.79	0.63
8:I:536:ASP:HA	8:I:665:ARG:HB2	1.81	0.63
1:H:170:ARG:HD2	1:H:179:ILE:HG21	1.81	0.63
1:H:251:ILE:HG21	1:H:255:ALA:HB3	1.79	0.63
8:R:141:LEU:O	8:R:171:LYS:NZ	2.31	0.63
13:V:874:MET:HA	13:V:877:ALA:HB3	1.79	0.63
8:R:302:LEU:HD22	8:R:342:LEU:HD23	1.80	0.63
8:R:524:LEU:HB3	8:R:547:LYS:HB3	1.80	0.63
10:U:462:ALA:O	10:U:467:GLU:N	2.32	0.63
13:S:781:GLY:O	13:S:782:LEU:HD22	1.99	0.62
1:H:418:LYS:HD2	9:T:277:GLN:HE22	1.64	0.62
8:R:180:ASN:ND2	8:R:216:PHE:O	2.31	0.62
13:V:267:ARG:HD2	13:V:269:TYR:HE1	1.64	0.62
3:C:522:SER:O	3:C:525:GLN:NE2	2.32	0.62
8:I:756:SER:O	8:I:763:ARG:NH1	2.32	0.62
11:W:114:VAL:O	11:W:118:GLN:NE2	2.31	0.62
1:H:312:MET:HB3	1:H:373:ILE:HD11	1.81	0.62
1:H:485:GLU:OE1	1:H:486:ARG:NH1	2.33	0.62
9:T:259:PHE:HA	9:T:262:LEU:HD12	1.82	0.62
1:A:447:PHE:HB2	1:A:478:ASN:HD21	1.63	0.62
2:B:419:ARG:HH11	4:D:344:LEU:HB3	1.65	0.62
13:S:133:LEU:HB2	13:S:139:ARG:HH12	1.64	0.62
8:R:276:TRP:HA	8:R:283:LEU:HA	1.81	0.62
7:G:199:LEU:HD12	7:G:203:GLY:HA3	1.82	0.62
13:S:375:ALA:HB3	13:S:382:LEU:HB2	1.81	0.62
8:R:266:ASN:HA	11:Y:75:ARG:HH21	1.64	0.62
11:Y:94:LEU:HD13	12:Z:471:LEU:HG	1.81	0.62
6:F:210:LEU:HD11	7:G:218:LEU:HD21	1.80	0.62
8:I:714:ARG:HE	8:I:727:ILE:HD11	1.65	0.62
2:J:268:ASP:OD1	9:T:272:TYR:OH	2.15	0.62
7:Q:199:LEU:HD12	7:Q:203:GLY:HA3	1.81	0.62
2:B:54:ARG:HE	2:B:79:PHE:HB2	1.64	0.62
2:J:189:ALA:HB1	2:J:209:VAL:O	2.00	0.62
4:N:321:GLU:O	4:N:325:ASP:N	2.30	0.62
8:R:379:LEU:HB2	8:R:386:LEU:HB3	1.79	0.62
13:V:896:ASP:OD1	13:V:921:ARG:NH1	2.32	0.62
5:E:151:ILE:HG12	5:E:177:LEU:HB3	1.80	0.62
6:F:196:LYS:NZ	7:G:203:GLY:O	2.33	0.62
10:M:411:ASN:HA	10:M:415:ALA:HB3	1.80	0.62
11:W:25:ASN:HA	11:W:28:LYS:HE2	1.81	0.62
13:S:503:HIS:HB3	13:S:515:LEU:HD11	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:26:LYS:HA	5:E:45:LEU:HB3	1.81	0.62
8:I:574:VAL:HG21	11:W:92:ARG:HD2	1.82	0.62
9:L:259:PHE:HA	9:L:262:LEU:HD12	1.82	0.62
11:W:56:ASP:OD1	11:W:57:GLN:N	2.33	0.62
3:K:247:ALA:HB2	3:K:263:LEU:HD21	1.82	0.62
3:K:502:THR:O	3:K:504:GLN:NE2	2.32	0.62
6:P:35:GLN:NE2	6:P:52:ASP:OD1	2.33	0.62
8:R:11:ASN:ND2	8:R:290:GLY:O	2.32	0.62
1:A:669:ILE:O	1:A:673:HIS:N	2.27	0.62
8:I:525:CYS:HA	8:I:546:THR:HA	1.81	0.62
10:M:462:ALA:O	10:M:467:GLU:N	2.33	0.62
13:S:443:LEU:HA	13:S:495:LEU:HD21	1.81	0.62
4:N:266:MET:HE1	4:N:273:LEU:HG	1.82	0.62
5:O:125:ARG:NE	5:O:152:GLU:OE1	2.31	0.62
3:C:134:GLN:HA	3:C:137:LYS:HE2	1.82	0.62
3:C:247:ALA:HB2	3:C:263:LEU:HD21	1.80	0.62
2:J:419:ARG:O	2:J:423:GLN:NE2	2.30	0.62
1:A:449:TYR:HD1	1:A:458:ALA:HB2	1.61	0.61
2:B:394:MET:HE1	2:B:405:GLN:HB2	1.82	0.61
6:F:315:THR:HA	6:F:318:HIS:CD2	2.35	0.61
13:S:309:GLY:HA2	13:S:315:VAL:HA	1.81	0.61
1:H:447:PHE:HB2	1:H:478:ASN:HD21	1.65	0.61
1:A:625:TYR:HA	1:A:628:ALA:HB3	1.81	0.61
2:B:189:ALA:HB1	2:B:209:VAL:O	2.00	0.61
8:I:138:ARG:NH1	8:I:138:ARG:O	2.33	0.61
8:I:379:LEU:HB2	8:I:386:LEU:HB3	1.80	0.61
13:S:896:ASP:OD1	13:S:921:ARG:NH1	2.33	0.61
2:J:189:ALA:HB1	2:J:210:TRP:HA	1.82	0.61
2:B:419:ARG:O	2:B:423:GLN:NE2	2.32	0.61
2:B:434:THR:HG21	4:D:344:LEU:HD23	1.81	0.61
9:L:204:ARG:HE	10:M:378:ASN:HB3	1.66	0.61
13:S:697:LYS:HG3	13:S:698:GLN:HG2	1.83	0.61
13:S:942:ALA:HB3	13:S:944:MET:HE2	1.82	0.61
3:K:134:GLN:HA	3:K:137:LYS:HE2	1.83	0.61
5:O:220:ALA:O	5:O:224:ASN:HB2	2.00	0.61
7:Q:183:LYS:O	7:Q:186:LYS:NZ	2.33	0.61
2:B:210:TRP:NE1	2:B:212:GLN:OE1	2.33	0.61
3:C:163:ARG:HH22	3:C:190:THR:HG1	1.45	0.61
1:H:567:LEU:O	1:H:571:VAL:N	2.31	0.61
3:C:542:GLY:O	3:C:546:CYS:N	2.32	0.61
6:F:210:LEU:HG	6:F:214:GLN:HE22	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:339:LYS:HE3	8:I:377:LEU:HA	1.82	0.61
8:I:535:VAL:HG12	8:I:539:LEU:HD23	1.81	0.61
8:I:647:VAL:HG11	8:I:656:ARG:HA	1.82	0.61
2:J:65:LYS:HA	2:J:98:ALA:HB1	1.82	0.61
6:P:196:LYS:NZ	7:Q:203:GLY:O	2.33	0.61
8:R:309:VAL:HG12	8:R:319:VAL:HG22	1.82	0.61
11:Y:55:ILE:HD12	12:Z:436:MET:HE1	1.83	0.61
3:K:195:PRO:O	3:K:199:HIS:ND1	2.24	0.61
13:V:1077:TRP:HA	13:V:1081:LEU:HD23	1.83	0.61
2:B:90:MET:HB2	2:B:222:GLY:HA2	1.81	0.61
2:B:189:ALA:HB1	2:B:210:TRP:HA	1.83	0.61
13:S:823:TYR:HB3	13:S:828:ARG:HB3	1.82	0.61
3:K:455:VAL:HA	3:K:458:THR:HG22	1.83	0.61
8:R:470:ALA:H	8:R:509:TRP:HE1	1.48	0.61
8:R:535:VAL:HG12	8:R:539:LEU:HD23	1.82	0.61
8:R:711:LEU:HD12	8:R:733:MET:HG3	1.80	0.61
6:F:35:GLN:NE2	6:F:52:ASP:OD1	2.33	0.61
2:J:192:VAL:HG13	2:J:193:LEU:HG	1.82	0.61
6:P:70:LYS:HD2	6:P:75:ARG:HE	1.65	0.61
8:R:373:ASP:HB3	8:R:389:ASP:HB2	1.82	0.61
2:B:270:LYS:NZ	9:L:268:GLU:OE1	2.25	0.61
4:D:252:GLU:HG2	4:D:254:PRO:HD3	1.82	0.61
5:E:261:ARG:HE	5:E:264:LEU:HD21	1.66	0.61
8:I:711:LEU:HD22	8:I:739:VAL:HB	1.82	0.61
13:S:507:ARG:NH1	13:S:531:GLN:O	2.34	0.61
1:H:304:TYR:C	1:H:306:LEU:H	2.09	0.61
1:H:522:GLU:HB3	1:H:526:ALA:H	1.66	0.61
8:I:141:LEU:O	8:I:171:LYS:NZ	2.32	0.60
13:V:375:ALA:HB3	13:V:382:LEU:HB2	1.83	0.60
13:V:758:GLU:HB2	13:V:780:GLY:HA3	1.83	0.60
1:A:522:GLU:HB3	1:A:526:ALA:H	1.66	0.60
2:B:11:ILE:HD12	2:B:34:LEU:HD21	1.82	0.60
3:C:455:VAL:HA	3:C:458:THR:HG22	1.82	0.60
6:F:6:TYR:HB2	7:G:334:THR:HG21	1.83	0.60
13:S:926:TYR:HA	13:S:929:THR:HG22	1.83	0.60
1:A:231:HIS:CD2	1:A:243:MET:SD	2.94	0.60
8:I:596:TRP:NE1	8:I:627:THR:OG1	2.31	0.60
11:Y:61:ARG:HB3	12:Z:440:TYR:HE2	1.66	0.60
13:V:668:VAL:O	13:V:672:GLN:CB	2.48	0.60
8:I:155:TYR:HB2	8:I:196:PRO:HB2	1.83	0.60
1:H:296:GLY:HA2	1:H:299:LEU:HD12	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:90:MET:HB2	2:J:222:GLY:HA2	1.82	0.60
13:V:737:HIS:NE2	13:V:747:TYR:OH	2.33	0.60
5:O:26:LYS:HA	5:O:45:LEU:HB3	1.81	0.60
8:R:386:LEU:HB2	8:R:424:LEU:HD22	1.82	0.60
12:X:433:ILE:HG22	12:X:437:ARG:HE	1.67	0.60
8:R:498:ALA:HB1	8:R:533:VAL:HG21	1.83	0.60
13:V:550:LEU:HB2	13:V:565:PHE:HB3	1.83	0.60
8:I:282:GLN:HB2	8:I:336:ARG:HH22	1.67	0.60
9:L:136:ILE:HD11	12:X:409:ARG:HH22	1.66	0.60
8:R:1:MET:O	8:R:261:SER:OG	2.15	0.60
8:R:756:SER:O	8:R:763:ARG:NH1	2.35	0.60
13:V:405:HIS:HB2	13:V:413:MET:HB2	1.83	0.60
1:A:181:LEU:HA	1:A:184:MET:HG3	1.83	0.60
3:C:220:THR:O	3:C:264:THR:OG1	2.19	0.60
2:J:426:MET:HB2	4:N:255:PRO:HA	1.83	0.60
3:C:60:THR:HG23	3:C:62:GLN:H	1.67	0.60
8:I:498:ALA:HB1	8:I:533:VAL:HG21	1.84	0.60
1:H:651:SER:O	1:H:654:ARG:NH1	2.35	0.60
1:H:663:LEU:HD23	1:H:667:LYS:HE2	1.83	0.60
5:O:37:ARG:HE	5:O:69:HIS:HB2	1.66	0.60
2:B:451:GLN:NE2	4:D:312:PRO:O	2.34	0.60
8:I:481:ILE:HG23	8:I:485:ARG:HA	1.84	0.60
13:S:613:GLU:OE1	13:S:650:ARG:NH1	2.34	0.60
13:S:788:GLN:O	13:S:792:SER:OG	2.15	0.60
2:J:354:GLU:OE2	3:K:89:GLN:NE2	2.35	0.60
3:K:310:GLU:O	3:K:314:ASN:ND2	2.35	0.60
3:K:522:SER:O	3:K:525:GLN:NE2	2.35	0.60
5:O:132:GLN:HB2	5:O:160:ILE:HD11	1.83	0.60
8:I:211:LYS:HG2	8:I:222:GLN:HA	1.83	0.59
13:S:408:ASN:HB2	13:S:411:VAL:HG22	1.83	0.59
5:O:25:PRO:O	5:O:49:ARG:NH1	2.34	0.59
9:T:104:LEU:HA	9:T:106:LYS:HG2	1.84	0.59
13:V:309:GLY:HA2	13:V:315:VAL:HA	1.83	0.59
13:V:668:VAL:HA	13:V:691:MET:HE2	1.83	0.59
13:V:776:LEU:HD23	13:V:779:LYS:HD3	1.84	0.59
13:V:912:PRO:HB3	13:V:919:PHE:HE2	1.67	0.59
1:A:283:PHE:HA	1:A:286:VAL:HG22	1.85	0.59
8:I:357:VAL:HB	8:I:367:HIS:HB2	1.84	0.59
9:L:53:ALA:HB3	9:L:62:ARG:HH12	1.68	0.59
12:X:491:GLN:HG2	12:X:494:ARG:HH21	1.67	0.59
13:S:889:LYS:HA	13:S:892:LYS:HE2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:O:202:TYR:HB2	5:O:233:MET:HE2	1.82	0.59
12:Z:409:ARG:NH1	12:Z:410:GLU:OE1	2.35	0.59
13:V:790:VAL:HG23	13:V:791:MET:HG3	1.84	0.59
1:A:230:ILE:O	1:A:234:GLN:NE2	2.35	0.59
2:B:422:ALA:HB1	2:B:425:LYS:HE2	1.84	0.59
10:M:312:GLU:O	10:M:316:HIS:ND1	2.29	0.59
10:M:384:VAL:O	10:M:388:ASN:ND2	2.35	0.59
13:S:720:GLN:O	13:S:725:TRP:NE1	2.35	0.59
3:K:249:ILE:O	3:K:252:THR:OG1	2.20	0.59
1:A:300:VAL:HA	1:A:303:ASN:HD22	1.68	0.59
1:A:418:LYS:HD2	9:L:277:GLN:HE22	1.67	0.59
11:W:34:THR:HA	11:W:37:PHE:CE2	2.37	0.59
13:S:445:SER:HB2	13:S:495:LEU:O	2.03	0.59
13:S:848:LEU:HD23	13:S:860:ILE:HD11	1.83	0.59
4:N:318:MET:SD	4:N:322:ASN:ND2	2.76	0.59
2:B:10:ARG:HG2	2:B:39:ARG:HD2	1.84	0.59
6:F:321:ILE:HD11	7:G:330:LYS:HB2	1.85	0.59
8:I:699:LEU:O	8:I:703:HIS:HB2	2.03	0.59
9:L:133:PRO:HA	9:L:136:ILE:HB	1.83	0.59
13:S:550:LEU:HB2	13:S:565:PHE:HB3	1.85	0.59
1:H:230:ILE:O	1:H:234:GLN:NE2	2.36	0.59
2:J:451:GLN:NE2	4:N:312:PRO:O	2.35	0.59
8:R:339:LYS:HE3	8:R:377:LEU:HA	1.83	0.59
8:R:485:ARG:O	8:R:504:CYS:N	2.33	0.59
10:U:312:GLU:O	10:U:316:HIS:ND1	2.29	0.59
1:A:485:GLU:OE1	1:A:486:ARG:NH1	2.36	0.59
3:C:557:ARG:HA	3:C:560:LYS:HG3	1.83	0.59
2:J:282:LEU:O	10:U:453:ASN:ND2	2.35	0.59
8:R:469:GLN:H	8:R:509:TRP:CD1	2.21	0.59
2:B:190:VAL:HG13	2:B:261:ALA:HB2	1.84	0.59
8:I:316:ARG:NH1	8:I:330:LEU:O	2.36	0.59
8:R:597:ASP:HB2	12:Z:503:LEU:HD12	1.83	0.59
13:V:106:ILE:HB	13:V:109:LYS:HZ1	1.67	0.59
13:V:371:ARG:NH1	13:V:385:ASP:OD2	2.36	0.59
13:V:861:GLU:OE1	13:V:880:HIS:ND1	2.36	0.59
2:B:354:GLU:OE2	3:C:89:GLN:NE2	2.35	0.59
8:I:729:ARG:NH1	8:I:733:MET:SD	2.76	0.59
13:S:371:ARG:NH1	13:S:385:ASP:OD2	2.36	0.59
2:J:10:ARG:HG2	2:J:39:ARG:HD2	1.84	0.59
2:J:276:ALA:O	2:J:281:LYS:NZ	2.36	0.59
3:K:476:VAL:HA	3:K:479:LYS:HG2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:ARG:HE	1:A:173:ASN:HB2	1.68	0.59
1:A:542:GLU:OE2	1:A:546:GLN:NE2	2.36	0.59
7:G:183:LYS:O	7:G:186:LYS:NZ	2.35	0.59
8:I:319:VAL:O	8:I:328:ASP:N	2.36	0.59
13:S:737:HIS:NE2	13:S:747:TYR:OH	2.34	0.59
3:K:195:PRO:HA	3:K:198:LYS:HG2	1.84	0.59
9:T:107:ALA:HB1	9:T:110:LYS:HB2	1.84	0.59
9:T:284:GLU:OE1	9:T:288:LYS:NZ	2.35	0.59
3:C:604:MET:HA	3:C:639:LYS:HZ1	1.68	0.59
8:I:629:GLU:OE2	13:V:724:ARG:NH2	2.35	0.59
8:I:668:GLU:O	8:I:672:SER:HB3	2.03	0.59
13:S:846:ILE:HA	13:S:849:ALA:HB2	1.84	0.59
5:O:81:LYS:NZ	5:O:113:GLN:OE1	2.27	0.59
8:R:525:CYS:HA	8:R:546:THR:HA	1.84	0.59
8:R:574:VAL:HG21	11:Y:92:ARG:HD2	1.84	0.58
2:B:121:THR:O	9:L:258:ARG:NH2	2.36	0.58
8:I:1:MET:HE1	8:I:252:LEU:HD23	1.84	0.58
13:S:137:LYS:O	13:S:139:ARG:NH1	2.37	0.58
1:H:355:MET:SD	1:H:356:ARG:NH1	2.76	0.58
8:R:35:GLN:OE1	8:R:57:PHE:N	2.30	0.58
13:V:995:GLU:HB2	13:V:1006:VAL:HG13	1.85	0.58
5:E:37:ARG:HE	5:E:69:HIS:HB2	1.68	0.58
8:I:63:TYR:HB3	8:I:75:THR:HA	1.84	0.58
8:I:243:ALA:HB2	8:I:276:TRP:HE1	1.68	0.58
13:S:639:ALA:HB1	13:S:648:ALA:HA	1.86	0.58
2:J:54:ARG:HE	2:J:79:PHE:HB2	1.68	0.58
2:J:90:MET:HE1	2:J:220:VAL:HB	1.86	0.58
2:J:182:THR:HG22	2:J:206:VAL:HG12	1.84	0.58
8:R:129:LYS:HB3	8:R:137:LEU:HD11	1.84	0.58
8:R:379:LEU:HD12	8:R:386:LEU:HD22	1.84	0.58
13:V:507:ARG:NH1	13:V:531:GLN:O	2.35	0.58
5:E:39:TYR:O	5:E:43:ILE:N	2.31	0.58
7:G:320:GLN:OE1	7:G:324:ARG:NH1	2.36	0.58
10:M:441:VAL:HA	10:M:444:HIS:CD2	2.38	0.58
13:S:690:ALA:O	13:S:722:ASN:ND2	2.33	0.58
8:R:323:LEU:HD22	12:Z:479:LYS:HZ1	1.67	0.58
8:R:643:PHE:HE2	8:R:663:TYR:HB3	1.68	0.58
10:U:379:ARG:NH1	10:U:382:GLU:OE1	2.37	0.58
1:A:663:LEU:HD23	1:A:667:LYS:HE2	1.85	0.58
1:A:678:GLU:HA	1:A:681:ARG:HE	1.68	0.58
8:I:270:SER:O	8:I:288:GLY:N	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:276:TRP:HA	8:I:283:LEU:HA	1.85	0.58
8:I:576:VAL:HG22	11:W:92:ARG:HH12	1.67	0.58
2:B:426:MET:HB2	4:D:255:PRO:HA	1.85	0.58
3:C:249:ILE:O	3:C:252:THR:OG1	2.21	0.58
8:R:688:ILE:HG21	8:R:706:HIS:CE1	2.38	0.58
9:T:228:SER:OG	10:U:404:MET:SD	2.55	0.58
3:C:607:LEU:HD22	3:C:639:LYS:HZ3	1.69	0.58
8:I:379:LEU:HD12	8:I:386:LEU:HD22	1.83	0.58
13:S:106:ILE:HB	13:S:109:LYS:HZ1	1.68	0.58
1:H:549:THR:HG22	1:H:553:MET:HE1	1.86	0.58
2:J:190:VAL:HG13	2:J:261:ALA:HB2	1.85	0.58
8:R:270:SER:O	8:R:288:GLY:N	2.36	0.58
13:V:688:VAL:HG23	13:V:691:MET:HE3	1.86	0.58
13:S:224:VAL:HB	13:S:237:PHE:HB2	1.85	0.58
13:V:821:GLU:O	13:V:825:HIS:ND1	2.28	0.58
13:V:926:TYR:HA	13:V:929:THR:HG22	1.85	0.58
1:A:257:GLU:HB3	3:C:646:ARG:HH22	1.67	0.58
8:I:597:ASP:HB2	12:X:503:LEU:HD12	1.86	0.58
1:H:483:LEU:HA	1:H:486:ARG:HB2	1.86	0.58
2:J:69:THR:HG23	2:J:71:PRO:HD2	1.86	0.58
8:R:138:ARG:NH1	8:R:138:ARG:O	2.37	0.58
8:R:316:ARG:NH1	8:R:330:LEU:O	2.37	0.58
1:A:659:LEU:HA	1:A:662:ALA:HB3	1.85	0.58
8:I:180:ASN:ND2	8:I:216:PHE:O	2.36	0.58
9:L:193:ARG:HH11	10:M:371:THR:HG23	1.69	0.58
1:H:268:LEU:HD22	2:J:304:LEU:HD21	1.86	0.58
9:T:59:GLU:OE1	9:T:87:TYR:OH	2.21	0.58
11:Y:118:GLN:O	11:Y:122:ILE:HG13	2.03	0.58
2:B:192:VAL:HG13	2:B:193:LEU:HG	1.84	0.57
6:F:13:LEU:O	6:F:17:SER:N	2.36	0.57
6:F:70:LYS:HD2	6:F:75:ARG:HE	1.68	0.57
13:S:266:ASN:HA	13:S:291:PHE:HB3	1.85	0.57
13:S:916:MET:HB3	13:S:920:ARG:HH12	1.69	0.57
1:H:625:TYR:HA	1:H:628:ALA:HB3	1.86	0.57
3:C:468:GLU:OE1	3:C:471:ARG:NH1	2.37	0.57
6:F:117:GLY:HA2	6:F:120:LEU:HB2	1.86	0.57
2:J:424:TYR:HA	4:N:255:PRO:HD3	1.86	0.57
6:P:117:GLY:HA2	6:P:120:LEU:HB2	1.86	0.57
8:R:533:VAL:HG23	8:R:537:LYS:HD3	1.86	0.57
2:B:11:ILE:HG12	2:B:58:ILE:HD12	1.87	0.57
2:B:141:ARG:HH22	2:B:151:LEU:HD21	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:846:ILE:HB	13:S:863:GLU:HG3	1.85	0.57
1:H:669:ILE:O	1:H:673:HIS:N	2.24	0.57
3:K:23:LEU:O	3:K:27:GLN:N	2.35	0.57
13:V:550:LEU:HD21	13:V:571:VAL:HG21	1.86	0.57
11:W:103:ARG:NH1	11:W:107:GLU:OE1	2.37	0.57
13:S:618:THR:HG23	13:S:619:LEU:HD12	1.86	0.57
1:H:277:PRO:HG3	1:H:303:ASN:HD22	1.69	0.57
1:H:592:ALA:O	1:H:596:HIS:HB2	2.04	0.57
2:J:210:TRP:NE1	2:J:212:GLN:OE1	2.37	0.57
5:O:1:MET:HE2	5:O:191:TYR:HB3	1.86	0.57
9:T:53:ALA:HB3	9:T:62:ARG:HH12	1.70	0.57
2:B:273:PRO:HA	9:L:269:LEU:HD22	1.86	0.57
7:G:168:GLN:O	7:G:172:ASN:ND2	2.38	0.57
13:S:454:ILE:HD13	13:S:610:GLN:HB3	1.85	0.57
13:S:933:GLU:OE1	13:S:937:ARG:NH1	2.38	0.57
3:K:510:GLU:HA	3:K:513:ARG:HB2	1.86	0.57
10:U:357:GLU:OE2	10:U:361:GLN:NE2	2.37	0.57
10:U:441:VAL:HA	10:U:444:HIS:CD2	2.39	0.57
13:V:683:THR:O	13:V:689:ARG:NH2	2.38	0.57
6:F:249:GLN:O	6:F:253:GLN:HB2	2.04	0.57
10:M:346:GLN:HB2	10:M:350:LYS:HB2	1.87	0.57
13:S:141:GLY:HA2	13:S:148:SER:HA	1.85	0.57
13:S:719:TYR:HB2	13:S:728:ALA:HB2	1.87	0.57
1:H:239:SER:O	1:H:243:MET:HG3	2.04	0.57
3:K:320:CYS:HA	3:K:327:TYR:HE1	1.69	0.57
8:R:428:THR:HG23	8:R:467:LEU:HD13	1.86	0.57
9:T:193:ARG:HH11	10:U:371:THR:HG23	1.69	0.57
6:F:305:MET:O	6:F:309:ARG:NH1	2.37	0.57
13:S:861:GLU:OE1	13:S:880:HIS:ND1	2.37	0.57
3:K:463:ASP:HA	3:K:466:TYR:HE1	1.70	0.57
11:Y:108:GLU:HG3	12:Z:488:MET:HG3	1.86	0.57
13:V:180:ALA:HA	13:V:198:GLN:HE22	1.69	0.57
13:V:945:ALA:HB1	13:V:964:VAL:HB	1.86	0.57
3:C:502:THR:O	3:C:504:GLN:NE2	2.38	0.57
4:D:221:TRP:O	4:D:225:ILE:HB	2.04	0.57
7:G:167:LYS:O	7:G:171:TYR:CB	2.52	0.57
9:L:114:MET:HE3	12:X:432:ASP:HB2	1.85	0.57
1:H:166:LEU:HD22	1:H:183:LEU:HD12	1.86	0.57
8:R:647:VAL:HG11	8:R:656:ARG:HA	1.87	0.57
9:T:290:MET:HG2	9:T:293:ARG:HH21	1.70	0.57
13:V:933:GLU:OE1	13:V:937:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:MET:SD	1:A:356:ARG:NH1	2.78	0.57
5:E:36:LYS:NZ	5:E:38:ASP:O	2.29	0.57
8:I:323:LEU:HD22	12:X:479:LYS:HZ1	1.70	0.57
3:K:493:ALA:HB2	3:K:537:ILE:HA	1.87	0.57
11:Y:121:MET:SD	12:Z:499:LEU:HD13	2.44	0.57
3:C:38:TYR:O	3:C:42:ASN:ND2	2.38	0.57
8:I:35:GLN:OE1	8:I:57:PHE:N	2.32	0.57
8:I:129:LYS:HB3	8:I:137:LEU:HD11	1.86	0.57
8:I:536:ASP:HB2	8:I:664:ARG:HG2	1.86	0.57
8:I:537:LYS:HD2	8:I:540:LEU:HD13	1.86	0.57
1:H:243:MET:HE3	1:H:244:TYR:CE1	2.40	0.57
1:H:530:PHE:HA	1:H:533:LEU:HB2	1.87	0.57
6:P:13:LEU:O	6:P:17:SER:N	2.36	0.57
9:T:293:ARG:NH1	9:T:297:GLU:OE1	2.37	0.57
13:V:612:TYR:HE2	13:V:638:GLN:HB3	1.70	0.57
1:A:166:LEU:HD21	1:A:179:ILE:HB	1.87	0.56
2:B:69:THR:HG23	2:B:71:PRO:HD2	1.87	0.56
3:C:320:CYS:HA	3:C:327:TYR:HE1	1.70	0.56
5:E:152:GLU:HA	5:E:155:LEU:HB2	1.86	0.56
1:H:148:ASP:H	1:H:197:MET:HG3	1.69	0.56
2:J:121:THR:O	9:T:258:ARG:NH2	2.38	0.56
2:J:324:VAL:HG11	3:K:582:LEU:HD12	1.86	0.56
9:T:56:ILE:HG13	9:T:62:ARG:HH21	1.70	0.56
11:Y:121:MET:HA	11:Y:124:LYS:HG2	1.87	0.56
1:A:210:ALA:HA	1:A:213:ARG:HG2	1.85	0.56
1:A:449:TYR:CD2	1:A:454:GLU:HG3	2.40	0.56
3:C:23:LEU:O	3:C:27:GLN:N	2.36	0.56
8:I:381:ALA:O	8:I:399:TYR:OH	2.22	0.56
8:I:543:THR:HA	8:I:610:THR:HG23	1.87	0.56
13:S:549:ASN:ND2	13:S:564:MET:SD	2.78	0.56
2:J:11:ILE:HG12	2:J:58:ILE:HD12	1.87	0.56
2:J:412:HIS:O	2:J:416:GLU:N	2.38	0.56
6:P:325:GLN:HA	6:P:328:LYS:HG2	1.86	0.56
11:Y:79:LEU:O	12:Z:461:GLN:NE2	2.37	0.56
1:A:531:LYS:HD3	1:A:547:ILE:HD12	1.87	0.56
2:B:276:ALA:O	2:B:281:LYS:NZ	2.37	0.56
13:S:142:MET:SD	13:S:144:LYS:NZ	2.78	0.56
13:S:380:THR:HA	13:S:395:PRO:HA	1.87	0.56
13:S:912:PRO:HB3	13:S:919:PHE:HE2	1.70	0.56
2:J:204:ARG:HD2	2:J:205:PRO:HD2	1.86	0.56
2:J:434:THR:HG21	4:N:344:LEU:HD23	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:607:LEU:HD21	3:K:638:LEU:HB3	1.88	0.56
5:O:77:LEU:HG	5:O:104:MET:HE1	1.86	0.56
5:O:132:GLN:HA	5:O:140:LEU:HD11	1.87	0.56
6:P:6:TYR:HB2	7:Q:334:THR:HG21	1.87	0.56
8:R:33:ASP:OD1	9:T:7:ARG:NH2	2.27	0.56
13:V:445:SER:HB2	13:V:495:LEU:O	2.05	0.56
13:V:663:PHE:HE2	13:V:696:ASN:HD21	1.52	0.56
1:A:474:ARG:HA	2:B:285:CYS:HB2	1.86	0.56
2:B:189:ALA:CB	2:B:210:TRP:HA	2.34	0.56
3:C:64:ASP:OD1	3:C:65:MET:N	2.38	0.56
3:C:169:ALA:O	3:C:173:LEU:CB	2.54	0.56
8:I:469:GLN:H	8:I:509:TRP:CD1	2.23	0.56
8:I:493:MET:N	8:I:493:MET:SD	2.79	0.56
10:M:458:GLN:NE2	10:M:468:GLU:OE2	2.38	0.56
8:R:468:SER:HB2	8:R:476:ARG:HA	1.86	0.56
13:V:408:ASN:HB2	13:V:411:VAL:HG22	1.87	0.56
3:C:36:LEU:HB3	3:C:53:LEU:HD11	1.87	0.56
3:C:269:ARG:NH2	3:C:273:GLU:O	2.38	0.56
3:C:637:MET:HE2	3:C:640:LYS:HZ1	1.71	0.56
8:I:219:LEU:HD21	8:I:222:GLN:HB2	1.87	0.56
10:M:379:ARG:NH1	10:M:382:GLU:OE1	2.39	0.56
13:S:306:MET:HE1	13:S:308:VAL:HB	1.87	0.56
13:S:901:ALA:HA	13:S:904:ALA:HB3	1.86	0.56
4:N:212:GLU:OE1	4:N:214:LYS:NZ	2.38	0.56
8:R:89:ILE:HD13	8:R:98:LYS:HB2	1.88	0.56
3:C:618:ARG:NH1	3:C:619:VAL:O	2.38	0.56
3:C:628:SER:OG	3:C:629:ARG:N	2.39	0.56
8:I:533:VAL:HG23	8:I:537:LYS:HD3	1.87	0.56
5:O:198:LYS:HG3	5:O:232:ARG:HH12	1.70	0.56
8:R:32:SER:OG	8:R:33:ASP:N	2.39	0.56
8:R:441:VAL:N	8:R:456:TRP:O	2.37	0.56
11:Y:59:VAL:HA	11:Y:62:LEU:HD12	1.87	0.56
4:D:304:LEU:O	4:D:308:PHE:HB2	2.05	0.56
4:D:321:GLU:O	4:D:325:ASP:N	2.33	0.56
10:M:357:GLU:OE2	10:M:361:GLN:NE2	2.39	0.56
8:R:699:LEU:O	8:R:703:HIS:HB2	2.05	0.56
11:Y:34:THR:HA	11:Y:37:PHE:CE2	2.40	0.56
13:V:139:ARG:HA	13:V:150:THR:HA	1.87	0.56
13:V:187:PRO:HD3	13:V:194:PRO:HB3	1.87	0.56
2:B:204:ARG:HD2	2:B:205:PRO:HD2	1.87	0.56
3:C:240:ILE:HG23	3:C:266:MET:HE1	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:651:PRO:O	8:I:763:ARG:NH2	2.39	0.56
9:L:293:ARG:NH1	9:L:297:GLU:OE1	2.38	0.56
2:J:135:SER:HA	2:J:174:GLU:HA	1.88	0.56
2:J:318:LEU:HA	2:J:321:LYS:HG2	1.87	0.56
5:O:151:ILE:HG12	5:O:177:LEU:HB3	1.87	0.56
8:I:11:ASN:ND2	8:I:290:GLY:O	2.39	0.56
8:I:525:CYS:SG	8:I:544:ARG:NH2	2.79	0.56
2:J:106:LEU:O	2:J:110:GLY:N	2.38	0.56
7:Q:137:ASN:HA	7:Q:140:MET:HE2	1.87	0.56
8:R:7:GLN:HE22	8:R:9:SER:HB2	1.71	0.56
8:R:23:ASN:ND2	8:R:75:THR:O	2.39	0.56
8:R:668:GLU:O	8:R:672:SER:HB3	2.06	0.56
1:A:268:LEU:HD22	2:B:304:LEU:HD21	1.87	0.56
3:C:385:THR:HA	3:C:388:ILE:HD12	1.88	0.56
5:E:198:LYS:HG3	5:E:232:ARG:HH12	1.69	0.56
8:I:265:LEU:O	11:W:75:ARG:NH2	2.38	0.56
8:I:266:ASN:HA	11:W:75:ARG:HH21	1.70	0.56
9:L:71:GLN:OE1	9:L:80:LYS:NZ	2.40	0.56
13:S:904:ALA:HB1	13:S:922:ILE:HG21	1.88	0.56
8:R:69:LYS:NZ	8:R:155:TYR:OH	2.39	0.56
8:R:138:ARG:HH22	13:V:435:ARG:HD2	1.71	0.56
8:R:587:LEU:HD23	8:R:614:THR:HG23	1.87	0.56
10:U:452:ARG:HH12	10:U:455:ARG:HH21	1.53	0.56
8:I:149:TYR:H	8:I:163:CYS:HB2	1.71	0.55
9:L:56:ILE:HG13	9:L:62:ARG:HH21	1.71	0.55
11:W:122:ILE:HD11	12:X:495:ASN:HA	1.88	0.55
8:R:487:LEU:N	8:R:501:ALA:O	2.38	0.55
3:C:401:LYS:O	3:C:405:ASN:ND2	2.39	0.55
3:C:425:TYR:O	3:C:430:LEU:N	2.35	0.55
13:S:139:ARG:HA	13:S:150:THR:HA	1.88	0.55
13:S:180:ALA:HA	13:S:198:GLN:HE22	1.71	0.55
2:J:370:ALA:O	2:J:375:ARG:NH2	2.39	0.55
3:K:63:TYR:HA	3:K:66:ALA:HB3	1.87	0.55
8:R:429:ILE:HB	8:R:444:PHE:HB2	1.87	0.55
8:R:481:ILE:HG23	8:R:485:ARG:HA	1.87	0.55
10:U:389:GLN:HA	10:U:392:HIS:CE1	2.40	0.55
13:V:697:LYS:HG3	13:V:698:GLN:HG2	1.88	0.55
1:A:565:GLU:O	9:T:231:GLN:NE2	2.39	0.55
2:B:103:ASN:HA	2:B:106:LEU:HB2	1.89	0.55
2:B:135:SER:HA	2:B:174:GLU:HA	1.88	0.55
5:E:60:LEU:HD11	5:E:83:LEU:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:23:ASN:ND2	8:I:75:THR:O	2.39	0.55
8:I:379:LEU:HD11	8:I:422:ILE:HG23	1.88	0.55
11:W:49:ASP:HA	11:W:52:VAL:HG22	1.89	0.55
13:S:945:ALA:HB1	13:S:964:VAL:HB	1.88	0.55
3:K:220:THR:O	3:K:264:THR:OG1	2.24	0.55
7:Q:168:GLN:O	7:Q:172:ASN:ND2	2.39	0.55
9:T:104:LEU:C	9:T:106:LYS:H	2.13	0.55
10:U:384:VAL:O	10:U:388:ASN:ND2	2.40	0.55
11:Y:49:ASP:HA	11:Y:52:VAL:HG22	1.88	0.55
1:A:530:PHE:HA	1:A:533:LEU:HB2	1.89	0.55
2:B:60:VAL:HG12	2:B:87:LEU:HB3	1.87	0.55
3:C:364:GLU:OE2	3:C:368:ARG:NH2	2.39	0.55
4:D:282:VAL:HG23	4:D:286:LEU:HD12	1.87	0.55
8:I:32:SER:OG	8:I:33:ASP:N	2.40	0.55
13:S:347:LYS:HG3	13:S:348:THR:HG23	1.87	0.55
8:R:700:ALA:HA	8:R:703:HIS:HB3	1.89	0.55
2:B:324:VAL:HG11	3:C:582:LEU:HD12	1.89	0.55
3:C:480:ASN:HD21	3:C:483:ASN:HB3	1.72	0.55
8:I:468:SER:HB2	8:I:476:ARG:HA	1.88	0.55
8:I:525:CYS:HB2	8:I:544:ARG:HE	1.70	0.55
13:S:554:TYR:HE1	13:S:596:LEU:HD21	1.71	0.55
13:S:874:MET:HB3	13:S:898:ARG:HD2	1.88	0.55
2:B:30:LEU:HA	2:B:33:ARG:HG2	1.87	0.55
3:K:628:SER:OG	3:K:629:ARG:N	2.39	0.55
10:U:346:GLN:HB2	10:U:350:LYS:HB2	1.89	0.55
1:A:584:ILE:HG23	1:A:587:ARG:HH21	1.72	0.55
1:A:632:PHE:O	1:A:645:TRP:NE1	2.37	0.55
3:C:219:ASN:HA	3:C:265:ASP:HA	1.88	0.55
3:C:419:MET:HE1	3:C:438:PHE:HE1	1.72	0.55
9:L:5:GLU:HG2	9:L:94:VAL:HG21	1.87	0.55
13:S:1:MET:HE1	13:S:320:ALA:HB1	1.87	0.55
1:H:641:GLN:NE2	1:H:642:GLU:OE2	2.40	0.55
2:J:30:LEU:HA	2:J:33:ARG:HG2	1.88	0.55
2:J:110:GLY:CA	2:J:188:PRO:HG3	2.25	0.55
3:K:445:CYS:SG	3:K:446:SER:N	2.73	0.55
13:V:618:THR:HG23	13:V:619:LEU:HD12	1.88	0.55
3:C:604:MET:HG3	3:C:639:LYS:HZ2	1.70	0.55
13:S:652:TYR:HB3	13:S:663:PHE:HB3	1.87	0.55
2:J:186:GLN:O	2:J:188:PRO:HD2	2.07	0.55
3:K:38:TYR:O	3:K:42:ASN:ND2	2.40	0.55
7:Q:192:LEU:O	7:Q:196:ASN:HB2	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:298:LYS:HA	7:Q:301:GLN:HG3	1.89	0.55
8:R:2:ARG:NE	8:R:261:SER:OG	2.36	0.55
13:V:549:ASN:ND2	13:V:564:MET:SD	2.80	0.55
13:V:716:ILE:HA	13:V:728:ALA:HB1	1.89	0.55
1:A:447:PHE:CE2	2:B:286:LEU:HB2	2.42	0.55
2:B:106:LEU:O	2:B:110:GLY:N	2.40	0.55
8:I:421:MET:HE2	8:I:432:LEU:HD22	1.87	0.55
8:I:664:ARG:HH21	8:I:667:PRO:HA	1.72	0.55
9:T:253:GLN:HA	9:T:256:LEU:HG	1.89	0.55
13:V:323:LYS:HG3	13:V:335:TYR:HB2	1.89	0.55
13:V:811:ALA:O	13:V:838:ARG:NH1	2.40	0.55
2:B:133:LEU:HD22	2:B:176:VAL:HA	1.89	0.55
2:B:370:ALA:O	2:B:375:ARG:NH2	2.40	0.55
6:F:180:LYS:HA	6:F:183:LEU:HD12	1.89	0.55
8:I:28:LEU:HD22	8:I:40:TRP:HB2	1.89	0.55
13:S:422:ILE:HD11	13:S:475:LEU:HG	1.89	0.55
2:B:380:THR:OG1	4:D:234:ALA:O	2.22	0.54
3:C:467:LYS:HD3	3:C:502:THR:HG22	1.89	0.54
6:F:210:LEU:HD12	6:F:213:GLN:HE21	1.72	0.54
1:H:449:TYR:CD2	1:H:454:GLU:HG3	2.42	0.54
2:J:189:ALA:CB	2:J:210:TRP:HA	2.37	0.54
8:R:89:ILE:HG22	8:R:97:GLU:HB2	1.89	0.54
2:B:176:VAL:HG11	2:B:231:TRP:HB3	1.87	0.54
2:B:318:LEU:HA	2:B:321:LYS:HG2	1.89	0.54
2:B:434:THR:HA	4:D:262:LYS:HE2	1.89	0.54
3:C:63:TYR:HA	3:C:66:ALA:HB3	1.89	0.54
5:E:25:PRO:O	5:E:49:ARG:NH1	2.38	0.54
10:M:389:GLN:HA	10:M:392:HIS:CE1	2.41	0.54
1:H:358:ARG:HA	1:H:361:ILE:HD12	1.90	0.54
1:H:515:LEU:HD22	1:H:519:ARG:HH22	1.72	0.54
3:K:243:PHE:HD1	3:K:246:LYS:HZ3	1.55	0.54
8:R:265:LEU:O	11:Y:75:ARG:NH2	2.39	0.54
10:U:310:LEU:O	10:U:314:HIS:ND1	2.39	0.54
11:Y:52:VAL:HA	11:Y:55:ILE:HG12	1.89	0.54
1:A:143:ASP:HA	1:A:149:ILE:HD11	1.89	0.54
1:A:264:ARG:HD2	2:B:304:LEU:HA	1.89	0.54
1:A:352:LYS:N	1:A:354:GLU:OE1	2.40	0.54
2:B:268:ASP:OD1	9:L:272:TYR:OH	2.19	0.54
2:B:433:GLN:NE2	4:D:258:GLU:OE2	2.39	0.54
5:E:152:GLU:HG3	5:E:155:LEU:HD22	1.88	0.54
5:E:294:HIS:O	5:E:297:ARG:NH1	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:3:LEU:HD11	8:I:252:LEU:HD22	1.89	0.54
8:I:690:LEU:HD21	13:V:695:LEU:HD11	1.89	0.54
13:S:498:ASN:HD21	13:S:502:THR:H	1.54	0.54
3:K:467:LYS:HD3	3:K:502:THR:HG22	1.89	0.54
8:R:247:PHE:HA	8:R:270:SER:HA	1.89	0.54
11:Y:123:GLN:NE2	11:Y:127:ASP:OD2	2.40	0.54
9:L:33:GLU:HB3	9:L:56:ILE:HG21	1.89	0.54
1:H:482:VAL:O	1:H:486:ARG:N	2.36	0.54
2:J:376:LEU:HD22	2:J:400:LEU:HD21	1.89	0.54
13:V:376:ARG:NH2	13:V:397:ASP:OD1	2.41	0.54
8:I:89:ILE:HD13	8:I:98:LYS:HB2	1.90	0.54
13:S:228:ASP:OD1	13:S:232:ARG:N	2.35	0.54
2:J:405:GLN:HG2	2:J:413:VAL:HB	1.89	0.54
5:O:125:ARG:HG3	5:O:152:GLU:HB3	1.89	0.54
7:Q:167:LYS:O	7:Q:171:TYR:CB	2.56	0.54
1:A:371:GLN:O	1:A:374:SER:N	2.40	0.54
2:B:343:LEU:HD21	3:C:317:LEU:HD21	1.88	0.54
2:B:412:HIS:O	2:B:416:GLU:N	2.40	0.54
5:E:77:LEU:HD21	5:E:101:LEU:HG	1.89	0.54
8:I:529:TYR:HE2	8:I:618:MET:HB3	1.70	0.54
9:L:253:GLN:HA	9:L:256:LEU:HG	1.90	0.54
9:L:284:GLU:OE1	9:L:288:LYS:NZ	2.37	0.54
13:S:376:ARG:NH2	13:S:397:ASP:OD1	2.41	0.54
1:H:264:ARG:HD2	2:J:304:LEU:HA	1.90	0.54
1:H:305:ALA:HB3	9:T:299:LEU:HD22	1.90	0.54
1:H:474:ARG:HA	2:J:285:CYS:HB2	1.89	0.54
6:F:11:LEU:HG	6:F:18:TYR:HB2	1.90	0.54
8:I:434:GLN:HA	8:I:438:GLY:HA2	1.90	0.54
1:H:479:LYS:HB3	1:H:495:LEU:HD13	1.90	0.54
2:J:422:ALA:HB1	2:J:425:LYS:HE2	1.90	0.54
2:J:451:GLN:HG2	4:N:316:GLN:HB3	1.88	0.54
11:Y:103:ARG:NH1	11:Y:107:GLU:OE1	2.40	0.54
1:A:236:LYS:O	1:A:239:SER:OG	2.21	0.54
1:A:531:LYS:HZ2	1:A:547:ILE:HG23	1.73	0.54
5:E:37:ARG:NH2	5:E:39:TYR:OH	2.40	0.54
5:E:56:ASP:HB3	5:E:59:ASN:HB2	1.90	0.54
9:L:110:LYS:HE3	12:X:436:MET:SD	2.47	0.54
13:S:1025:LEU:O	13:S:1028:GLN:NE2	2.40	0.54
2:J:419:ARG:HD3	4:N:344:LEU:HD13	1.88	0.54
3:K:480:ASN:HD21	3:K:483:ASN:HB3	1.73	0.54
3:K:518:GLU:HA	3:K:521:ARG:HE	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:R:87:VAL:HB	8:R:100:ILE:HG13	1.89	0.54
8:R:185:HIS:ND1	8:R:207:ASP:OD2	2.41	0.54
8:R:434:GLN:HA	8:R:438:GLY:HA2	1.90	0.54
9:T:240:GLU:HA	9:T:243:ARG:HD3	1.89	0.54
9:T:293:ARG:HH22	9:T:294:LEU:HG	1.72	0.54
1:A:305:ALA:HB3	9:L:299:LEU:HD22	1.90	0.54
2:B:57:HIS:HA	2:B:79:PHE:HZ	1.73	0.54
6:F:125:MET:O	6:F:130:ASN:ND2	2.41	0.54
9:L:243:ARG:NH2	10:M:414:ASP:O	2.40	0.54
11:W:66:LYS:HE3	11:W:70:ILE:HD11	1.90	0.54
1:H:471:TYR:HB3	6:P:182:ARG:HH22	1.72	0.54
5:O:7:ARG:HH12	5:O:256:ASP:HB3	1.72	0.54
8:R:537:LYS:HD2	8:R:540:LEU:HD13	1.89	0.54
8:R:591:ILE:HG21	8:R:618:MET:HG3	1.89	0.54
11:Y:94:LEU:HG	11:Y:98:GLN:HE22	1.73	0.54
13:V:373:LEU:HD23	13:V:386:LEU:HG	1.90	0.54
13:V:513:LEU:HB2	13:V:527:LEU:HB2	1.90	0.54
4:D:212:GLU:OE1	4:D:214:LYS:NZ	2.40	0.54
11:W:83:ARG:NH2	11:W:87:GLN:OE1	2.38	0.54
13:S:325:HIS:HB3	13:S:333:PHE:HB2	1.89	0.54
3:K:57:TYR:HA	3:K:60:THR:HG22	1.90	0.54
3:K:637:MET:O	3:K:640:LYS:NZ	2.38	0.54
6:P:144:ALA:O	6:P:147:GLN:NE2	2.41	0.54
8:R:729:ARG:HG2	8:R:732:GLN:HE21	1.73	0.54
9:T:214:GLU:HG3	9:T:217:LYS:HE3	1.89	0.54
1:A:549:THR:HG22	1:A:553:MET:HE1	1.90	0.53
4:D:246:ILE:HG13	4:D:304:LEU:HD22	1.89	0.53
5:E:13:ARG:HB3	5:E:250:SER:HA	1.89	0.53
5:E:176:ARG:HG3	5:E:177:LEU:HG	1.89	0.53
13:S:82:ILE:HB	13:S:90:PHE:HB2	1.89	0.53
13:S:267:ARG:NH1	13:S:269:TYR:OH	2.42	0.53
1:H:678:GLU:HA	1:H:681:ARG:HE	1.72	0.53
2:J:141:ARG:HH22	2:J:151:LEU:HD21	1.72	0.53
13:V:554:TYR:HE1	13:V:596:LEU:HD21	1.73	0.53
13:V:846:ILE:HB	13:V:863:GLU:HG3	1.90	0.53
1:A:178:GLN:HE21	1:A:181:LEU:HB3	1.73	0.53
1:A:304:TYR:CG	1:A:376:LYS:HE3	2.43	0.53
1:A:527:LEU:O	1:A:531:LYS:HG2	2.09	0.53
2:B:379:LEU:HD23	2:B:399:ILE:HD11	1.90	0.53
8:I:470:ALA:H	8:I:509:TRP:HE1	1.57	0.53
1:H:527:LEU:O	1:H:531:LYS:HG2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:364:GLU:OE2	3:K:368:ARG:NH2	2.39	0.53
13:V:546:SER:OG	13:V:547:ARG:N	2.41	0.53
6:F:144:ALA:O	6:F:147:GLN:NE2	2.40	0.53
8:I:730:PHE:O	8:I:734:ASN:ND2	2.32	0.53
6:P:13:LEU:HB3	6:P:15:PRO:HD2	1.90	0.53
7:Q:250:MET:O	7:Q:254:GLN:HB2	2.08	0.53
8:R:536:ASP:HB2	8:R:664:ARG:HG2	1.88	0.53
9:T:175:ASP:HB3	9:T:177:VAL:HG22	1.91	0.53
10:U:453:ASN:HA	10:U:456:LEU:HD12	1.90	0.53
13:V:960:ALA:HA	13:V:963:ARG:HE	1.74	0.53
1:A:293:HIS:HA	1:A:319:LEU:HD21	1.89	0.53
2:B:33:ARG:NH2	2:B:233:ASP:OD1	2.41	0.53
3:C:190:THR:HG1	3:C:192:GLN:CD	2.16	0.53
9:L:214:GLU:HG3	9:L:217:LYS:HE3	1.89	0.53
1:H:670:HIS:HE1	1:H:676:ASN:HB3	1.73	0.53
5:O:43:ILE:HA	5:O:46:LEU:HB2	1.91	0.53
6:P:151:GLU:HA	6:P:154:LYS:HG2	1.89	0.53
8:R:87:VAL:N	8:R:100:ILE:O	2.40	0.53
13:V:442:TYR:O	13:V:495:LEU:HG	2.09	0.53
13:V:901:ALA:HA	13:V:904:ALA:HB3	1.90	0.53
5:E:220:ALA:HA	5:E:246:LEU:HD11	1.90	0.53
8:I:87:VAL:HB	8:I:100:ILE:HG13	1.89	0.53
12:X:488:MET:O	12:X:492:ILE:HG13	2.09	0.53
13:S:310:SER:HB2	13:S:314:ALA:H	1.73	0.53
1:H:483:LEU:HB3	1:H:488:ASP:HB2	1.90	0.53
1:H:632:PHE:O	1:H:645:TRP:NE1	2.39	0.53
2:J:51:ASP:OD1	2:J:52:THR:N	2.42	0.53
3:K:169:ALA:O	3:K:173:LEU:CB	2.57	0.53
8:R:107:CYS:HA	8:R:123:GLY:HA2	1.91	0.53
8:R:350:ALA:HB2	8:R:378:LEU:HD22	1.91	0.53
11:Y:47:LEU:HA	11:Y:50:LYS:HE3	1.91	0.53
13:V:729:ILE:HG12	13:V:743:LEU:HD11	1.91	0.53
2:B:182:THR:HG22	2:B:206:VAL:HG12	1.90	0.53
2:B:186:GLN:O	2:B:188:PRO:HD2	2.09	0.53
8:I:39:LYS:HG3	8:I:47:GLU:HB2	1.90	0.53
9:L:128:LEU:HD22	12:X:417:HIS:CG	2.43	0.53
1:H:189:PHE:HE2	2:J:309:THR:HG23	1.74	0.53
2:J:114:ASN:OD1	2:J:204:ARG:NH2	2.41	0.53
5:O:63:LEU:O	5:O:67:TYR:N	2.41	0.53
5:O:152:GLU:HG3	5:O:155:LEU:HD22	1.90	0.53
6:P:125:MET:O	6:P:130:ASN:ND2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:V:310:SER:HB2	13:V:314:ALA:H	1.73	0.53
1:A:358:ARG:HA	1:A:361:ILE:HD12	1.91	0.53
1:A:567:LEU:O	1:A:571:VAL:N	2.28	0.53
8:I:485:ARG:O	8:I:504:CYS:N	2.39	0.53
9:L:265:LEU:O	9:L:269:LEU:HD12	2.08	0.53
13:S:89:VAL:HB	13:S:110:PHE:HB2	1.90	0.53
13:S:184:PHE:HD1	13:S:196:SER:HB2	1.73	0.53
13:S:187:PRO:HD3	13:S:194:PRO:HB3	1.90	0.53
13:S:636:ALA:HB2	13:S:655:LEU:HD11	1.89	0.53
1:H:371:GLN:O	1:H:374:SER:N	2.41	0.53
3:K:36:LEU:HB3	3:K:53:LEU:HD11	1.89	0.53
6:P:220:LEU:O	6:P:224:ILE:HG23	2.09	0.53
8:R:130:ILE:HD11	8:R:141:LEU:HB2	1.91	0.53
13:V:325:HIS:HB3	13:V:333:PHE:HB2	1.91	0.53
1:A:193:HIS:HA	1:A:196:HIS:HD1	1.74	0.53
7:G:166:ARG:HH21	7:G:170:GLN:HE22	1.55	0.53
8:I:87:VAL:N	8:I:100:ILE:O	2.41	0.53
9:L:243:ARG:O	9:L:246:GLY:N	2.42	0.53
10:M:451:LEU:HA	10:M:454:LYS:HG2	1.90	0.53
13:S:223:ARG:NE	13:S:236:SER:OG	2.39	0.53
13:S:546:SER:OG	13:S:547:ARG:N	2.42	0.53
3:K:468:GLU:HA	3:K:471:ARG:HG2	1.91	0.53
4:N:282:VAL:HG23	4:N:286:LEU:HD12	1.91	0.53
8:R:111:ARG:HG3	8:R:153:TRP:HD1	1.73	0.53
8:R:604:ARG:HH22	8:R:635:ILE:HG22	1.74	0.53
2:B:419:ARG:HD3	4:D:344:LEU:HD13	1.89	0.53
8:I:432:LEU:HD23	8:I:434:GLN:HG3	1.90	0.53
1:H:283:PHE:O	1:H:287:MET:HG2	2.08	0.53
3:K:58:TYR:O	3:K:63:TYR:OH	2.26	0.53
3:K:382:ARG:HA	3:K:385:THR:HG22	1.89	0.53
8:R:81:ALA:HA	8:R:87:VAL:HA	1.91	0.53
8:R:394:ILE:O	8:R:408:ARG:NH2	2.41	0.53
9:T:128:LEU:HD22	12:Z:417:HIS:CG	2.44	0.53
3:C:607:LEU:HD21	3:C:638:LEU:HB3	1.91	0.53
3:C:637:MET:O	3:C:640:LYS:NZ	2.38	0.53
6:F:203:TYR:OH	7:G:207:PRO:O	2.25	0.53
9:L:243:ARG:HH22	10:M:415:ALA:HA	1.74	0.53
3:K:599:SER:HA	3:K:602:GLU:HG2	1.91	0.53
2:B:194:SER:HA	2:B:205:PRO:HA	1.91	0.52
3:C:110:HIS:HB3	3:C:113:ALA:HB3	1.90	0.52
5:E:129:HIS:HA	5:E:132:GLN:HE21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:598:LYS:HD2	8:I:602:LEU:HD23	1.91	0.52
9:L:240:GLU:HA	9:L:243:ARG:HD3	1.90	0.52
3:K:541:ILE:HG23	3:K:557:ARG:HE	1.74	0.52
5:O:155:LEU:HA	5:O:174:TYR:HE1	1.74	0.52
13:V:719:TYR:HB2	13:V:728:ALA:HB2	1.91	0.52
4:D:217:LYS:HZ3	5:E:248:GLU:HG2	1.74	0.52
6:F:13:LEU:HB3	6:F:15:PRO:HD2	1.91	0.52
13:S:849:ALA:O	13:S:850:ARG:HD3	2.09	0.52
1:H:130:GLU:HG3	1:H:134:HIS:CE1	2.44	0.52
6:P:315:THR:O	6:P:319:ASN:ND2	2.42	0.52
8:R:63:TYR:HB3	8:R:75:THR:HA	1.90	0.52
8:R:109:SER:O	8:R:121:THR:OG1	2.26	0.52
9:T:204:ARG:NE	10:U:378:ASN:HB3	2.23	0.52
1:A:287:MET:HE1	1:A:295:THR:HB	1.91	0.52
1:A:515:LEU:HD22	1:A:519:ARG:HH22	1.75	0.52
6:F:41:PHE:HA	6:F:44:ILE:HG12	1.90	0.52
8:I:111:ARG:HG3	8:I:153:TRP:HD1	1.74	0.52
8:I:373:ASP:HB3	8:I:389:ASP:HB2	1.91	0.52
9:L:277:GLN:HA	9:L:280:MET:HG2	1.91	0.52
13:S:931:ALA:HB1	13:S:934:GLU:HB2	1.90	0.52
1:H:542:GLU:OE2	1:H:546:GLN:NE2	2.42	0.52
3:K:508:ALA:HA	3:K:511:LEU:HB2	1.90	0.52
3:K:618:ARG:NH1	3:K:619:VAL:O	2.41	0.52
4:N:246:ILE:HG23	4:N:249:LEU:HD22	1.90	0.52
5:O:56:ASP:HB3	5:O:59:ASN:HB2	1.92	0.52
8:R:28:LEU:HD22	8:R:40:TRP:HB2	1.91	0.52
8:R:131:TRP:HA	8:R:137:LEU:HA	1.90	0.52
8:R:236:ALA:HB3	8:R:241:LEU:HB3	1.91	0.52
9:T:297:GLU:HA	9:T:300:ARG:HG2	1.91	0.52
10:U:452:ARG:NH1	10:U:455:ARG:HH21	2.06	0.52
13:V:545:GLN:NE2	13:V:546:SER:O	2.42	0.52
13:V:723:HIS:ND1	13:V:723:HIS:O	2.39	0.52
1:A:511:TYR:HD2	2:B:283:LYS:HB2	1.75	0.52
2:B:88:ILE:HB	2:B:220:VAL:HG12	1.91	0.52
3:C:200:LEU:HD11	3:C:245:LEU:HG	1.92	0.52
7:G:192:LEU:O	7:G:196:ASN:HB2	2.10	0.52
8:I:130:ILE:HD11	8:I:141:LEU:HB2	1.92	0.52
13:S:550:LEU:HD21	13:S:571:VAL:HG21	1.92	0.52
13:S:580:ARG:HA	13:S:601:ILE:HD13	1.90	0.52
2:J:372:GLU:HA	2:J:375:ARG:HG2	1.90	0.52
8:R:389:ASP:OD1	8:R:395:GLN:NE2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:432:SER:O	3:C:435:GLU:HG2	2.10	0.52
3:C:480:ASN:ND2	3:C:483:ASN:O	2.42	0.52
7:G:137:ASN:HA	7:G:140:MET:HE2	1.91	0.52
8:I:487:LEU:N	8:I:501:ALA:O	2.40	0.52
8:I:644:VAL:HG21	13:V:724:ARG:HH21	1.74	0.52
12:X:432:ASP:O	12:X:436:MET:HG2	2.10	0.52
13:S:511:ARG:NH1	13:S:530:CYS:O	2.38	0.52
2:J:11:ILE:HD12	2:J:34:LEU:HD21	1.92	0.52
5:O:11:ALA:HB1	5:O:217:PRO:HB2	1.92	0.52
8:R:195:SER:HB3	8:R:235:TRP:CE2	2.44	0.52
8:R:319:VAL:O	8:R:328:ASP:N	2.36	0.52
9:T:243:ARG:O	9:T:246:GLY:N	2.42	0.52
13:V:141:GLY:HA2	13:V:148:SER:HA	1.90	0.52
13:V:846:ILE:HA	13:V:849:ALA:HB2	1.90	0.52
1:A:305:ALA:O	9:L:292:LYS:NZ	2.38	0.52
2:B:76:LEU:HD11	2:B:86:ILE:HG13	1.91	0.52
3:C:317:LEU:HA	3:C:320:CYS:HB2	1.92	0.52
5:E:274:LEU:HG	5:E:307:LEU:HD13	1.91	0.52
5:E:301:VAL:HA	5:E:304:ALA:HB3	1.91	0.52
13:S:828:ARG:HE	13:S:830:SER:HB3	1.74	0.52
13:S:911:ASP:OD1	13:S:911:ASP:N	2.43	0.52
1:H:280:LEU:CD2	1:H:302:CYS:HB3	2.39	0.52
1:H:474:ARG:NH2	1:H:508:GLU:OE1	2.42	0.52
1:H:493:ARG:O	1:H:497:ASN:ND2	2.43	0.52
5:O:5:LYS:HE2	5:O:257:HIS:CE1	2.45	0.52
8:R:85:GLY:O	8:R:102:GLY:N	2.35	0.52
2:B:112:SER:O	2:B:184:SER:N	2.42	0.52
6:F:315:THR:O	6:F:319:ASN:ND2	2.43	0.52
8:I:18:ALA:HB2	9:L:7:ARG:HH12	1.74	0.52
8:I:394:ILE:O	8:I:408:ARG:NH2	2.42	0.52
8:I:733:MET:HA	8:I:736:SER:HB3	1.91	0.52
11:W:115:LYS:O	12:X:495:ASN:ND2	2.43	0.52
2:J:425:LYS:HD3	4:N:286:LEU:HB3	1.91	0.52
4:N:309:LYS:O	4:N:315:ARG:NH1	2.40	0.52
8:R:589:ASP:O	8:R:593:LYS:NZ	2.43	0.52
1:A:251:ILE:HG21	1:A:255:ALA:HB3	1.91	0.52
2:B:413:VAL:HA	2:B:416:GLU:HB2	1.91	0.52
3:C:91:LEU:HA	3:C:96:MET:HE2	1.91	0.52
8:I:89:ILE:HG22	8:I:97:GLU:HB2	1.92	0.52
8:I:485:ARG:NH2	8:I:503:MET:O	2.43	0.52
8:I:706:HIS:HA	8:I:747:LYS:HD3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:M:309:HIS:HE1	11:W:38:ILE:HG12	1.75	0.52
1:H:550:THR:HA	1:H:553:MET:SD	2.50	0.52
5:O:60:LEU:HD11	5:O:83:LEU:HD13	1.91	0.52
6:P:321:ILE:HA	6:P:324:ILE:HG12	1.91	0.52
13:V:187:PRO:HB3	13:V:194:PRO:HD3	1.91	0.52
3:C:482:ASP:OD1	3:C:483:ASN:N	2.43	0.52
5:E:34:LEU:HD12	5:E:35:THR:HG23	1.90	0.52
5:E:63:LEU:O	5:E:67:TYR:N	2.42	0.52
6:F:286:ARG:HD2	7:G:296:LEU:HB2	1.91	0.52
9:L:260:ARG:NH2	10:M:431:GLU:OE1	2.38	0.52
1:H:139:LYS:NZ	1:H:151:SER:O	2.43	0.52
5:O:209:LEU:HB3	5:O:226:LYS:HZ2	1.75	0.52
5:O:220:ALA:HA	5:O:246:LEU:HD11	1.92	0.52
9:T:74:LEU:O	10:U:306:TRP:NE1	2.41	0.52
13:V:342:ILE:HG12	13:V:353:VAL:HG13	1.92	0.52
8:I:81:ALA:HA	8:I:87:VAL:HA	1.92	0.52
8:I:107:CYS:HA	8:I:123:GLY:HA2	1.92	0.52
8:I:206:GLU:HA	8:I:229:PRO:HB3	1.92	0.52
8:I:714:ARG:O	8:I:714:ARG:NH1	2.41	0.52
13:S:443:LEU:O	13:S:495:LEU:HD11	2.10	0.52
1:H:304:TYR:C	1:H:306:LEU:N	2.68	0.52
2:J:92:GLU:O	2:J:97:LYS:NZ	2.41	0.52
2:J:204:ARG:NH1	2:J:205:PRO:O	2.43	0.52
6:P:41:PHE:HA	6:P:44:ILE:HG12	1.91	0.52
8:R:68:LYS:HG3	8:R:73:GLY:HA2	1.92	0.52
8:R:608:ASP:HB3	8:R:611:MET:HG2	1.92	0.52
12:Z:406:SER:O	12:Z:410:GLU:HG2	2.10	0.52
1:A:636:SER:HB3	1:A:645:TRP:HD1	1.75	0.51
3:C:243:PHE:HD1	3:C:246:LYS:HZ3	1.58	0.51
3:C:382:ARG:HA	3:C:385:THR:HG22	1.91	0.51
8:I:124:GLU:HG3	9:L:2:SER:HB2	1.91	0.51
8:I:558:ILE:HA	8:I:568:VAL:HG12	1.92	0.51
9:L:46:TYR:CZ	9:L:104:LEU:HB2	2.45	0.51
9:L:228:SER:OG	10:M:404:MET:SD	2.59	0.51
10:M:398:LEU:HB3	10:M:402:LYS:HZ3	1.75	0.51
13:S:555:SER:N	13:S:627:GLU:OE1	2.30	0.51
1:H:464:MET:HG2	1:H:467:LYS:HZ3	1.75	0.51
7:Q:215:PHE:O	7:Q:219:LYS:HB2	2.10	0.51
9:T:71:GLN:OE1	9:T:80:LYS:NZ	2.43	0.51
11:Y:44:MET:HE1	12:Z:421:PRO:HB2	1.93	0.51
13:V:383:MET:O	13:V:392:SER:N	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:110:GLY:CA	2:B:188:PRO:HG3	2.28	0.51
2:B:397:GLY:HA2	2:B:400:LEU:HD12	1.92	0.51
3:C:401:LYS:HA	3:C:404:ILE:HG12	1.90	0.51
5:E:132:GLN:HB2	5:E:160:ILE:HD11	1.93	0.51
5:E:220:ALA:O	5:E:224:ASN:HB2	2.10	0.51
8:I:109:SER:O	8:I:121:THR:OG1	2.27	0.51
8:I:428:THR:HG23	8:I:467:LEU:HD13	1.91	0.51
8:I:433:ASP:OD1	8:I:435:GLN:NE2	2.43	0.51
13:S:1046:GLU:HG2	13:S:1070:MET:HE1	1.92	0.51
3:K:269:ARG:NH2	3:K:273:GLU:O	2.43	0.51
3:K:385:THR:HA	3:K:388:ILE:HD12	1.91	0.51
4:N:333:GLY:O	4:N:334:MET:C	2.53	0.51
13:V:443:LEU:O	13:V:495:LEU:HD11	2.09	0.51
13:V:536:VAL:HG11	13:V:541:VAL:HB	1.92	0.51
1:A:312:MET:N	1:A:312:MET:SD	2.83	0.51
3:C:58:TYR:O	3:C:63:TYR:OH	2.22	0.51
3:C:310:GLU:O	3:C:314:ASN:ND2	2.44	0.51
3:C:373:LEU:O	3:C:377:HIS:ND1	2.35	0.51
6:F:324:ILE:HA	6:F:327:ARG:HG2	1.93	0.51
13:S:442:TYR:O	13:S:495:LEU:HG	2.11	0.51
6:P:140:GLU:HA	6:P:143:LYS:HE2	1.92	0.51
6:P:210:LEU:HD12	6:P:213:GLN:HE21	1.76	0.51
8:R:82:CYS:SG	8:R:83:THR:N	2.81	0.51
13:V:889:LYS:HA	13:V:892:LYS:HE2	1.93	0.51
13:V:911:ASP:OD1	13:V:911:ASP:N	2.42	0.51
1:A:188:ASP:O	1:A:208:TYR:OH	2.24	0.51
3:C:518:GLU:HA	3:C:521:ARG:HE	1.74	0.51
8:I:441:VAL:N	8:I:456:TRP:O	2.42	0.51
13:S:383:MET:O	13:S:392:SER:N	2.42	0.51
13:S:449:GLN:HB3	13:S:458:SER:HB2	1.92	0.51
1:H:511:TYR:HD2	2:J:283:LYS:HB2	1.76	0.51
5:O:223:VAL:HA	5:O:226:LYS:HE2	1.93	0.51
8:R:115:ASP:OD1	8:R:115:ASP:N	2.41	0.51
13:V:228:ASP:OD1	13:V:232:ARG:N	2.38	0.51
1:A:259:ARG:NH1	1:A:288:ASP:OD1	2.43	0.51
2:B:67:LYS:NZ	2:B:101:ASN:OD1	2.44	0.51
6:F:23:LEU:O	6:F:26:THR:OG1	2.28	0.51
7:G:209:TYR:O	7:G:213:GLN:NE2	2.33	0.51
8:I:602:LEU:HB2	8:I:606:ILE:HD13	1.93	0.51
11:W:109:GLN:HA	11:W:112:ILE:HD12	1.92	0.51
11:W:124:LYS:HD2	11:W:125:LEU:HG	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:799:ASP:HB3	13:S:802:LEU:H	1.76	0.51
1:H:449:TYR:CZ	1:H:454:GLU:HG3	2.46	0.51
1:H:602:HIS:HB2	1:H:611:VAL:HG11	1.91	0.51
6:P:181:GLU:OE2	6:P:182:ARG:NH1	2.43	0.51
3:C:15:GLN:OE1	3:C:18:GLN:NE2	2.40	0.51
5:E:422:ASP:OD1	5:E:422:ASP:N	2.43	0.51
8:I:130:ILE:HG22	8:I:138:ARG:HB3	1.93	0.51
1:H:531:LYS:HD3	1:H:547:ILE:HD12	1.92	0.51
7:Q:167:LYS:O	7:Q:171:TYR:HB3	2.10	0.51
8:R:379:LEU:HD11	8:R:422:ILE:HG23	1.92	0.51
8:R:381:ALA:O	8:R:399:TYR:OH	2.27	0.51
8:R:543:THR:HA	8:R:610:THR:HG23	1.93	0.51
8:R:567:LEU:HD11	8:R:575:LEU:HD12	1.92	0.51
6:F:83:LEU:HA	6:F:86:GLN:HG3	1.93	0.51
1:H:293:HIS:HA	1:H:319:LEU:HD21	1.93	0.51
1:H:531:LYS:HZ2	1:H:547:ILE:HG23	1.75	0.51
3:K:341:ALA:HB1	3:K:345:LEU:HD11	1.93	0.51
6:P:11:LEU:HG	6:P:18:TYR:HB2	1.92	0.51
7:Q:143:LEU:O	7:Q:147:ARG:HG2	2.10	0.51
8:R:662:VAL:HG21	8:R:674:LEU:HD22	1.92	0.51
1:A:268:LEU:O	1:A:272:ARG:HG2	2.10	0.51
1:A:449:TYR:CZ	1:A:454:GLU:HG3	2.46	0.51
2:B:376:LEU:HD22	2:B:400:LEU:HD21	1.93	0.51
3:C:132:ARG:NH2	3:C:156:GLU:OE1	2.44	0.51
8:I:559:GLN:HB2	8:I:567:LEU:HG	1.92	0.51
9:L:136:ILE:HD12	12:X:410:GLU:HB2	1.92	0.51
13:S:4:ARG:O	13:S:319:ASP:N	2.40	0.51
13:S:781:GLY:C	13:S:782:LEU:HD22	2.35	0.51
1:H:412:THR:HA	1:H:415:MET:HE2	1.91	0.51
13:V:352:ILE:HD11	13:V:391:LEU:HD21	1.93	0.51
13:V:360:TYR:CE2	13:V:379:TYR:HB3	2.46	0.51
3:C:213:GLU:HG2	3:C:214:LEU:HG	1.92	0.51
3:C:458:THR:HA	3:C:461:MET:HE2	1.93	0.51
8:I:539:LEU:HD12	8:I:542:LYS:HD3	1.92	0.51
8:I:584:PRO:HB3	8:I:611:MET:HE1	1.93	0.51
13:S:719:TYR:HE2	13:S:731:VAL:HG11	1.74	0.51
13:S:837:ARG:HG3	13:S:842:TYR:HB3	1.92	0.51
13:S:881:PHE:HA	13:S:884:SER:HB3	1.93	0.51
1:H:178:GLN:HE21	1:H:181:LEU:HB3	1.75	0.51
1:H:559:ASN:HA	1:H:562:LYS:HE2	1.92	0.51
2:J:403:LYS:HE2	4:N:326:GLY:HA2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:231:SER:HB3	3:K:234:LEU:HD13	1.93	0.51
2:B:120:ARG:NH1	2:B:128:HIS:O	2.44	0.51
3:C:176:GLN:NE2	5:E:275:GLN:OE1	2.43	0.51
3:C:282:SER:HA	3:C:285:ILE:HG22	1.92	0.51
3:C:463:ASP:HA	3:C:466:TYR:HE1	1.76	0.51
9:L:145:LYS:HG2	10:M:322:LYS:HZ3	1.75	0.51
13:S:231:GLY:O	13:S:232:ARG:NH1	2.44	0.51
13:S:513:LEU:HB2	13:S:527:LEU:HB2	1.93	0.51
1:H:304:TYR:O	1:H:304:TYR:HD1	1.94	0.51
1:H:304:TYR:O	1:H:306:LEU:N	2.44	0.51
3:K:401:LYS:O	3:K:405:ASN:ND2	2.44	0.51
8:R:251:GLN:HG3	8:R:262:LYS:HA	1.93	0.51
10:U:314:HIS:HA	10:U:317:LYS:HG2	1.93	0.51
13:V:493:ASP:OD1	13:V:493:ASP:N	2.44	0.51
1:A:559:ASN:HA	1:A:562:LYS:HE2	1.93	0.50
2:B:27:PHE:HB2	2:B:31:PHE:HE2	1.76	0.50
3:C:450:VAL:HG22	3:C:451:TRP:H	1.76	0.50
6:F:151:GLU:HA	6:F:154:LYS:HG2	1.93	0.50
8:I:2:ARG:NE	8:I:261:SER:OG	2.42	0.50
8:I:131:TRP:HA	8:I:137:LEU:HA	1.93	0.50
8:I:247:PHE:HA	8:I:270:SER:HA	1.93	0.50
13:S:667:VAL:HG12	13:S:691:MET:HG2	1.93	0.50
1:H:437:VAL:HG13	1:H:440:ARG:HH21	1.76	0.50
2:J:397:GLY:HA2	2:J:400:LEU:HD12	1.93	0.50
3:K:19:THR:O	3:K:23:LEU:HB2	2.10	0.50
3:K:480:ASN:ND2	3:K:483:ASN:O	2.44	0.50
3:K:559:ILE:HG21	3:K:602:GLU:HB2	1.93	0.50
5:O:197:CYS:SG	5:O:229:ASN:ND2	2.83	0.50
6:P:169:LEU:HA	6:P:172:LYS:HE2	1.93	0.50
13:V:7:LYS:HE2	13:V:9:ILE:HG13	1.92	0.50
13:V:142:MET:SD	13:V:144:LYS:NZ	2.85	0.50
13:V:422:ILE:HG13	13:V:431:LEU:HB2	1.93	0.50
2:B:425:LYS:HZ2	4:D:288:ILE:HB	1.76	0.50
3:C:57:TYR:HA	3:C:60:THR:HG22	1.93	0.50
7:G:143:LEU:O	7:G:147:ARG:HG2	2.11	0.50
8:I:80:VAL:O	8:I:88:LYS:N	2.42	0.50
8:I:598:LYS:HE2	12:X:496:ASP:HB3	1.92	0.50
10:M:316:HIS:HB3	11:W:31:GLN:HE22	1.75	0.50
12:X:501:LYS:HB3	12:X:505:MET:HE3	1.93	0.50
13:S:536:VAL:HG11	13:S:541:VAL:HB	1.93	0.50
1:H:434:GLU:O	1:H:438:LYS:N	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:508:GLU:OE2	1:H:512:ASN:ND2	2.45	0.50
2:J:60:VAL:HG12	2:J:87:LEU:HB3	1.92	0.50
6:P:28:LYS:HE2	6:P:36:LEU:HD22	1.92	0.50
8:R:18:ALA:HB2	9:T:7:ARG:HH12	1.76	0.50
8:R:202:ILE:HG22	8:R:212:VAL:HG22	1.92	0.50
8:R:619:ALA:O	8:R:623:LYS:N	2.44	0.50
11:Y:66:LYS:HE3	11:Y:70:ILE:HD11	1.92	0.50
13:V:1014:LYS:HB2	13:V:1033:LYS:HZ1	1.76	0.50
8:I:448:GLN:O	8:I:450:ARG:NH1	2.44	0.50
8:I:460:LEU:HB3	8:I:482:ASP:HB2	1.93	0.50
13:S:292:TYR:HD2	13:S:311:MET:HG3	1.76	0.50
13:S:713:ASP:OD1	13:S:713:ASP:N	2.42	0.50
13:S:729:ILE:HG12	13:S:743:LEU:HD11	1.93	0.50
6:P:23:LEU:O	6:P:26:THR:OG1	2.20	0.50
13:V:292:TYR:HD2	13:V:311:MET:HG3	1.76	0.50
13:V:713:ASP:OD1	13:V:713:ASP:N	2.42	0.50
13:V:758:GLU:H	13:V:780:GLY:HA3	1.76	0.50
2:B:273:PRO:HA	9:L:269:LEU:HD13	1.93	0.50
2:B:403:LYS:HE2	4:D:326:GLY:HA2	1.94	0.50
8:I:567:LEU:HD11	8:I:575:LEU:HD12	1.93	0.50
10:M:377:TYR:O	10:M:381:THR:OG1	2.27	0.50
13:S:817:GLU:HA	13:S:835:SER:HB3	1.94	0.50
13:S:922:ILE:HA	13:S:925:HIS:HB3	1.94	0.50
2:J:165:PRO:O	2:J:166:GLN:NE2	2.45	0.50
2:J:413:VAL:HA	2:J:416:GLU:HB2	1.93	0.50
3:K:202:GLU:HA	3:K:205:GLU:HG3	1.93	0.50
6:P:210:LEU:HD11	7:Q:218:LEU:HD21	1.93	0.50
1:A:568:THR:OG1	9:T:231:GLN:OE1	2.27	0.50
5:E:290:ASN:O	5:E:294:HIS:HB3	2.11	0.50
7:G:271:GLU:HA	7:G:274:THR:HG22	1.93	0.50
8:I:138:ARG:HH22	13:S:435:ARG:HD2	1.76	0.50
8:I:688:ILE:HG12	8:I:710:VAL:HA	1.94	0.50
9:L:136:ILE:HG13	12:X:410:GLU:HG3	1.92	0.50
11:W:53:SER:HA	11:W:56:ASP:OD2	2.11	0.50
13:S:140:LEU:HD21	13:S:186:PHE:HE1	1.77	0.50
3:K:463:ASP:N	3:K:463:ASP:OD1	2.41	0.50
7:Q:268:GLN:HG3	7:Q:271:GLU:OE2	2.12	0.50
12:Z:409:ARG:NH2	12:Z:410:GLU:OE1	2.44	0.50
13:V:1021:GLN:HA	13:V:1024:ARG:HB3	1.94	0.50
1:A:466:LEU:HD12	1:A:470:ARG:HD3	1.94	0.50
6:F:220:LEU:O	6:F:224:ILE:HG23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:425:SER:OG	8:I:426:ASN:N	2.45	0.50
13:S:692:MET:HE3	13:S:696:ASN:ND2	2.27	0.50
13:S:778:LEU:O	13:S:780:GLY:N	2.36	0.50
1:H:231:HIS:HD2	1:H:243:MET:SD	2.33	0.50
6:P:216:GLU:OE2	7:Q:226:ARG:NH2	2.37	0.50
8:R:118:ALA:HA	8:R:132:SER:HA	1.93	0.50
11:Y:101:LEU:HD22	12:Z:478:ILE:HG12	1.93	0.50
1:A:257:GLU:HB3	3:C:646:ARG:HH12	1.76	0.50
5:E:155:LEU:HA	5:E:174:TYR:HE1	1.77	0.50
6:F:169:LEU:HD11	7:G:175:ASP:HB3	1.94	0.50
8:I:429:ILE:HB	8:I:444:PHE:HB2	1.93	0.50
8:I:632:PHE:HA	8:I:635:ILE:HG12	1.93	0.50
9:L:274:GLN:O	9:L:277:GLN:NE2	2.42	0.50
13:S:24:TRP:HH2	13:S:45:GLU:HA	1.77	0.50
8:R:2:ARG:NH2	8:R:260:TYR:O	2.44	0.50
13:V:399:ASP:N	13:V:399:ASP:OD1	2.42	0.50
1:A:259:ARG:NH2	1:A:286:VAL:O	2.44	0.50
1:A:550:THR:HA	1:A:553:MET:SD	2.51	0.50
1:A:592:ALA:O	1:A:596:HIS:HB2	2.12	0.50
2:B:295:ASP:OD1	2:B:295:ASP:N	2.45	0.50
4:D:246:ILE:HA	4:D:249:LEU:HD13	1.94	0.50
6:F:286:ARG:HH11	7:G:296:LEU:HD22	1.77	0.50
8:I:66:SER:HA	8:I:69:LYS:HZ1	1.77	0.50
8:I:600:THR:O	8:I:604:ARG:NH1	2.45	0.50
9:L:175:ASP:HB3	9:L:177:VAL:HG22	1.92	0.50
13:S:74:SER:OG	13:S:79:LYS:O	2.28	0.50
13:S:1083:VAL:HA	13:S:1086:VAL:HG12	1.94	0.50
3:K:60:THR:HG23	3:K:62:GLN:H	1.76	0.50
3:K:450:VAL:HG22	3:K:451:TRP:H	1.77	0.50
5:O:36:LYS:HE2	5:O:38:ASP:HB3	1.94	0.50
7:Q:225:GLN:OE1	7:Q:228:ARG:NH2	2.44	0.50
9:T:166:ARG:HB3	10:U:344:LYS:HG2	1.94	0.50
9:T:281:GLU:HB3	9:T:285:ARG:NH1	2.27	0.50
13:V:586:ASP:HA	13:V:591:THR:HA	1.92	0.50
13:V:698:GLN:O	13:V:702:SER:N	2.38	0.50
3:C:463:ASP:N	3:C:463:ASP:OD1	2.41	0.50
9:L:239:ASP:O	9:L:242:GLU:HG3	2.11	0.50
11:W:117:GLU:HA	13:V:781:GLY:O	2.12	0.50
13:S:471:ARG:HH21	13:S:473:GLN:HG3	1.77	0.50
2:J:194:SER:HA	2:J:205:PRO:HA	1.93	0.50
12:Z:491:GLN:HG2	12:Z:494:ARG:HH21	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:V:9:ILE:HD11	13:V:317:MET:HB2	1.93	0.50
13:V:777:TYR:HB3	13:V:786:ALA:HB2	1.94	0.50
5:E:306:GLY:HA2	5:E:309:LYS:HD3	1.93	0.49
8:I:207:ASP:OD1	8:I:207:ASP:N	2.45	0.49
8:I:518:ALA:HB3	8:I:527:TRP:HZ3	1.76	0.49
13:S:360:TYR:CE2	13:S:379:TYR:HB3	2.47	0.49
3:K:282:SER:HA	3:K:285:ILE:HG22	1.94	0.49
4:N:300:VAL:O	4:N:303:THR:OG1	2.25	0.49
5:O:84:LEU:HD21	5:O:93:PHE:HB2	1.94	0.49
9:T:213:ILE:HA	9:T:216:LYS:HZ3	1.77	0.49
12:Z:488:MET:O	12:Z:492:ILE:HG13	2.12	0.49
13:V:799:ASP:HB3	13:V:802:LEU:H	1.77	0.49
6:F:210:LEU:O	6:F:213:GLN:HG2	2.13	0.49
8:I:249:THR:HA	8:I:264:HIS:HA	1.94	0.49
11:W:101:LEU:HD22	12:X:478:ILE:HG12	1.94	0.49
13:S:549:ASN:HA	13:S:566:PRO:HA	1.95	0.49
1:H:304:TYR:CE2	2:J:296:TRP:HZ2	2.29	0.49
1:H:447:PHE:CD2	1:H:448:LEU:HG	2.46	0.49
3:K:317:LEU:HA	3:K:320:CYS:HB2	1.95	0.49
3:K:377:HIS:CD2	3:K:414:TYR:HB2	2.47	0.49
3:K:557:ARG:HA	3:K:560:LYS:HG3	1.93	0.49
8:R:532:GLU:HA	8:R:535:VAL:HB	1.94	0.49
9:T:150:LEU:HD21	11:Y:23:LYS:HG2	1.94	0.49
11:Y:111:LEU:HD21	12:Z:492:ILE:HG12	1.93	0.49
13:V:383:MET:HB3	13:V:392:SER:HB2	1.94	0.49
13:V:664:LEU:HD11	13:V:694:GLN:HE21	1.77	0.49
13:V:837:ARG:HG3	13:V:842:TYR:HB3	1.94	0.49
1:A:170:ARG:HD2	1:A:179:ILE:HG21	1.93	0.49
3:C:38:TYR:HD1	3:C:41:GLN:HE21	1.60	0.49
3:C:485:LEU:O	3:C:533:HIS:NE2	2.45	0.49
13:S:598:GLU:HA	13:S:601:ILE:HD12	1.94	0.49
13:S:833:MET:HE1	13:S:848:LEU:HB2	1.95	0.49
2:J:14:SER:HB3	2:J:61:LEU:HD13	1.94	0.49
13:V:931:ALA:HB1	13:V:934:GLU:HB2	1.93	0.49
9:L:178:GLU:HA	9:L:181:ILE:HD12	1.94	0.49
13:S:508:ASP:OD1	13:S:512:HIS:N	2.44	0.49
13:S:729:ILE:HB	13:S:750:TRP:HE1	1.77	0.49
1:H:184:MET:HG2	1:H:216:ASN:HD21	1.77	0.49
2:J:33:ARG:HD2	2:J:241:MET:HE1	1.95	0.49
8:R:425:SER:OG	8:R:426:ASN:N	2.46	0.49
13:V:347:LYS:HG3	13:V:348:THR:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:LYS:HA	3:C:636:ARG:HD3	1.93	0.49
1:A:508:GLU:OE2	1:A:512:ASN:ND2	2.45	0.49
6:F:28:LYS:HE2	6:F:36:LEU:HD22	1.92	0.49
6:F:145:MET:HA	6:F:148:GLU:HB3	1.95	0.49
8:I:69:LYS:HE2	8:I:413:ARG:HH22	1.77	0.49
8:I:725:GLU:CD	8:I:731:MET:HE3	2.37	0.49
9:L:213:ILE:HA	9:L:216:LYS:HZ3	1.77	0.49
13:S:612:TYR:HE2	13:S:638:GLN:HB3	1.77	0.49
13:S:716:ILE:HA	13:S:728:ALA:HB1	1.94	0.49
13:S:758:GLU:HG3	13:S:782:LEU:H	1.77	0.49
1:H:466:LEU:HD12	1:H:470:ARG:HD3	1.93	0.49
1:H:618:TYR:HA	1:H:621:LYS:HG2	1.94	0.49
3:K:611:GLU:HB3	3:K:615:LYS:HE2	1.94	0.49
8:R:108:ILE:HD11	9:T:2:SER:HB3	1.94	0.49
13:V:218:ALA:HB2	13:V:224:VAL:HG22	1.95	0.49
13:V:847:ASP:OD1	13:V:848:LEU:N	2.45	0.49
3:C:341:ALA:HB1	3:C:345:LEU:HD11	1.95	0.49
8:I:347:LEU:HB3	8:I:358:TYR:HB2	1.94	0.49
13:S:43:PHE:HE1	13:S:49:LYS:HG3	1.77	0.49
1:H:659:LEU:HA	1:H:662:ALA:HB3	1.95	0.49
3:K:512:MET:HA	3:K:515:VAL:HG22	1.94	0.49
5:O:363:GLN:HG3	5:O:395:PHE:HZ	1.77	0.49
8:R:119:LEU:HB2	8:R:131:TRP:HB2	1.94	0.49
8:R:431:VAL:O	8:R:442:ARG:N	2.46	0.49
8:R:600:THR:O	8:R:604:ARG:HG2	2.11	0.49
9:T:124:VAL:HA	9:T:127:SER:HB3	1.94	0.49
9:T:232:SER:HB2	10:U:404:MET:HE1	1.94	0.49
13:V:904:ALA:HB1	13:V:922:ILE:HG21	1.94	0.49
3:C:246:LYS:HA	3:C:249:ILE:HG22	1.93	0.49
4:D:213:ASN:HD21	4:D:217:LYS:HE3	1.77	0.49
6:F:28:LYS:O	6:F:93:ARG:NH1	2.46	0.49
11:W:79:LEU:O	12:X:461:GLN:NE2	2.45	0.49
13:S:577:HIS:HE1	13:S:582:GLU:HG2	1.77	0.49
13:S:776:LEU:HD23	13:S:779:LYS:HD2	1.95	0.49
1:H:225:VAL:HG21	1:H:264:ARG:HH22	1.77	0.49
1:H:287:MET:HE1	1:H:295:THR:HB	1.93	0.49
2:J:103:ASN:HA	2:J:106:LEU:HB2	1.95	0.49
2:J:112:SER:O	2:J:184:SER:N	2.38	0.49
4:N:243:MET:HE3	4:N:246:ILE:HD11	1.94	0.49
6:P:10:SER:HB2	6:P:104:VAL:HG21	1.94	0.49
8:R:149:TYR:H	8:R:163:CYS:HB2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:T:266:GLU:HA	9:T:269:LEU:HD12	1.93	0.49
13:V:184:PHE:HD1	13:V:196:SER:HB2	1.78	0.49
13:V:719:TYR:HE2	13:V:731:VAL:HG11	1.78	0.49
3:C:512:MET:HA	3:C:515:VAL:HG22	1.94	0.49
5:E:151:ILE:HA	5:E:177:LEU:HD13	1.94	0.49
9:L:4:ARG:HG3	9:L:95:LYS:HZ2	1.78	0.49
13:S:332:GLU:HG3	13:S:344:LYS:HB2	1.95	0.49
13:S:960:ALA:HA	13:S:963:ARG:HE	1.78	0.49
1:H:143:ASP:OD1	1:H:151:SER:OG	2.31	0.49
1:H:449:TYR:CD1	1:H:449:TYR:C	2.91	0.49
1:H:584:ILE:HG23	1:H:587:ARG:HH21	1.78	0.49
2:J:106:LEU:HA	2:J:109:PHE:HB2	1.95	0.49
3:K:458:THR:HA	3:K:461:MET:HE2	1.95	0.49
5:O:34:LEU:HD12	5:O:35:THR:HG23	1.94	0.49
8:R:529:TYR:HE2	8:R:618:MET:HB3	1.77	0.49
9:T:26:ASN:HB2	9:T:35:VAL:HG13	1.94	0.49
9:T:270:GLU:HG3	10:U:445:THR:HB	1.93	0.49
13:V:942:ALA:HB3	13:V:944:MET:HE2	1.93	0.49
1:A:475:ALA:HA	1:A:478:ASN:HB2	1.95	0.49
2:B:114:ASN:OD1	2:B:204:ARG:NH2	2.42	0.49
2:B:120:ARG:HH22	2:B:127:LEU:HA	1.78	0.49
3:C:536:ILE:HG12	3:C:573:THR:HG21	1.95	0.49
8:I:467:LEU:O	8:I:469:GLN:NE2	2.40	0.49
8:I:587:LEU:HD11	8:I:615:LEU:HD13	1.94	0.49
13:S:174:SER:HB2	13:S:182:TRP:HB2	1.95	0.49
1:H:507:VAL:HG13	7:Q:201:LYS:HD3	1.95	0.49
2:J:72:GLU:HA	2:J:75:MET:HG3	1.94	0.49
6:P:9:ASP:OD1	6:P:19:GLN:NE2	2.35	0.49
7:Q:225:GLN:O	7:Q:229:VAL:HG23	2.13	0.49
8:R:39:LYS:HG3	8:R:47:GLU:HB2	1.95	0.49
13:V:422:ILE:HD11	13:V:475:LEU:HG	1.95	0.49
1:A:238:PRO:HA	1:A:241:ILE:HG12	1.95	0.49
2:B:128:HIS:HB3	2:B:131:GLU:HB2	1.95	0.49
3:C:99:GLU:OE1	3:C:102:LYS:NZ	2.37	0.49
5:E:209:LEU:HB3	5:E:226:LYS:HZ2	1.78	0.49
8:I:41:ASN:HB3	8:I:45:GLU:HB3	1.95	0.49
8:I:186:ASP:OD1	8:I:186:ASP:N	2.45	0.49
8:I:195:SER:HB3	8:I:235:TRP:CE2	2.48	0.49
8:I:389:ASP:OD1	8:I:395:GLN:NE2	2.46	0.49
8:I:482:ASP:OD1	8:I:486:ASP:N	2.46	0.49
8:I:532:GLU:HA	8:I:535:VAL:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:M:309:HIS:CE1	11:W:38:ILE:HG12	2.48	0.49
1:H:236:LYS:O	1:H:239:SER:OG	2.23	0.49
2:J:94:GLY:HA3	2:J:115:ASN:HA	1.95	0.49
4:N:319:GLU:OE1	4:N:323:LYS:NZ	2.39	0.49
5:O:13:ARG:NH2	5:O:16:VAL:O	2.46	0.49
5:O:151:ILE:HA	5:O:177:LEU:HD13	1.94	0.49
5:O:176:ARG:HG3	5:O:177:LEU:HG	1.94	0.49
7:Q:246:ALA:HB1	7:Q:250:MET:HE1	1.95	0.49
8:R:243:ALA:HB2	8:R:276:TRP:HE1	1.77	0.49
8:R:489:LEU:N	8:R:498:ALA:O	2.41	0.49
9:T:223:GLN:O	9:T:226:ARG:HG3	2.12	0.49
1:A:449:TYR:HA	1:A:452:GLU:HG3	1.93	0.48
1:A:467:LYS:HZ2	6:F:304:GLU:CD	2.21	0.48
2:B:318:LEU:HD12	2:B:321:LYS:HZ2	1.78	0.48
2:B:372:GLU:HA	2:B:375:ARG:HG2	1.94	0.48
2:B:424:TYR:HA	4:D:255:PRO:HD3	1.95	0.48
3:C:373:LEU:HD23	3:C:376:ARG:HH11	1.77	0.48
5:E:63:LEU:HA	5:E:66:CYS:HB2	1.94	0.48
6:F:93:ARG:NH2	6:F:97:TYR:OH	2.46	0.48
6:F:325:GLN:HA	6:F:328:LYS:HG2	1.95	0.48
8:I:322:ILE:HG23	12:X:479:LYS:HZ2	1.78	0.48
8:I:333:PHE:HE2	8:I:349:VAL:HG11	1.77	0.48
8:I:596:TRP:HE1	8:I:627:THR:HG1	1.57	0.48
13:S:924:GLN:OE1	13:S:939:TYR:OH	2.27	0.48
2:J:78:LYS:HD3	2:J:81:LYS:HZ3	1.78	0.48
3:K:21:TYR:HE2	4:N:226:ASN:HD21	1.58	0.48
3:K:555:VAL:O	3:K:559:ILE:HG12	2.13	0.48
8:R:448:GLN:O	8:R:450:ARG:NH1	2.46	0.48
8:R:559:GLN:HB2	8:R:567:LEU:HG	1.93	0.48
9:T:136:ILE:CD1	12:Z:410:GLU:HG3	2.43	0.48
1:A:143:ASP:OD1	1:A:151:SER:OG	2.31	0.48
3:C:21:TYR:HE2	4:D:226:ASN:HD21	1.60	0.48
3:C:493:ALA:HB2	3:C:537:ILE:HA	1.95	0.48
5:E:223:VAL:HB	5:E:246:LEU:HD22	1.94	0.48
8:I:36:THR:HG22	8:I:52:THR:HG23	1.94	0.48
8:I:370:ASP:OD1	8:I:370:ASP:N	2.46	0.48
8:I:485:ARG:HB2	8:I:503:MET:HA	1.94	0.48
13:S:255:PRO:HG3	13:S:301:PRO:HA	1.95	0.48
2:J:176:VAL:HG11	2:J:231:TRP:HB3	1.94	0.48
2:J:295:ASP:OD1	2:J:295:ASP:N	2.46	0.48
5:O:422:ASP:N	5:O:422:ASP:OD1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:P:180:LYS:HA	6:P:183:LEU:HD12	1.95	0.48
6:P:335:ARG:HH12	7:Q:340:SER:HB3	1.76	0.48
8:R:36:THR:HG22	8:R:52:THR:HG23	1.95	0.48
8:R:206:GLU:HA	8:R:229:PRO:HB3	1.94	0.48
9:T:178:GLU:HA	9:T:181:ILE:HD12	1.94	0.48
13:V:138:VAL:HG23	13:V:151:CYS:HB2	1.95	0.48
13:V:380:THR:HA	13:V:395:PRO:HA	1.95	0.48
3:C:383:ARG:HG3	3:C:386:LYS:HE3	1.95	0.48
8:I:89:ILE:O	8:I:97:GLU:N	2.46	0.48
13:S:800:PRO:O	13:S:804:ASP:HB2	2.14	0.48
1:H:466:LEU:HD22	1:H:479:LYS:HG2	1.95	0.48
2:J:27:PHE:HB2	2:J:31:PHE:HE2	1.78	0.48
5:O:54:ARG:HH21	5:O:83:LEU:HD11	1.77	0.48
8:R:249:THR:HA	8:R:264:HIS:HA	1.96	0.48
8:R:593:LYS:HB2	8:R:595:GLN:HE21	1.78	0.48
13:V:89:VAL:HB	13:V:110:PHE:HB2	1.94	0.48
13:V:829:SER:H	13:V:852:GLU:HA	1.78	0.48
13:V:867:TRP:O	13:V:870:THR:OG1	2.30	0.48
2:B:19:GLU:HA	2:B:65:LYS:HG3	1.95	0.48
13:S:581:THR:HG23	13:S:601:ILE:HG12	1.94	0.48
6:P:280:PRO:HA	6:P:283:VAL:HG22	1.94	0.48
8:R:89:ILE:O	8:R:97:GLU:N	2.46	0.48
8:R:480:VAL:HG13	8:R:488:TYR:HD1	1.77	0.48
13:V:447:VAL:HB	13:V:499:GLN:HA	1.94	0.48
13:V:939:TYR:HD1	13:V:944:MET:HG3	1.79	0.48
1:A:309:ARG:NH2	1:A:378:ASP:HB3	2.29	0.48
2:B:186:GLN:C	2:B:188:PRO:HD3	2.38	0.48
8:I:350:ALA:HB2	8:I:378:LEU:HD22	1.95	0.48
13:S:7:LYS:HE2	13:S:9:ILE:HG13	1.95	0.48
13:S:499:GLN:HG3	13:S:500:ARG:HD3	1.95	0.48
13:S:514:HIS:HB3	13:S:523:ARG:HG2	1.96	0.48
13:S:778:LEU:C	13:S:780:GLY:H	2.21	0.48
2:J:19:GLU:HA	2:J:65:LYS:HG3	1.95	0.48
3:K:398:ASP:N	3:K:398:ASP:OD1	2.47	0.48
8:R:130:ILE:HG22	8:R:138:ARG:HB3	1.96	0.48
8:R:347:LEU:HB3	8:R:358:TYR:HB2	1.95	0.48
13:V:1083:VAL:HA	13:V:1086:VAL:HG12	1.96	0.48
2:B:337:GLU:OE2	3:C:454:ASN:ND2	2.47	0.48
3:C:122:SER:HA	3:C:125:GLN:HG2	1.95	0.48
6:F:78:VAL:HG11	6:F:83:LEU:HD11	1.96	0.48
8:I:431:VAL:HB	8:I:442:ARG:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:554:TYR:CZ	13:S:600:LEU:HD13	2.48	0.48
1:H:181:LEU:HA	1:H:184:MET:HG3	1.95	0.48
1:H:670:HIS:NE2	1:H:679:CYS:SG	2.84	0.48
3:K:132:ARG:NH2	3:K:156:GLU:OE1	2.47	0.48
3:K:460:PHE:O	3:K:466:TYR:OH	2.23	0.48
5:O:14:THR:OG1	5:O:17:ALA:O	2.32	0.48
6:P:44:ILE:HD11	6:P:68:PHE:HZ	1.78	0.48
7:Q:209:TYR:O	7:Q:213:GLN:NE2	2.34	0.48
8:R:505:ASP:OD1	8:R:505:ASP:N	2.46	0.48
8:R:517:SER:HG	8:R:566:CYS:HG	1.60	0.48
12:Z:409:ARG:CZ	12:Z:410:GLU:OE1	2.62	0.48
13:V:471:ARG:HH21	13:V:473:GLN:HG3	1.79	0.48
13:V:508:ASP:OD1	13:V:512:HIS:N	2.46	0.48
13:V:652:TYR:CD2	13:V:692:MET:HE2	2.48	0.48
1:A:280:LEU:HD11	1:A:303:ASN:OD1	2.14	0.48
2:B:186:GLN:O	2:B:188:PRO:CD	2.61	0.48
2:B:426:MET:HE1	4:D:287:ASP:H	1.76	0.48
5:E:282:ASP:OD1	5:E:288:ARG:NH1	2.46	0.48
6:F:169:LEU:HA	6:F:172:LYS:HE2	1.95	0.48
8:I:437:SER:OG	8:I:461:GLU:OE2	2.30	0.48
8:I:596:TRP:CE2	12:X:503:LEU:HD11	2.49	0.48
9:L:161:ARG:HA	9:L:164:ARG:HE	1.77	0.48
13:S:198:GLN:NE2	13:S:200:VAL:O	2.47	0.48
1:H:268:LEU:O	1:H:272:ARG:HG2	2.13	0.48
1:H:511:TYR:CZ	1:H:515:LEU:HD11	2.48	0.48
3:K:543:THR:HA	3:K:546:CYS:HB2	1.95	0.48
8:R:479:ILE:HB	8:R:487:LEU:HD11	1.95	0.48
11:Y:122:ILE:HD11	12:Z:495:ASN:HA	1.94	0.48
13:V:514:HIS:HB3	13:V:523:ARG:HG2	1.96	0.48
13:V:729:ILE:HB	13:V:750:TRP:HE1	1.78	0.48
1:A:434:GLU:O	1:A:438:LYS:N	2.45	0.48
2:B:53:LEU:HB3	2:B:54:ARG:HH11	1.77	0.48
2:B:427:GLY:N	4:D:254:PRO:O	2.41	0.48
3:C:260:LYS:HA	3:C:285:ILE:HD11	1.95	0.48
5:E:132:GLN:HA	5:E:140:LEU:HD11	1.96	0.48
6:F:252:TYR:HB3	7:G:257:MET:HE3	1.95	0.48
8:I:645:ARG:HH22	13:V:725:TRP:CD1	2.31	0.48
8:I:700:ALA:HA	8:I:703:HIS:HB3	1.94	0.48
9:L:204:ARG:NE	10:M:378:ASN:HB3	2.28	0.48
2:J:186:GLN:O	2:J:188:PRO:CD	2.61	0.48
3:K:275:ASP:O	3:K:279:LEU:N	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:474:GLU:HA	3:K:477:VAL:HB	1.96	0.48
5:O:129:HIS:HA	5:O:132:GLN:HG2	1.95	0.48
7:Q:150:ILE:HA	7:Q:153:VAL:HG22	1.96	0.48
8:R:211:LYS:HG2	8:R:222:GLN:HA	1.95	0.48
8:R:518:ALA:HB3	8:R:527:TRP:HZ3	1.78	0.48
13:V:30:ARG:NH1	13:V:77:SER:O	2.47	0.48
1:A:210:ALA:O	1:A:214:ASN:ND2	2.47	0.48
2:B:7:GLU:O	2:B:39:ARG:N	2.47	0.48
4:D:318:MET:O	4:D:322:ASN:ND2	2.47	0.48
8:I:489:LEU:N	8:I:498:ALA:O	2.41	0.48
13:S:384:GLY:HA3	13:S:391:LEU:HD23	1.95	0.48
5:O:13:ARG:HH11	5:O:18:GLN:HG2	1.79	0.48
6:P:210:LEU:O	6:P:213:GLN:HG2	2.14	0.48
8:R:587:LEU:HD11	8:R:615:LEU:HD13	1.95	0.48
9:T:235:PRO:HD2	9:T:237:TYR:CZ	2.48	0.48
11:Y:77:ALA:O	11:Y:80:SER:OG	2.25	0.48
6:F:127:GLU:HA	6:F:130:ASN:HB2	1.95	0.48
6:F:186:LYS:O	6:F:190:ALA:HB2	2.14	0.48
1:H:542:GLU:OE2	1:H:545:HIS:ND1	2.47	0.48
1:H:658:ASN:O	1:H:662:ALA:N	2.45	0.48
3:K:432:SER:O	3:K:435:GLU:HG2	2.14	0.48
7:Q:271:GLU:HA	7:Q:274:THR:HG22	1.96	0.48
13:V:549:ASN:HA	13:V:566:PRO:HA	1.96	0.48
1:A:228:GLY:HA2	1:A:231:HIS:CD2	2.48	0.47
3:C:96:MET:O	3:C:100:ALA:N	2.34	0.47
13:S:373:LEU:HD23	13:S:386:LEU:HG	1.94	0.47
13:S:664:LEU:HD11	13:S:694:GLN:HE21	1.79	0.47
13:S:874:MET:HG3	13:S:878:ILE:HG23	1.95	0.47
13:S:960:ALA:HB2	13:S:963:ARG:HH21	1.79	0.47
1:H:143:ASP:HA	1:H:149:ILE:HD11	1.96	0.47
13:V:531:GLN:N	13:V:545:GLN:O	2.41	0.47
13:V:560:ASP:OD1	13:V:561:ASN:N	2.47	0.47
13:V:849:ALA:O	13:V:850:ARG:HD3	2.14	0.47
1:A:148:ASP:H	1:A:197:MET:HG3	1.80	0.47
1:A:308:ASP:N	1:A:308:ASP:OD1	2.44	0.47
1:A:483:LEU:HA	1:A:486:ARG:HB2	1.95	0.47
2:B:187:LYS:NZ	2:B:261:ALA:HB1	2.29	0.47
4:D:219:GLN:HA	4:D:222:ILE:HD12	1.96	0.47
5:E:14:THR:OG1	5:E:17:ALA:O	2.33	0.47
8:I:153:TRP:HA	8:I:160:LEU:HG	1.96	0.47
8:I:202:ILE:HG22	8:I:212:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:259:ARG:O	1:H:263:MET:HG3	2.14	0.47
6:P:78:VAL:HG11	6:P:83:LEU:HD11	1.96	0.47
11:Y:109:GLN:HA	11:Y:112:ILE:HD12	1.95	0.47
13:V:498:ASN:HD21	13:V:502:THR:H	1.60	0.47
1:A:155:ASN:OD1	1:A:156:ALA:N	2.47	0.47
1:A:449:TYR:CD1	1:A:449:TYR:C	2.91	0.47
3:C:221:ASP:OD1	3:C:221:ASP:N	2.44	0.47
5:E:43:ILE:HA	5:E:46:LEU:HB2	1.96	0.47
6:F:335:ARG:HH12	7:G:340:SER:HB3	1.80	0.47
8:I:252:LEU:HA	8:I:252:LEU:HD12	1.74	0.47
8:I:300:LEU:HB2	8:I:311:VAL:HB	1.96	0.47
8:I:480:VAL:HG13	8:I:488:TYR:HD1	1.79	0.47
13:S:709:GLN:OE1	13:S:711:LYS:NZ	2.46	0.47
1:H:576:GLY:HA3	2:J:272:LEU:HD23	1.95	0.47
2:J:7:GLU:O	2:J:39:ARG:N	2.46	0.47
8:R:211:LYS:HE2	8:R:222:GLN:HG3	1.96	0.47
8:R:275:SER:O	8:R:284:ALA:N	2.48	0.47
9:T:239:ASP:O	9:T:242:GLU:HG3	2.13	0.47
11:Y:108:GLU:O	11:Y:112:ILE:HG13	2.14	0.47
13:V:554:TYR:CZ	13:V:600:LEU:HD13	2.50	0.47
1:A:577:VAL:HA	1:A:580:ARG:HE	1.79	0.47
5:E:223:VAL:HA	5:E:226:LYS:HE2	1.97	0.47
8:I:322:ILE:HG23	12:X:479:LYS:NZ	2.29	0.47
13:S:342:ILE:HG12	13:S:353:VAL:HG22	1.95	0.47
13:S:493:ASP:OD1	13:S:494:TRP:N	2.47	0.47
13:S:899:GLN:HG2	13:S:900:PHE:H	1.80	0.47
1:H:352:LYS:N	1:H:354:GLU:OE1	2.47	0.47
3:K:219:ASN:HA	3:K:265:ASP:HA	1.97	0.47
8:R:366:PRO:HG2	8:R:368:ILE:HD11	1.95	0.47
9:T:277:GLN:HA	9:T:280:MET:HG3	1.96	0.47
1:A:283:PHE:O	1:A:287:MET:HG2	2.13	0.47
1:A:304:TYR:CD2	1:A:376:LYS:HE3	2.48	0.47
12:X:409:ARG:HA	12:X:412:VAL:HG22	1.96	0.47
1:H:308:ASP:OD1	1:H:308:ASP:N	2.47	0.47
3:K:298:LEU:HD23	3:K:301:LEU:HD12	1.97	0.47
5:O:183:ASP:H	5:O:186:ARG:HB2	1.80	0.47
6:P:83:LEU:HA	6:P:86:GLN:HG3	1.97	0.47
6:P:224:ILE:HG22	7:Q:229:VAL:HG22	1.97	0.47
7:Q:272:TYR:HA	7:Q:275:LEU:HD12	1.96	0.47
8:R:277:THR:N	8:R:282:GLN:O	2.39	0.47
8:R:389:ASP:OD1	8:R:389:ASP:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:R:433:ASP:OD1	8:R:435:GLN:NE2	2.47	0.47
13:V:639:ALA:HB1	13:V:648:ALA:HA	1.96	0.47
1:A:437:VAL:HG13	1:A:440:ARG:HH21	1.79	0.47
3:C:207:ALA:HA	3:C:210:GLU:HG3	1.96	0.47
3:C:555:VAL:O	3:C:559:ILE:HG12	2.14	0.47
7:G:146:LYS:HB3	7:G:147:ARG:NH2	2.30	0.47
7:G:264:MET:HE1	7:G:269:ARG:HG2	1.97	0.47
8:I:182:TRP:HE1	8:I:184:ALA:HB2	1.78	0.47
12:X:499:LEU:HA	12:X:502:LEU:HG	1.96	0.47
13:S:372:TYR:HB3	13:S:383:MET:HE1	1.95	0.47
1:H:270:PHE:HD2	1:H:279:ALA:HB2	1.78	0.47
8:R:756:SER:HB3	8:R:763:ARG:HH12	1.79	0.47
13:V:159:TYR:HB3	13:V:177:MET:HB2	1.96	0.47
1:A:576:GLY:HA3	2:B:272:LEU:HD23	1.96	0.47
3:C:169:ALA:O	3:C:173:LEU:HB3	2.14	0.47
3:C:599:SER:HA	3:C:602:GLU:HG2	1.97	0.47
5:E:13:ARG:NH2	5:E:16:VAL:O	2.48	0.47
8:I:82:CYS:SG	8:I:83:THR:N	2.83	0.47
8:I:95:ARG:NE	8:I:97:GLU:OE2	2.48	0.47
8:I:153:TRP:CE3	8:I:160:LEU:HD11	2.50	0.47
8:I:158:ASP:OD1	8:I:158:ASP:N	2.42	0.47
8:I:568:VAL:HG22	8:I:576:VAL:HB	1.96	0.47
8:I:593:LYS:HE2	8:I:595:GLN:NE2	2.30	0.47
9:L:16:LEU:O	9:L:45:ARG:NE	2.47	0.47
13:S:12:PRO:HG3	13:S:314:ALA:HB2	1.96	0.47
13:S:399:ASP:OD1	13:S:399:ASP:N	2.44	0.47
1:H:136:LEU:HD11	1:H:158:GLU:HG3	1.97	0.47
1:H:544:ILE:HG21	1:H:566:LEU:HD22	1.97	0.47
2:J:57:HIS:HA	2:J:79:PHE:HZ	1.79	0.47
5:O:69:HIS:NE2	5:O:187:SER:OG	2.43	0.47
5:O:347:GLN:HG2	5:O:368:CYS:HB2	1.96	0.47
6:P:222:THR:O	6:P:226:THR:HG23	2.15	0.47
8:R:20:VAL:HG12	8:R:30:THR:HG22	1.95	0.47
8:R:460:LEU:HB3	8:R:482:ASP:HB2	1.96	0.47
8:R:725:GLU:OE1	8:R:731:MET:HE3	2.15	0.47
8:R:730:PHE:O	8:R:734:ASN:ND2	2.38	0.47
9:T:5:GLU:HG2	9:T:94:VAL:HG21	1.96	0.47
13:V:415:HIS:HA	13:V:420:LEU:HA	1.96	0.47
2:B:92:GLU:O	2:B:97:LYS:NZ	2.41	0.47
3:C:543:THR:HA	3:C:546:CYS:HB2	1.97	0.47
8:I:218:ARG:HH21	8:I:219:LEU:HB3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:341:VAL:O	13:S:354:LEU:N	2.40	0.47
13:S:402:GLU:HG2	13:S:414:VAL:HB	1.97	0.47
13:S:836:TYR:HB2	13:S:845:ALA:HB2	1.96	0.47
2:J:111:MET:HE1	2:J:185:VAL:HG13	1.97	0.47
8:R:207:ASP:OD1	8:R:207:ASP:N	2.43	0.47
13:V:978:TYR:HD2	13:V:1001:ALA:HA	1.80	0.47
13:V:998:TYR:OH	13:V:1008:LYS:NZ	2.46	0.47
1:A:208:TYR:HB3	1:A:223:LEU:HD11	1.96	0.47
3:C:223:MET:N	3:C:223:MET:SD	2.88	0.47
13:S:698:GLN:O	13:S:702:SER:N	2.39	0.47
13:S:719:TYR:HD2	13:S:728:ALA:HA	1.80	0.47
13:S:867:TRP:O	13:S:870:THR:OG1	2.31	0.47
2:J:180:GLY:HA2	2:J:223:SER:HB2	1.97	0.47
5:O:63:LEU:HA	5:O:66:CYS:HB2	1.96	0.47
8:R:519:MET:HE1	8:R:552:PHE:CD2	2.49	0.47
11:Y:72:LEU:O	11:Y:76:VAL:HG13	2.15	0.47
13:V:324:ARG:HH22	13:V:332:GLU:HB2	1.80	0.47
13:V:459:LYS:HG3	13:V:475:LEU:HB2	1.97	0.47
13:V:577:HIS:HE1	13:V:582:GLU:HG2	1.80	0.47
13:V:874:MET:HE2	13:V:894:ALA:HB3	1.96	0.47
1:A:227:MET:SD	1:A:243:MET:SD	3.12	0.47
2:B:295:ASP:H	2:B:298:SER:HG	1.63	0.47
8:I:216:PHE:HZ	13:V:547:ARG:HH22	1.63	0.47
8:I:277:THR:N	8:I:282:GLN:O	2.39	0.47
3:K:458:THR:O	3:K:462:GLN:N	2.46	0.47
3:K:559:ILE:HD12	3:K:606:PHE:HB2	1.95	0.47
5:O:461:TYR:OH	5:O:496:TYR:OH	2.32	0.47
6:P:186:LYS:O	6:P:190:ALA:HB2	2.15	0.47
7:Q:180:ASP:OD1	7:Q:181:LEU:N	2.48	0.47
7:Q:195:TYR:HA	7:Q:198:VAL:HG22	1.97	0.47
1:A:511:TYR:CZ	1:A:515:LEU:HD11	2.50	0.46
2:B:140:ASN:HD21	2:B:256:LEU:HD12	1.79	0.46
3:C:153:MET:HE2	3:C:158:LYS:HD2	1.97	0.46
3:C:243:PHE:HA	3:C:246:LYS:HG2	1.96	0.46
5:E:7:ARG:HH12	5:E:256:ASP:HB3	1.81	0.46
5:E:196:TYR:HB3	5:E:204:VAL:HG13	1.96	0.46
6:F:217:GLU:HG3	7:G:222:ASN:CG	2.39	0.46
6:F:306:ASP:N	6:F:306:ASP:OD1	2.45	0.46
8:I:27:GLU:HB3	8:I:92:ARG:NH2	2.29	0.46
8:I:275:SER:O	8:I:284:ALA:N	2.48	0.46
8:I:692:ASN:H	13:V:662:ARG:H	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L:221:GLU:O	9:L:225:LYS:HG2	2.15	0.46
1:H:311:GLY:O	1:H:315:ALA:HB3	2.15	0.46
2:J:186:GLN:C	2:J:188:PRO:HD3	2.39	0.46
3:K:573:THR:HA	3:K:576:TYR:HB2	1.97	0.46
5:O:14:THR:HG23	5:O:18:GLN:HE22	1.80	0.46
5:O:173:ILE:HG13	5:O:176:ARG:HH21	1.80	0.46
8:R:129:LYS:HA	8:R:140:THR:HA	1.96	0.46
8:R:227:ASP:OD1	8:R:227:ASP:N	2.48	0.46
9:T:107:ALA:HA	11:Y:59:VAL:HG21	1.97	0.46
13:V:402:GLU:HG3	13:V:416:TYR:HB2	1.96	0.46
13:V:916:MET:HB3	13:V:920:ARG:HH12	1.80	0.46
1:A:670:HIS:HE1	1:A:676:ASN:HB3	1.80	0.46
2:B:391:TYR:OH	5:E:26:LYS:NZ	2.33	0.46
2:B:432:GLY:H	4:D:254:PRO:HB3	1.80	0.46
8:I:129:LYS:HA	8:I:140:THR:HA	1.97	0.46
8:I:514:ALA:HB1	8:I:530:PRO:HG3	1.96	0.46
8:I:598:LYS:HE2	12:X:496:ASP:CG	2.40	0.46
13:S:415:HIS:HD2	13:S:420:LEU:HB2	1.80	0.46
2:J:116:ASP:OD1	2:J:116:ASP:N	2.48	0.46
2:J:394:MET:HB2	2:J:404:LEU:HD11	1.96	0.46
2:J:427:GLY:N	4:N:254:PRO:O	2.36	0.46
5:O:349:VAL:O	5:O:352:SER:OG	2.28	0.46
8:R:577:SER:HB2	11:Y:97:LYS:NZ	2.31	0.46
9:T:200:GLU:O	9:T:204:ARG:HG2	2.16	0.46
13:V:8:SER:OG	13:V:316:ASP:OD2	2.32	0.46
13:V:616:VAL:HG12	13:V:632:TRP:HZ3	1.80	0.46
13:V:791:MET:HE1	13:V:822:LEU:HB2	1.96	0.46
13:V:816:TYR:HE2	13:V:834:GLN:HB3	1.80	0.46
1:A:471:TYR:HB3	6:F:182:ARG:HH22	1.80	0.46
1:A:482:VAL:O	1:A:486:ARG:N	2.43	0.46
2:B:133:LEU:HD22	2:B:176:VAL:HG22	1.98	0.46
7:G:233:LEU:HD22	7:G:236:ARG:HH21	1.80	0.46
8:I:479:ILE:HB	8:I:487:LEU:HD11	1.97	0.46
9:L:96:GLU:OE2	9:L:99:LYS:NZ	2.34	0.46
12:X:485:ILE:O	12:X:489:LYS:HG2	2.15	0.46
2:J:67:LYS:NZ	2:J:101:ASN:OD1	2.48	0.46
2:J:106:LEU:O	2:J:111:MET:N	2.42	0.46
8:R:254:ASP:HB2	8:R:260:TYR:HE1	1.79	0.46
9:T:221:GLU:O	9:T:225:LYS:HG2	2.15	0.46
9:T:240:GLU:HA	9:T:243:ARG:HB2	1.98	0.46
13:V:82:ILE:HB	13:V:90:PHE:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:V:758:GLU:HG2	13:V:777:TYR:HA	1.98	0.46
2:B:106:LEU:O	2:B:111:MET:N	2.47	0.46
2:B:203:ASN:HB2	2:B:265:ASP:HB3	1.98	0.46
3:C:398:ASP:OD1	3:C:398:ASP:N	2.46	0.46
5:E:363:GLN:HG3	5:E:395:PHE:HZ	1.80	0.46
7:G:143:LEU:HG	7:G:147:ARG:NH1	2.31	0.46
8:I:200:LEU:HB2	8:I:255:ARG:HH11	1.80	0.46
9:L:166:ARG:HB3	10:M:344:LYS:HG2	1.97	0.46
11:W:115:LYS:HG2	12:X:495:ASN:ND2	2.31	0.46
1:H:228:GLY:HA2	1:H:231:HIS:CD2	2.50	0.46
1:H:304:TYR:CD2	2:J:296:TRP:HZ2	2.33	0.46
2:J:365:LEU:HD22	4:N:225:ILE:HG23	1.96	0.46
3:K:297:LYS:HA	3:K:300:PHE:HD2	1.80	0.46
5:O:128:PHE:CE1	5:O:143:TYR:HB3	2.50	0.46
5:O:178:LEU:HG	5:O:182:ARG:HH21	1.81	0.46
9:T:280:MET:O	9:T:283:GLN:HG3	2.16	0.46
13:V:540:ASP:OD1	13:V:540:ASP:N	2.46	0.46
13:V:795:ASN:OD1	13:V:796:VAL:N	2.48	0.46
13:V:924:GLN:OE1	13:V:939:TYR:OH	2.30	0.46
2:B:94:GLY:HA3	2:B:115:ASN:HA	1.98	0.46
2:B:388:ASP:HA	2:B:392:TYR:HB3	1.98	0.46
3:C:559:ILE:HD12	3:C:606:PHE:HB2	1.97	0.46
7:G:225:GLN:O	7:G:229:VAL:HG23	2.15	0.46
8:I:398:THR:HG22	8:I:402:ARG:H	1.81	0.46
13:S:218:ALA:HB2	13:S:224:VAL:HG22	1.98	0.46
13:S:616:VAL:HG12	13:S:632:TRP:HZ3	1.81	0.46
13:S:652:TYR:CD2	13:S:692:MET:HE2	2.50	0.46
13:S:957:LYS:HG2	13:S:960:ALA:HB3	1.98	0.46
2:J:312:ILE:HB	3:K:589:ALA:HB1	1.98	0.46
6:P:196:LYS:HG3	6:P:198:PRO:HD3	1.97	0.46
6:P:272:ARG:HA	6:P:275:VAL:HG12	1.97	0.46
8:R:186:ASP:OD1	8:R:186:ASP:N	2.48	0.46
3:C:458:THR:O	3:C:462:GLN:N	2.47	0.46
8:I:68:LYS:HG3	8:I:73:GLY:HA2	1.96	0.46
11:W:117:GLU:HG2	13:V:756:GLN:HG2	1.97	0.46
13:S:363:GLU:OE1	13:S:376:ARG:NH1	2.48	0.46
13:S:402:GLU:HG3	13:S:416:TYR:HB2	1.97	0.46
6:P:238:TYR:HE2	7:Q:239:LEU:HB3	1.80	0.46
13:V:140:LEU:HD21	13:V:186:PHE:HE1	1.80	0.46
1:A:189:PHE:HE2	2:B:309:THR:HG23	1.81	0.46
2:B:106:LEU:HA	2:B:109:PHE:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:291:ASP:N	2:B:291:ASP:OD1	2.43	0.46
5:E:14:THR:HG23	5:E:18:GLN:HE22	1.79	0.46
6:F:328:LYS:HA	6:F:331:GLN:HG3	1.97	0.46
8:I:347:LEU:N	8:I:358:TYR:O	2.38	0.46
11:W:56:ASP:CA	11:W:59:VAL:HG22	2.40	0.46
12:X:407:SER:O	12:X:411:LEU:HG	2.16	0.46
13:S:1069:GLN:NE2	13:S:1073:GLN:OE1	2.49	0.46
1:H:257:GLU:OE1	3:K:646:ARG:NH2	2.45	0.46
2:J:54:ARG:HH21	2:J:76:LEU:HA	1.80	0.46
3:K:428:MET:HG2	3:K:430:LEU:HG	1.97	0.46
8:R:80:VAL:O	8:R:88:LYS:N	2.47	0.46
9:T:16:LEU:O	9:T:45:ARG:NE	2.48	0.46
9:T:110:LYS:HE3	12:Z:436:MET:HG2	1.97	0.46
9:T:134:LYS:NZ	10:U:311:ASP:OD2	2.34	0.46
13:V:945:ALA:HB3	13:V:969:LEU:HD23	1.97	0.46
1:A:231:HIS:HD2	1:A:243:MET:SD	2.37	0.46
2:B:330:ASN:HD21	3:C:548:LYS:HB2	1.80	0.46
5:E:5:LYS:HE2	5:E:257:HIS:CE1	2.51	0.46
7:G:153:VAL:HA	7:G:156:ASN:ND2	2.31	0.46
8:I:108:ILE:HD11	9:L:2:SER:HB3	1.97	0.46
9:L:200:GLU:O	9:L:204:ARG:HG2	2.16	0.46
1:H:254:THR:OG1	1:H:255:ALA:N	2.47	0.46
1:H:283:PHE:HA	1:H:286:VAL:HG22	1.98	0.46
2:J:141:ARG:HH21	2:J:168:PHE:HA	1.80	0.46
9:T:70:ALA:HB2	9:T:83:ILE:HD11	1.97	0.46
1:A:454:GLU:OE2	10:M:443:SER:OG	2.25	0.46
2:B:71:PRO:O	2:B:75:MET:HG3	2.16	0.46
2:B:358:PRO:O	3:C:59:TYR:OH	2.33	0.46
3:C:17:THR:OG1	3:C:18:GLN:OE1	2.32	0.46
3:C:559:ILE:HG21	3:C:602:GLU:HB2	1.98	0.46
4:D:308:PHE:HE2	4:D:318:MET:HE3	1.80	0.46
5:E:125:ARG:HG3	5:E:152:GLU:HB3	1.97	0.46
6:F:210:LEU:O	6:F:214:GLN:NE2	2.49	0.46
9:L:74:LEU:O	10:M:306:TRP:NE1	2.47	0.46
10:M:398:LEU:HB3	10:M:402:LYS:NZ	2.31	0.46
13:S:412:CYS:O	13:S:423:VAL:N	2.46	0.46
13:S:422:ILE:HG13	13:S:431:LEU:HB2	1.97	0.46
13:S:545:GLN:NE2	13:S:546:SER:O	2.44	0.46
13:S:945:ALA:HB3	13:S:969:LEU:HD23	1.98	0.46
1:H:180:ASN:OD1	1:H:181:LEU:N	2.49	0.46
1:H:496:PHE:CE2	1:H:516:VAL:HG21	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:211:HIS:CE1	3:K:214:LEU:HB2	2.51	0.46
5:O:326:HIS:CD2	5:O:341:LYS:HD2	2.51	0.46
6:P:328:LYS:HA	6:P:331:GLN:HG3	1.98	0.46
8:R:153:TRP:CE3	8:R:160:LEU:HD11	2.50	0.46
8:R:158:ASP:OD1	8:R:158:ASP:N	2.43	0.46
8:R:527:TRP:HA	8:R:544:ARG:HA	1.98	0.46
8:R:539:LEU:HD12	8:R:542:LYS:HD3	1.97	0.46
8:R:729:ARG:HA	8:R:732:GLN:HG3	1.98	0.46
13:V:402:GLU:HG2	13:V:414:VAL:HB	1.98	0.46
13:V:653:ALA:HA	13:V:662:ARG:HA	1.98	0.46
1:A:306:LEU:HG	9:L:296:GLU:OE1	2.16	0.46
5:E:226:LYS:O	5:E:230:HIS:ND1	2.49	0.46
13:S:24:TRP:HZ2	13:S:317:MET:HE1	1.81	0.46
1:H:395:ARG:HG2	1:H:400:THR:HA	1.96	0.46
2:J:178:PRO:O	2:J:223:SER:OG	2.29	0.46
2:J:291:ASP:OD1	2:J:291:ASP:N	2.43	0.46
2:J:358:PRO:O	3:K:59:TYR:OH	2.34	0.46
3:K:64:ASP:OD1	3:K:65:MET:N	2.41	0.46
5:O:37:ARG:NH2	5:O:39:TYR:OH	2.49	0.46
5:O:223:VAL:HB	5:O:246:LEU:HD22	1.98	0.46
8:R:711:LEU:HD22	8:R:739:VAL:HB	1.98	0.46
13:V:12:PRO:HG3	13:V:314:ALA:HB2	1.97	0.46
13:V:511:ARG:NH1	13:V:530:CYS:O	2.45	0.46
2:B:123:HIS:CG	9:L:258:ARG:HH12	2.34	0.45
8:I:529:TYR:CD1	8:I:532:GLU:HG2	2.50	0.45
8:I:619:ALA:O	8:I:623:LYS:N	2.48	0.45
8:I:688:ILE:HG13	8:I:713:TYR:HD2	1.81	0.45
1:H:239:SER:O	1:H:242:LYS:HG2	2.16	0.45
2:J:339:PRO:HD3	3:K:419:MET:HE2	1.98	0.45
3:K:326:PHE:HB3	3:K:329:LEU:HD11	1.98	0.45
3:K:367:PHE:CE1	3:K:421:MET:HE2	2.51	0.45
5:O:274:LEU:HG	5:O:307:LEU:HD13	1.97	0.45
7:Q:166:ARG:HH21	7:Q:170:GLN:HE22	1.62	0.45
8:R:398:THR:HG22	8:R:402:ARG:H	1.81	0.45
8:R:425:SER:HB2	8:R:467:LEU:HB3	1.97	0.45
13:V:26:PRO:HA	13:V:301:PRO:HG3	1.97	0.45
1:A:270:PHE:HD2	1:A:279:ALA:HB2	1.82	0.45
1:A:578:LEU:HD23	1:A:597:TYR:HA	1.99	0.45
8:I:425:SER:OG	8:I:476:ARG:NE	2.48	0.45
8:I:458:HIS:NE2	8:I:480:VAL:HG21	2.31	0.45
8:I:510:HIS:HB2	8:I:515:MET:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:28:LYS:HA	2:J:31:PHE:HD2	1.81	0.45
2:J:120:ARG:HH22	2:J:127:LEU:HA	1.81	0.45
2:J:380:THR:OG1	4:N:234:ALA:O	2.21	0.45
3:K:541:ILE:HG23	3:K:557:ARG:NE	2.31	0.45
7:Q:137:ASN:N	7:Q:137:ASN:OD1	2.49	0.45
10:U:451:LEU:HA	10:U:454:LYS:HG2	1.98	0.45
13:V:577:HIS:CE1	13:V:582:GLU:HG2	2.51	0.45
2:B:141:ARG:HH21	2:B:168:PHE:HA	1.81	0.45
2:B:283:LYS:HZ1	10:M:457:LEU:HD22	1.82	0.45
3:C:175:TYR:H	5:E:275:GLN:HE22	1.64	0.45
3:C:275:ASP:O	3:C:279:LEU:N	2.42	0.45
5:E:13:ARG:HH11	5:E:18:GLN:HG2	1.81	0.45
5:E:54:ARG:HH21	5:E:83:LEU:HD11	1.81	0.45
5:E:326:HIS:CD2	5:E:341:LYS:HD2	2.51	0.45
8:I:76:ASP:O	8:I:92:ARG:N	2.49	0.45
9:L:124:VAL:HA	9:L:127:SER:HB3	1.98	0.45
10:M:453:ASN:HA	10:M:456:LEU:HD12	1.98	0.45
11:W:56:ASP:O	11:W:59:VAL:HG22	2.16	0.45
11:W:119:GLU:HB2	12:X:495:ASN:ND2	2.30	0.45
13:S:1053:GLU:HA	13:S:1056:LYS:HE2	1.98	0.45
1:H:600:GLU:HG2	1:H:603:ARG:HH21	1.81	0.45
1:H:659:LEU:HD22	1:H:686:LEU:HD21	1.97	0.45
2:J:76:LEU:HD11	2:J:86:ILE:HG13	1.99	0.45
3:K:187:TYR:O	3:K:192:GLN:N	2.47	0.45
5:O:377:ASP:N	5:O:377:ASP:OD1	2.49	0.45
8:R:467:LEU:O	8:R:469:GLN:NE2	2.43	0.45
13:V:1100:TRP:HA	13:V:1103:THR:HG22	1.98	0.45
1:A:139:LYS:NZ	1:A:151:SER:O	2.49	0.45
1:A:600:GLU:HA	1:A:603:ARG:HG3	1.97	0.45
2:B:371:SER:OG	2:B:374:ASN:OD1	2.31	0.45
5:E:34:LEU:HA	5:E:39:TYR:HE1	1.82	0.45
7:G:180:ASP:OD1	7:G:181:LEU:N	2.49	0.45
9:L:235:PRO:HD2	9:L:237:TYR:CE1	2.52	0.45
11:W:108:GLU:HG3	12:X:488:MET:HG3	1.97	0.45
13:S:138:VAL:HG23	13:S:151:CYS:HB2	1.97	0.45
13:S:631:GLN:HE22	13:S:635:LEU:HD11	1.81	0.45
13:S:778:LEU:C	13:S:780:GLY:N	2.74	0.45
1:H:226:ASN:O	1:H:230:ILE:HG12	2.16	0.45
1:H:309:ARG:NH2	1:H:378:ASP:HB3	2.31	0.45
2:J:123:HIS:CG	9:T:258:ARG:HH12	2.34	0.45
3:K:349:LEU:HA	3:K:352:TYR:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:312:PRO:HA	4:N:315:ARG:HB2	1.98	0.45
5:O:96:TYR:OH	5:O:184:TYR:OH	2.23	0.45
7:Q:256:SER:HA	7:Q:259:GLN:HE22	1.81	0.45
8:R:182:TRP:HE1	8:R:184:ALA:HB2	1.80	0.45
8:R:701:THR:HG23	8:R:729:ARG:HH21	1.81	0.45
9:T:122:ILE:HD11	11:Y:48:VAL:HG21	1.99	0.45
13:V:228:ASP:HB3	13:V:234:ILE:HD11	1.98	0.45
3:C:73:LEU:HD22	3:C:83:TYR:CZ	2.52	0.45
3:C:535:CYS:HA	3:C:538:ASN:ND2	2.32	0.45
8:I:685:LYS:HA	8:I:688:ILE:HG22	1.99	0.45
9:L:107:ALA:HB1	9:L:110:LYS:HB2	1.99	0.45
9:L:108:THR:HG23	11:W:59:VAL:HG23	1.98	0.45
9:L:223:GLN:O	9:L:226:ARG:HG3	2.16	0.45
11:W:121:MET:HE3	13:V:780:GLY:O	2.16	0.45
13:S:26:PRO:HA	13:S:301:PRO:HG3	1.97	0.45
13:S:469:THR:HA	13:S:487:ASN:HA	1.98	0.45
5:O:15:ASN:ND2	5:O:250:SER:O	2.48	0.45
5:O:39:TYR:HB3	5:O:43:ILE:HG13	1.99	0.45
6:P:186:LYS:HZ3	7:Q:192:LEU:HB3	1.81	0.45
8:R:63:TYR:HB2	8:R:77:VAL:O	2.17	0.45
8:R:159:GLN:HA	8:R:172:SER:HA	1.98	0.45
8:R:322:ILE:HG23	12:Z:479:LYS:HZ2	1.82	0.45
10:U:377:TYR:O	10:U:381:THR:OG1	2.25	0.45
1:A:226:ASN:O	1:A:230:ILE:HG12	2.16	0.45
2:B:210:TRP:HB3	2:B:218:ILE:HG12	1.98	0.45
3:C:71:GLU:HB2	3:C:87:TYR:CE1	2.51	0.45
5:E:377:ASP:OD1	5:E:377:ASP:N	2.49	0.45
6:F:178:GLU:O	6:F:181:GLU:HG3	2.17	0.45
8:I:63:TYR:HB2	8:I:77:VAL:O	2.16	0.45
8:I:319:VAL:HB	8:I:328:ASP:HB3	1.98	0.45
8:I:536:ASP:O	8:I:539:LEU:N	2.38	0.45
13:S:776:LEU:CD2	13:S:779:LYS:HD2	2.47	0.45
1:H:161:LYS:HZ2	1:H:165:LYS:HE3	1.81	0.45
1:H:263:MET:HG2	1:H:286:VAL:HG21	1.99	0.45
1:H:575:PRO:HG3	1:H:605:TYR:HB3	1.99	0.45
1:H:619:HIS:ND1	1:H:624:VAL:HG13	2.32	0.45
8:R:249:THR:OG1	8:R:251:GLN:OE1	2.18	0.45
8:R:601:ARG:HA	8:R:601:ARG:HD3	1.71	0.45
13:V:274:ASN:HD21	13:V:281:GLU:HG2	1.82	0.45
13:V:499:GLN:HG3	13:V:500:ARG:HD3	1.98	0.45
13:V:829:SER:O	13:V:833:MET:HE3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:548:ALA:HB2	1:A:563:TRP:HB2	1.99	0.45
2:B:95:GLU:OE1	2:B:103:ASN:ND2	2.49	0.45
2:B:180:GLY:HA2	2:B:223:SER:HB2	1.98	0.45
3:C:297:LYS:HA	3:C:300:PHE:HD2	1.82	0.45
3:C:425:TYR:HB3	3:C:430:LEU:HB2	1.98	0.45
5:E:304:ALA:HA	5:E:307:LEU:HD12	1.98	0.45
13:S:176:HIS:HB2	13:S:180:ALA:HB3	1.98	0.45
13:S:586:ASP:HA	13:S:591:THR:HA	1.97	0.45
3:K:127:ASP:OD1	3:K:127:ASP:N	2.45	0.45
3:K:143:PRO:HG2	3:K:173:LEU:HD13	1.99	0.45
3:K:367:PHE:CE1	3:K:421:MET:HB2	2.52	0.45
3:K:373:LEU:HD23	3:K:376:ARG:HH11	1.82	0.45
3:K:559:ILE:HG13	3:K:602:GLU:HG3	1.98	0.45
4:N:264:MET:HE1	4:N:267:PRO:HG3	1.97	0.45
7:Q:233:LEU:HD22	7:Q:236:ARG:HH21	1.82	0.45
8:R:13:HIS:NE2	8:R:30:THR:OG1	2.33	0.45
8:R:282:GLN:HE21	8:R:294:PHE:HB3	1.81	0.45
13:V:847:ASP:CG	13:V:860:ILE:HD13	2.41	0.45
13:V:892:LYS:HA	13:V:895:ILE:HD12	1.98	0.45
1:A:296:GLY:HA2	1:A:299:LEU:HD12	1.99	0.45
3:C:97:TYR:CZ	3:C:124:GLU:HG2	2.51	0.45
3:C:195:PRO:HA	3:C:198:LYS:HG3	1.99	0.45
6:F:321:ILE:HA	6:F:324:ILE:HG12	1.98	0.45
3:K:38:TYR:HD1	3:K:41:GLN:HE21	1.65	0.45
5:O:263:ASN:HA	5:O:266:VAL:HG22	1.99	0.45
6:P:210:LEU:O	6:P:214:GLN:NE2	2.50	0.45
6:P:262:GLU:HA	6:P:265:ASN:HD22	1.82	0.45
6:P:290:GLN:O	6:P:294:SER:N	2.49	0.45
9:T:46:TYR:CZ	9:T:104:LEU:HB2	2.51	0.45
11:Y:93:MET:O	11:Y:97:LYS:HG2	2.16	0.45
13:V:137:LYS:O	13:V:139:ARG:NH1	2.50	0.45
13:V:449:GLN:HB3	13:V:458:SER:HB2	1.97	0.45
13:V:902:LYS:O	13:V:906:ILE:HG12	2.16	0.45
1:A:477:VAL:HG13	1:A:496:PHE:CE1	2.52	0.45
1:A:489:LEU:HD12	1:A:520:LEU:HD13	1.98	0.45
1:A:493:ARG:O	1:A:497:ASN:ND2	2.50	0.45
2:B:78:LYS:HD3	2:B:81:LYS:HZ3	1.81	0.45
5:E:8:PRO:HG2	5:E:69:HIS:CG	2.52	0.45
6:F:139:LYS:HD3	6:F:139:LYS:HA	1.73	0.45
6:F:252:TYR:O	6:F:256:SER:OG	2.30	0.45
8:I:119:LEU:HB2	8:I:131:TRP:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:193:ASP:HB2	8:I:233:VAL:HG23	1.99	0.45
9:L:168:VAL:HA	9:L:171:HIS:CE1	2.52	0.45
10:M:314:HIS:HA	10:M:317:LYS:HG2	1.99	0.45
13:S:274:ASN:HD21	13:S:281:GLU:HG2	1.82	0.45
1:H:257:GLU:HB3	3:K:646:ARG:HH22	1.81	0.45
1:H:478:ASN:O	1:H:482:VAL:HG23	2.17	0.45
2:J:326:LYS:HD2	2:J:326:LYS:HA	1.74	0.45
3:K:634:GLU:O	3:K:638:LEU:N	2.48	0.45
6:P:169:LEU:HD11	7:Q:175:ASP:HB3	1.99	0.45
8:R:510:HIS:HB2	8:R:515:MET:HB2	1.99	0.45
8:R:590:MET:HB2	8:R:598:LYS:HZ1	1.82	0.45
9:T:73:MET:SD	9:T:81:LEU:HB2	2.56	0.45
11:Y:81:GLU:HA	11:Y:84:LYS:HE2	1.98	0.45
12:Z:457:GLU:O	12:Z:461:GLN:HG2	2.17	0.45
13:V:774:ILE:HA	13:V:777:TYR:HB2	1.98	0.45
13:V:848:LEU:HD23	13:V:860:ILE:HD11	1.97	0.45
1:A:444:ASN:ND2	2:B:287:GLN:OE1	2.50	0.45
3:C:634:GLU:O	3:C:638:LEU:N	2.49	0.45
4:D:266:MET:HE2	4:D:271:VAL:HG22	1.98	0.45
6:F:290:GLN:O	6:F:294:SER:N	2.50	0.45
8:I:69:LYS:NZ	8:I:155:TYR:OH	2.35	0.45
13:S:693:ALA:HB1	13:S:699:TRP:HB2	1.98	0.45
1:H:435:PRO:HA	1:H:438:LYS:HB2	1.99	0.45
2:J:54:ARG:NH2	2:J:75:MET:SD	2.90	0.45
2:J:427:GLY:HA2	4:N:253:TRP:HA	1.98	0.45
4:N:219:GLN:HA	4:N:222:ILE:HD12	1.99	0.45
5:O:244:LYS:NZ	5:O:248:GLU:OE1	2.38	0.45
8:R:522:GLN:HE22	8:R:554:LYS:HA	1.81	0.45
8:R:536:ASP:O	8:R:539:LEU:N	2.38	0.45
13:V:922:ILE:HA	13:V:925:HIS:HB3	1.99	0.45
3:C:150:GLY:HA2	3:C:165:LYS:HD3	1.99	0.44
5:E:4:SER:HB3	5:E:133:ARG:HE	1.81	0.44
13:S:160:VAL:HA	13:S:176:HIS:HA	1.99	0.44
1:H:258:VAL:HA	1:H:261:LYS:HD2	1.99	0.44
3:K:298:LEU:HD22	3:K:315:LEU:HD13	1.99	0.44
8:R:482:ASP:OD1	8:R:482:ASP:N	2.49	0.44
9:T:123:ASP:HA	10:U:306:TRP:N	2.32	0.44
12:Z:485:ILE:O	12:Z:489:LYS:HG2	2.17	0.44
13:V:330:LYS:O	13:V:346:LEU:N	2.43	0.44
1:A:430:PHE:HB3	1:A:433:LYS:HZ1	1.83	0.44
1:A:496:PHE:CE2	1:A:516:VAL:HG21	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:326:PHE:HB3	3:C:329:LEU:HD11	1.99	0.44
4:D:309:LYS:O	4:D:315:ARG:NH1	2.48	0.44
6:F:44:ILE:HD11	6:F:68:PHE:HZ	1.82	0.44
9:L:283:GLN:O	9:L:286:ARG:NH1	2.50	0.44
13:S:375:ALA:O	13:S:382:LEU:N	2.44	0.44
1:H:399:TYR:HB3	1:H:402:LEU:HD13	1.98	0.44
8:R:427:ASP:N	8:R:427:ASP:OD1	2.49	0.44
9:T:243:ARG:HH22	10:U:415:ALA:HA	1.82	0.44
13:V:67:ILE:H	13:V:85:SER:HB3	1.82	0.44
13:V:74:SER:OG	13:V:79:LYS:O	2.29	0.44
13:V:668:VAL:HG12	13:V:691:MET:HE1	1.98	0.44
13:V:873:GLN:NE2	13:V:875:ASP:OD1	2.51	0.44
1:A:430:PHE:O	1:A:432:LYS:N	2.51	0.44
1:A:474:ARG:NH2	1:A:508:GLU:OE1	2.50	0.44
1:A:602:HIS:HB2	1:A:611:VAL:HG11	1.98	0.44
3:C:298:LEU:HD22	3:C:315:LEU:HD13	1.99	0.44
5:E:349:VAL:O	5:E:352:SER:OG	2.30	0.44
8:I:652:THR:O	8:I:656:ARG:NH1	2.50	0.44
13:S:677:GLU:HB2	13:S:685:ALA:HA	1.98	0.44
8:R:19:ALA:HB3	8:R:31:CYS:HB2	1.98	0.44
8:R:76:ASP:O	8:R:92:ARG:N	2.49	0.44
8:R:695:ARG:HA	8:R:695:ARG:HD2	1.70	0.44
13:V:374:ILE:HG12	13:V:383:MET:SD	2.58	0.44
13:V:1080:ALA:HA	13:V:1083:VAL:HG12	2.00	0.44
3:C:54:GLY:O	3:C:70:TYR:OH	2.34	0.44
3:C:377:HIS:CD2	3:C:414:TYR:HB2	2.53	0.44
3:C:575:TYR:HA	3:C:578:LYS:HB2	1.98	0.44
4:D:273:LEU:HB3	4:D:277:THR:HB	2.00	0.44
8:I:85:GLY:O	8:I:102:GLY:N	2.34	0.44
8:I:196:PRO:HD2	8:I:197:ILE:HD12	1.99	0.44
13:S:902:LYS:O	13:S:906:ILE:HG12	2.17	0.44
5:O:26:LYS:HB3	5:O:26:LYS:HE2	1.80	0.44
5:O:282:ASP:OD1	5:O:288:ARG:NH1	2.50	0.44
8:R:69:LYS:HE2	8:R:413:ARG:HH22	1.83	0.44
8:R:153:TRP:HA	8:R:160:LEU:HG	1.99	0.44
8:R:340:VAL:HG22	8:R:349:VAL:HG23	1.99	0.44
8:R:596:TRP:CE2	12:Z:503:LEU:HD11	2.53	0.44
13:V:568:LYS:HD2	13:V:568:LYS:HA	1.76	0.44
13:V:868:LEU:HB2	13:V:877:ALA:HB2	1.98	0.44
2:B:14:SER:HB3	2:B:61:LEU:HD13	2.00	0.44
3:C:554:GLY:O	3:C:558:ILE:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:501:ALA:HB1	8:I:520:VAL:HG21	1.99	0.44
8:I:554:LYS:O	8:I:571:SER:OG	2.26	0.44
9:L:280:MET:O	9:L:283:GLN:HG3	2.18	0.44
13:S:790:VAL:HG23	13:S:791:MET:SD	2.57	0.44
13:S:1052:ARG:NH1	10:U:362:GLN:OE1	2.50	0.44
1:H:244:TYR:CZ	1:H:265:ASN:HB3	2.53	0.44
1:H:369:ALA:HA	1:H:372:LEU:HG	1.99	0.44
3:K:243:PHE:HA	3:K:246:LYS:HG2	1.99	0.44
3:K:596:LYS:O	3:K:599:SER:OG	2.33	0.44
5:O:5:LYS:HG2	5:O:105:GLY:HA2	2.00	0.44
8:R:432:LEU:HD23	8:R:434:GLN:HG3	2.00	0.44
8:R:456:TRP:HE1	8:R:458:HIS:CE1	2.36	0.44
9:T:101:ALA:O	9:T:105:TYR:HB2	2.17	0.44
11:Y:119:GLU:HB2	12:Z:495:ASN:HD21	1.81	0.44
13:V:412:CYS:O	13:V:423:VAL:N	2.49	0.44
13:V:748:LEU:O	13:V:752:LEU:HB3	2.17	0.44
5:E:1:MET:HB2	5:E:191:TYR:HD1	1.83	0.44
6:F:170:LYS:HD2	6:F:170:LYS:HA	1.80	0.44
8:I:340:VAL:HG22	8:I:349:VAL:HG23	2.00	0.44
9:L:299:LEU:O	9:L:303:ARG:N	2.51	0.44
12:X:455:ALA:HA	12:X:458:LEU:HG	2.00	0.44
1:H:208:TYR:HB3	1:H:223:LEU:HD11	1.98	0.44
1:H:519:ARG:HE	2:J:279:ALA:HB1	1.83	0.44
2:J:53:LEU:HB3	2:J:54:ARG:HH11	1.82	0.44
3:K:50:LEU:HB3	3:K:73:LEU:HD21	1.98	0.44
3:K:73:LEU:HD22	3:K:83:TYR:CZ	2.52	0.44
3:K:367:PHE:HE1	3:K:421:MET:HE2	1.82	0.44
4:N:266:MET:HE2	4:N:271:VAL:HG13	1.98	0.44
5:O:36:LYS:HA	5:O:217:PRO:HD2	2.00	0.44
5:O:310:ASP:N	5:O:310:ASP:OD1	2.50	0.44
8:R:196:PRO:HD2	8:R:197:ILE:HD12	2.00	0.44
8:R:525:CYS:HB2	8:R:544:ARG:HE	1.83	0.44
10:U:434:ASP:HA	10:U:437:VAL:HG22	1.99	0.44
1:A:273:MET:SD	1:A:273:MET:N	2.87	0.44
1:A:399:TYR:HB3	1:A:402:LEU:HD13	1.99	0.44
3:C:169:ALA:O	3:C:173:LEU:HB2	2.17	0.44
3:C:211:HIS:CE1	3:C:214:LEU:HB2	2.52	0.44
3:C:265:ASP:OD1	3:C:265:ASP:N	2.50	0.44
5:E:266:VAL:HG21	5:E:290:ASN:HD21	1.82	0.44
6:F:213:GLN:HE21	7:G:218:LEU:HD11	1.83	0.44
12:X:457:GLU:O	12:X:461:GLN:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:X:501:LYS:O	12:X:505:MET:HG2	2.18	0.44
1:H:181:LEU:HG	1:H:185:TYR:HD2	1.83	0.44
1:H:410:LYS:HE3	1:H:413:ARG:NH2	2.33	0.44
1:H:592:ALA:HA	1:H:595:LEU:HG	2.00	0.44
3:K:169:ALA:O	3:K:173:LEU:HB2	2.18	0.44
3:K:169:ALA:O	3:K:173:LEU:HB3	2.17	0.44
3:K:283:ALA:O	3:K:287:MET:HG2	2.18	0.44
3:K:447:GLU:HB3	3:K:452:LYS:HG3	2.00	0.44
5:O:8:PRO:HG2	5:O:69:HIS:CG	2.53	0.44
7:Q:254:GLN:HA	7:Q:257:MET:HE3	2.00	0.44
8:R:343:GLY:HA3	8:R:380:GLN:NE2	2.33	0.44
8:R:440:THR:HA	8:R:457:GLN:HA	2.00	0.44
11:Y:65:GLU:HB3	12:Z:443:TRP:HB3	1.98	0.44
13:V:174:SER:HB2	13:V:182:TRP:HB2	2.00	0.44
2:B:236:GLU:O	2:B:240:ILE:N	2.49	0.44
3:C:309:PRO:HB3	3:C:344:LEU:HG	1.99	0.44
5:E:39:TYR:HB3	5:E:43:ILE:HG13	2.00	0.44
6:F:280:PRO:HA	6:F:283:VAL:HG22	2.00	0.44
7:G:315:ARG:O	7:G:319:LEU:HB2	2.17	0.44
8:I:132:SER:HB3	8:I:138:ARG:HB2	2.00	0.44
8:I:474:ASN:OD1	8:I:475:ASP:N	2.50	0.44
8:I:508:ARG:NH1	8:I:561:PHE:HB3	2.33	0.44
9:L:59:GLU:OE1	9:L:87:TYR:OH	2.29	0.44
9:L:186:ALA:HB1	10:M:363:TYR:HD2	1.83	0.44
1:H:304:TYR:O	1:H:304:TYR:CD1	2.70	0.44
4:N:242:ARG:NH2	4:N:245:GLU:HA	2.33	0.44
5:O:226:LYS:O	5:O:230:HIS:ND1	2.51	0.44
7:Q:153:VAL:HA	7:Q:156:ASN:ND2	2.33	0.44
8:R:166:SER:OG	8:R:186:ASP:O	2.32	0.44
8:R:425:SER:OG	8:R:476:ARG:NE	2.51	0.44
10:U:342:LEU:HA	10:U:345:LEU:HB2	2.00	0.44
12:Z:410:GLU:O	12:Z:414:LYS:N	2.43	0.44
13:V:819:ALA:O	13:V:822:LEU:HB3	2.18	0.44
1:A:180:ASN:OD1	1:A:181:LEU:N	2.51	0.44
1:A:369:ALA:HA	1:A:372:LEU:HG	2.00	0.44
1:A:422:LYS:HD2	1:A:422:LYS:HA	1.79	0.44
2:B:427:GLY:HA2	4:D:253:TRP:HA	2.00	0.44
6:F:275:VAL:HG22	7:G:289:PHE:CZ	2.53	0.44
13:S:1100:TRP:HA	13:S:1103:THR:HG22	1.99	0.44
1:H:303:ASN:CG	9:T:299:LEU:HD11	2.43	0.44
2:J:188:PRO:O	2:J:210:TRP:CD1	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:210:TRP:HB3	2:J:218:ILE:HG12	1.99	0.44
5:O:101:LEU:HA	5:O:104:MET:SD	2.58	0.44
8:R:347:LEU:N	8:R:358:TYR:O	2.41	0.44
8:R:395:GLN:OE1	8:R:408:ARG:NH2	2.51	0.44
8:R:627:THR:HA	8:R:630:VAL:HG12	1.99	0.44
11:Y:83:ARG:NH2	11:Y:87:GLN:OE1	2.40	0.44
13:V:489:ASP:OD1	13:V:490:THR:N	2.50	0.44
13:V:790:VAL:HG12	13:V:798:TRP:CE2	2.53	0.44
13:V:817:GLU:HA	13:V:835:SER:HB3	1.99	0.44
13:V:848:LEU:HD22	13:V:854:PRO:HA	2.00	0.44
13:V:864:TRP:HE3	13:V:880:HIS:CE1	2.36	0.44
1:A:653:TYR:HE2	1:A:665:LYS:HG2	1.83	0.43
2:B:411:LYS:HD3	2:B:415:SER:HB3	2.00	0.43
3:C:257:GLU:O	3:C:260:LYS:HB2	2.18	0.43
3:C:349:LEU:HA	3:C:352:TYR:HB2	2.00	0.43
4:D:251:GLN:HE22	4:D:253:TRP:NE1	2.15	0.43
5:E:97:SER:HB2	5:E:113:GLN:NE2	2.33	0.43
8:I:16:LEU:HD21	8:I:272:MET:HE3	2.00	0.43
8:I:282:GLN:HE21	8:I:294:PHE:HB3	1.84	0.43
1:H:304:TYR:HB2	1:H:308:ASP:OD1	2.18	0.43
6:P:322:THR:O	6:P:325:GLN:HG3	2.18	0.43
8:R:248:ASN:O	8:R:265:LEU:N	2.51	0.43
8:R:370:ASP:N	8:R:370:ASP:OD1	2.47	0.43
1:A:193:HIS:ND1	2:B:309:THR:OG1	2.51	0.43
1:A:311:GLY:O	1:A:315:ALA:HB3	2.18	0.43
1:A:677:VAL:HA	1:A:680:LEU:HD12	2.00	0.43
2:B:183:LEU:O	2:B:204:ARG:NH1	2.42	0.43
6:F:238:TYR:CE2	7:G:239:LEU:HB3	2.50	0.43
8:I:227:ASP:OD1	8:I:227:ASP:N	2.51	0.43
8:I:720:ASN:ND2	13:V:649:GLU:HG3	2.32	0.43
9:L:123:ASP:HA	10:M:306:TRP:N	2.33	0.43
11:W:83:ARG:NH1	11:W:87:GLN:HG2	2.34	0.43
1:H:198:ASN:O	1:H:200:ASN:N	2.47	0.43
3:K:517:LYS:HA	3:K:517:LYS:HD2	1.78	0.43
5:O:97:SER:HB2	5:O:113:GLN:HE22	1.83	0.43
6:P:324:ILE:HA	6:P:327:ARG:HE	1.83	0.43
8:R:398:THR:HG23	8:R:400:GLU:H	1.82	0.43
8:R:602:LEU:HB2	8:R:606:ILE:HD13	2.00	0.43
9:T:90:ASP:N	9:T:90:ASP:OD1	2.51	0.43
13:V:367:ILE:HG13	13:V:373:LEU:HA	2.00	0.43
13:V:580:ARG:HA	13:V:601:ILE:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:28:LYS:HA	2:B:31:PHE:HD2	1.83	0.43
5:E:7:ARG:HE	5:E:71:GLY:HA2	1.83	0.43
5:E:166:HIS:ND1	5:E:169:GLU:OE1	2.51	0.43
5:E:438:TYR:OH	5:E:450:ARG:NH1	2.52	0.43
7:G:195:TYR:HA	7:G:198:VAL:HG22	2.00	0.43
13:S:568:LYS:HD2	13:S:568:LYS:HA	1.76	0.43
1:H:304:TYR:CE2	2:J:296:TRP:CZ2	3.07	0.43
1:H:551:TYR:OH	1:H:559:ASN:ND2	2.46	0.43
2:J:69:THR:OG1	2:J:70:ALA:N	2.49	0.43
8:R:47:GLU:HG3	13:V:900:PHE:CE2	2.53	0.43
8:R:505:ASP:OD1	8:R:519:MET:HB3	2.19	0.43
10:U:452:ARG:NE	10:U:456:LEU:HG	2.34	0.43
1:A:390:CYS:HA	1:A:393:GLN:HE21	1.83	0.43
1:A:605:TYR:CZ	1:A:607:VAL:HB	2.53	0.43
3:C:153:MET:HE1	3:C:161:ALA:HB3	2.00	0.43
4:D:308:PHE:CE2	4:D:314:PHE:HB3	2.53	0.43
8:I:60:MET:HG2	8:I:80:VAL:HG22	1.99	0.43
13:S:758:GLU:CD	13:S:782:LEU:HB2	2.43	0.43
13:S:841:ALA:O	13:S:845:ALA:N	2.51	0.43
1:H:470:ARG:HB2	1:H:475:ALA:HB3	2.00	0.43
3:K:70:TYR:HB3	3:K:87:TYR:HB2	2.00	0.43
3:K:101:SER:HA	3:K:104:VAL:HG12	2.00	0.43
3:K:418:LEU:HD12	3:K:421:MET:SD	2.59	0.43
4:N:318:MET:O	4:N:322:ASN:ND2	2.51	0.43
5:O:138:ASP:OD1	5:O:138:ASP:N	2.51	0.43
6:P:170:LYS:HD2	6:P:170:LYS:HA	1.80	0.43
6:P:213:GLN:HE21	7:Q:218:LEU:HD11	1.83	0.43
9:T:166:ARG:HD3	9:T:166:ARG:HA	1.66	0.43
13:V:836:TYR:HB2	13:V:845:ALA:HB2	2.01	0.43
13:V:1052:ARG:C	13:V:1056:LYS:HZ2	2.26	0.43
2:B:89:LEU:HD13	2:B:221:LEU:HB2	2.00	0.43
3:C:641:MET:SD	3:C:641:MET:N	2.89	0.43
4:D:226:ASN:O	4:D:229:HIS:NE2	2.51	0.43
6:F:224:ILE:HG22	7:G:229:VAL:HG22	2.00	0.43
6:F:272:ARG:HA	6:F:275:VAL:HG12	1.99	0.43
8:I:460:LEU:HD12	8:I:460:LEU:HA	1.92	0.43
8:I:600:THR:O	8:I:604:ARG:HG2	2.17	0.43
8:I:601:ARG:HD3	8:I:601:ARG:HA	1.56	0.43
8:I:646:LYS:HD3	8:I:646:LYS:HA	1.59	0.43
9:L:53:ALA:O	9:L:62:ARG:NH2	2.47	0.43
11:W:94:LEU:HD12	11:W:94:LEU:HA	1.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:762:ALA:HB2	13:S:785:ARG:HH11	1.83	0.43
13:S:775:GLY:O	13:S:779:LYS:HG3	2.18	0.43
13:S:962:GLN:HB2	13:S:966:ARG:NH2	2.33	0.43
13:S:965:ALA:HB2	13:S:974:MET:HE2	2.00	0.43
13:S:1021:GLN:HA	13:S:1024:ARG:HB3	2.00	0.43
1:H:131:LYS:HA	1:H:131:LYS:HD3	1.83	0.43
7:Q:143:LEU:HG	7:Q:147:ARG:NH1	2.33	0.43
8:R:322:ILE:HG23	12:Z:479:LYS:NZ	2.33	0.43
9:T:136:ILE:HD13	12:Z:410:GLU:HG3	1.99	0.43
13:V:368:TYR:CD1	13:V:374:ILE:HD12	2.52	0.43
13:V:471:ARG:CZ	13:V:482:THR:HB	2.48	0.43
1:A:449:TYR:O	1:A:452:GLU:HG2	2.19	0.43
8:I:248:ASN:O	8:I:265:LEU:N	2.52	0.43
13:S:531:GLN:N	13:S:545:GLN:O	2.47	0.43
1:H:125:GLN:O	1:H:129:MET:HG2	2.19	0.43
1:H:161:LYS:HD2	1:H:161:LYS:HA	1.85	0.43
1:H:238:PRO:HA	1:H:241:ILE:HG12	2.01	0.43
3:K:309:PRO:HB3	3:K:344:LEU:HG	2.00	0.43
3:K:368:ARG:O	3:K:372:GLU:HG3	2.19	0.43
6:P:290:GLN:HA	6:P:293:LEU:HB2	2.00	0.43
7:Q:158:LYS:HA	7:Q:158:LYS:HD2	1.72	0.43
7:Q:174:MET:SD	7:Q:177:ARG:NH2	2.89	0.43
8:R:476:ARG:HA	8:R:476:ARG:HD3	1.85	0.43
2:B:188:PRO:O	2:B:210:TRP:CD1	2.71	0.43
2:B:326:LYS:HD2	2:B:326:LYS:HA	1.79	0.43
3:C:187:TYR:CD2	3:C:195:PRO:HB2	2.54	0.43
3:C:600:PHE:CD2	3:C:604:MET:HE1	2.53	0.43
6:F:10:SER:HB2	6:F:104:VAL:HG21	2.00	0.43
8:I:643:PHE:HA	13:V:695:LEU:HD23	2.01	0.43
9:L:134:LYS:HD3	9:L:134:LYS:HA	1.88	0.43
3:K:97:TYR:CZ	3:K:124:GLU:HG2	2.54	0.43
3:K:535:CYS:HA	3:K:538:ASN:ND2	2.33	0.43
5:O:355:GLU:HG2	5:O:360:PRO:HG2	2.01	0.43
8:R:60:MET:HG2	8:R:80:VAL:HG22	2.01	0.43
8:R:300:LEU:HB3	8:R:311:VAL:HB	2.00	0.43
8:R:596:TRP:HA	8:R:599:ALA:HB3	2.00	0.43
8:R:658:ALA:HB2	8:R:673:ILE:HG13	2.01	0.43
9:T:104:LEU:C	9:T:106:LYS:N	2.77	0.43
9:T:214:GLU:HA	9:T:217:LYS:HG2	2.00	0.43
11:Y:115:LYS:HG2	12:Z:495:ASN:ND2	2.34	0.43
13:V:25:ALA:HA	13:V:73:PHE:HD2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:V:609:ASP:OD2	13:V:614:ARG:NH1	2.52	0.43
1:A:130:GLU:O	1:A:134:HIS:ND1	2.51	0.43
5:E:26:LYS:HE2	5:E:26:LYS:HB3	1.83	0.43
5:E:62:TRP:HD1	5:E:63:LEU:HD22	1.84	0.43
5:E:310:ASP:OD1	5:E:310:ASP:N	2.51	0.43
8:I:691:PHE:N	13:V:665:HIS:HE1	2.16	0.43
13:S:489:ASP:OD1	13:S:490:THR:N	2.50	0.43
13:S:816:TYR:HE2	13:S:834:GLN:HB3	1.84	0.43
1:H:507:VAL:O	1:H:511:TYR:HB3	2.19	0.43
1:H:541:VAL:HA	1:H:544:ILE:HD13	1.99	0.43
1:H:574:ASP:OD2	1:H:577:VAL:N	2.46	0.43
1:H:595:LEU:HA	1:H:598:TYR:CD2	2.53	0.43
2:J:95:GLU:OE1	2:J:103:ASN:ND2	2.52	0.43
2:J:133:LEU:HD22	2:J:176:VAL:HG22	2.01	0.43
3:K:153:MET:HE1	3:K:161:ALA:HB3	2.01	0.43
8:R:522:GLN:NE2	8:R:553:GLY:O	2.51	0.43
10:U:417:PRO:HA	10:U:420:ARG:NE	2.34	0.43
13:V:9:ILE:HG21	13:V:43:PHE:CE2	2.54	0.43
13:V:176:HIS:HB2	13:V:180:ALA:HB3	2.00	0.43
13:V:555:SER:N	13:V:627:GLU:OE1	2.31	0.43
1:A:130:GLU:HG3	1:A:134:HIS:CE1	2.54	0.43
1:A:192:ALA:N	1:A:208:TYR:OH	2.52	0.43
1:A:395:ARG:HG2	1:A:400:THR:HA	2.00	0.43
1:A:435:PRO:HA	1:A:438:LYS:HB2	2.00	0.43
3:C:485:LEU:HD21	3:C:519:GLU:HA	2.01	0.43
3:C:528:ASP:OD1	3:C:528:ASP:N	2.49	0.43
3:C:596:LYS:HD2	3:C:596:LYS:HA	1.88	0.43
3:C:601:THR:HA	3:C:604:MET:HE2	2.01	0.43
7:G:150:ILE:HA	7:G:153:VAL:HG22	2.01	0.43
8:I:29:PHE:CZ	8:I:39:LYS:HE2	2.54	0.43
8:I:166:SER:OG	8:I:186:ASP:O	2.34	0.43
8:I:377:LEU:HD12	8:I:419:ALA:HB2	2.01	0.43
9:L:122:ILE:HD11	11:W:48:VAL:HG21	2.00	0.43
11:W:66:LYS:NZ	11:W:73:ARG:HH22	2.17	0.43
13:S:939:TYR:HE2	13:S:951:MET:HE1	1.84	0.43
1:H:475:ALA:HA	1:H:478:ASN:HB2	2.01	0.43
1:H:577:VAL:HA	1:H:580:ARG:HE	1.84	0.43
3:K:554:GLY:O	3:K:558:ILE:HG12	2.19	0.43
5:O:50:ARG:HG2	5:O:54:ARG:HD3	2.01	0.43
8:R:130:ILE:O	8:R:138:ARG:N	2.52	0.43
9:T:186:ALA:HB2	10:U:364:ARG:NH1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:T:204:ARG:HA	9:T:204:ARG:HD3	1.88	0.43
1:A:206:ASN:OD1	1:A:207:LEU:N	2.52	0.43
1:A:225:VAL:HG21	1:A:264:ARG:HH22	1.84	0.43
1:A:447:PHE:HE2	2:B:286:LEU:HB2	1.82	0.43
6:F:16:PHE:HE1	6:F:40:VAL:HA	1.84	0.43
8:I:565:ARG:HA	8:I:579:ALA:HA	2.00	0.43
8:I:601:ARG:HG3	13:V:755:GLY:HA3	2.00	0.43
8:I:643:PHE:HB3	8:I:660:LEU:HA	2.00	0.43
8:I:655:GLY:HA2	8:I:658:ALA:HB3	2.01	0.43
9:L:26:ASN:HB2	9:L:35:VAL:HG13	2.01	0.43
11:W:79:LEU:HB3	12:X:461:GLN:HE21	1.84	0.43
11:W:121:MET:SD	12:X:499:LEU:HD13	2.59	0.43
13:S:154:HIS:CE1	13:S:156:GLU:HB2	2.54	0.43
1:H:444:ASN:ND2	2:J:287:GLN:OE1	2.51	0.43
1:H:619:HIS:CG	1:H:628:ALA:HB2	2.54	0.43
3:K:637:MET:HE2	3:K:640:LYS:HZ1	1.83	0.43
8:R:103:HIS:NE2	8:R:127:SER:O	2.51	0.43
8:R:124:GLU:HG3	9:T:2:SER:HB2	2.00	0.43
8:R:385:PHE:HE2	8:R:399:TYR:HA	1.84	0.43
9:T:208:THR:HG22	9:T:212:LYS:HZ3	1.83	0.43
13:V:878:ILE:O	13:V:882:ILE:HG12	2.19	0.43
1:A:161:LYS:HA	1:A:161:LYS:HD2	1.79	0.42
1:A:241:ILE:HG13	1:A:245:ARG:HH12	1.83	0.42
2:B:116:ASP:OD1	2:B:116:ASP:N	2.51	0.42
3:C:267:PRO:HA	3:C:268:PRO:HD3	1.88	0.42
3:C:550:ASN:OD1	3:C:550:ASN:N	2.52	0.42
5:E:260:ILE:HA	5:E:263:ASN:HD21	1.84	0.42
8:I:587:LEU:HA	8:I:590:MET:HG2	2.01	0.42
9:L:105:TYR:CE1	11:W:60:GLU:HG2	2.54	0.42
2:J:318:LEU:HD12	2:J:321:LYS:HZ3	1.84	0.42
3:K:153:MET:HE2	3:K:158:LYS:HD2	2.00	0.42
3:K:181:TYR:OH	3:K:241:GLU:HG2	2.18	0.42
5:O:438:TYR:OH	5:O:450:ARG:NH1	2.52	0.42
8:R:315:MET:HE3	8:R:316:ARG:HG2	2.01	0.42
8:R:688:ILE:CG2	8:R:706:HIS:HE1	2.28	0.42
9:T:243:ARG:NH2	10:U:414:ASP:O	2.52	0.42
13:V:198:GLN:NE2	13:V:200:VAL:O	2.52	0.42
13:V:1076:GLN:HG3	13:V:1079:ASP:H	1.84	0.42
1:A:239:SER:O	1:A:243:MET:HG3	2.20	0.42
1:A:261:LYS:HG2	1:A:264:ARG:HH21	1.84	0.42
2:B:204:ARG:NH1	2:B:205:PRO:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:266:VAL:HG21	5:E:290:ASN:ND2	2.34	0.42
11:W:125:LEU:HA	11:W:125:LEU:HD23	1.70	0.42
13:S:235:ARG:NH1	13:S:280:TRP:O	2.52	0.42
13:S:471:ARG:CZ	13:S:482:THR:HB	2.49	0.42
13:S:892:LYS:HG3	13:S:918:TYR:CE2	2.54	0.42
13:S:898:ARG:NH2	13:S:899:GLN:OE1	2.52	0.42
1:H:262:ILE:O	1:H:266:ILE:HG12	2.19	0.42
3:K:246:LYS:HA	3:K:249:ILE:HG22	2.01	0.42
5:O:213:LEU:HD11	5:O:226:LYS:HE3	2.01	0.42
5:O:436:ARG:HB3	5:O:440:MET:HE2	2.02	0.42
6:P:139:LYS:HD3	6:P:139:LYS:HA	1.71	0.42
6:P:320:GLN:O	6:P:323:GLU:HG2	2.18	0.42
8:R:458:HIS:NE2	8:R:480:VAL:HG21	2.34	0.42
9:T:186:ALA:HB1	10:U:363:TYR:HD2	1.83	0.42
13:V:71:MET:HE1	13:V:73:PHE:CE1	2.54	0.42
3:C:368:ARG:O	3:C:372:GLU:HG3	2.20	0.42
6:F:37:LEU:HD13	6:F:37:LEU:HA	1.90	0.42
6:F:322:THR:O	6:F:325:GLN:HG3	2.19	0.42
7:G:233:LEU:HD23	7:G:236:ARG:HE	1.85	0.42
7:G:256:SER:HA	7:G:259:GLN:HE22	1.84	0.42
8:I:33:ASP:OD1	9:L:7:ARG:NH2	2.29	0.42
8:I:84:ASP:OD1	8:I:84:ASP:N	2.48	0.42
8:I:130:ILE:O	8:I:138:ARG:N	2.52	0.42
8:I:398:THR:HG23	8:I:400:GLU:H	1.83	0.42
8:I:651:PRO:HB3	8:I:656:ARG:HH22	1.84	0.42
8:I:731:MET:N	8:I:731:MET:HE2	2.34	0.42
9:L:12:VAL:HG12	9:L:16:LEU:HD12	2.01	0.42
10:M:434:ASP:HA	10:M:437:VAL:HG22	2.00	0.42
13:S:919:PHE:HD2	13:S:942:ALA:HB2	1.83	0.42
1:H:210:ALA:O	1:H:214:ASN:ND2	2.52	0.42
1:H:264:ARG:HB2	2:J:303:SER:O	2.19	0.42
1:H:391:CYS:O	1:H:395:ARG:HG3	2.20	0.42
6:P:66:ILE:HD13	6:P:66:ILE:HA	1.94	0.42
6:P:122:PHE:CE2	6:P:142:ILE:HD11	2.54	0.42
8:R:248:ASN:OD1	8:R:268:THR:N	2.48	0.42
13:V:864:TRP:HE3	13:V:880:HIS:HE1	1.67	0.42
1:A:214:ASN:OD1	1:A:215:LYS:N	2.49	0.42
2:B:424:TYR:HD2	4:D:308:PHE:HE1	1.68	0.42
3:C:430:LEU:HD13	3:C:433:ASN:HD21	1.84	0.42
3:C:459:PHE:HB2	3:C:469:ALA:HB2	2.00	0.42
8:I:209:LYS:HE2	8:I:209:LYS:HB3	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:604:ARG:CZ	8:I:635:ILE:HA	2.50	0.42
8:I:646:LYS:HB3	8:I:689:LYS:HD3	2.00	0.42
8:I:648:LYS:HA	8:I:656:ARG:HH21	1.85	0.42
13:S:410:ARG:HH21	13:S:448:VAL:H	1.66	0.42
1:H:243:MET:HE3	1:H:243:MET:HB2	1.91	0.42
1:H:619:HIS:HD1	1:H:624:VAL:HG13	1.85	0.42
3:K:450:VAL:O	3:K:453:LEU:HG	2.19	0.42
6:P:186:LYS:HB3	6:P:186:LYS:HE3	1.77	0.42
8:R:593:LYS:HE2	8:R:595:GLN:NE2	2.34	0.42
9:T:161:ARG:HA	9:T:164:ARG:HE	1.84	0.42
13:V:962:GLN:HB2	13:V:966:ARG:NH2	2.34	0.42
1:A:387:PHE:HE2	1:A:413:ARG:HH12	1.67	0.42
2:B:23:HIS:CD2	2:B:23:HIS:H	2.36	0.42
2:B:157:ASP:OD1	2:B:157:ASP:N	2.53	0.42
2:B:382:LYS:HE3	5:E:23:GLU:HB3	2.00	0.42
3:C:421:MET:HA	3:C:424:ILE:HB	2.02	0.42
3:C:559:ILE:HG13	3:C:602:GLU:HG3	2.00	0.42
3:C:588:LEU:HD21	3:C:595:LEU:HD23	2.01	0.42
3:C:596:LYS:O	3:C:599:SER:OG	2.35	0.42
5:E:8:PRO:O	5:E:69:HIS:HB3	2.20	0.42
5:E:159:SER:OG	5:E:195:CYS:SG	2.72	0.42
5:E:187:SER:HB3	5:E:191:TYR:CE2	2.55	0.42
5:E:263:ASN:HA	5:E:266:VAL:HG22	2.02	0.42
8:I:658:ALA:HB2	8:I:673:ILE:HG13	2.01	0.42
10:M:444:HIS:O	10:M:447:LEU:HB3	2.19	0.42
11:W:87:GLN:O	11:W:91:GLU:HG2	2.20	0.42
13:S:577:HIS:CE1	13:S:582:GLU:HG2	2.53	0.42
13:S:1080:ALA:HA	13:S:1083:VAL:HG12	2.01	0.42
1:H:388:MET:HE2	1:H:388:MET:N	2.33	0.42
2:J:411:LYS:HB3	2:J:415:SER:HB3	2.02	0.42
7:Q:264:MET:HE1	7:Q:269:ARG:HG2	2.00	0.42
8:R:710:VAL:HG12	8:R:730:PHE:CE1	2.55	0.42
9:T:5:GLU:HG2	9:T:94:VAL:HG11	2.01	0.42
13:V:18:LYS:NZ	13:V:20:THR:HG22	2.34	0.42
13:V:1025:LEU:O	13:V:1028:GLN:NE2	2.49	0.42
1:A:522:GLU:HG2	1:A:525:TYR:HD2	1.84	0.42
1:A:546:GLN:NE2	2:B:276:ALA:HB3	2.35	0.42
2:B:294:ARG:HE	2:B:298:SER:HB2	1.85	0.42
3:C:467:LYS:HB2	3:C:467:LYS:HE2	1.83	0.42
5:E:197:CYS:SG	5:E:229:ASN:ND2	2.86	0.42
9:L:151:TYR:HA	9:L:154:LEU:HG	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:M:372:ASP:O	10:M:376:THR:OG1	2.25	0.42
1:H:148:ASP:N	1:H:197:MET:HG3	2.35	0.42
1:H:292:ASP:O	1:H:295:THR:OG1	2.38	0.42
1:H:390:CYS:HA	1:H:393:GLN:HE21	1.84	0.42
2:J:91:SER:HB2	2:J:224:CYS:HB3	2.01	0.42
13:V:631:GLN:HE22	13:V:635:LEU:HD11	1.84	0.42
13:V:783:PRO:HB2	13:V:810:LEU:HD23	2.00	0.42
13:V:960:ALA:HB2	13:V:963:ARG:HH21	1.84	0.42
1:A:479:LYS:HB3	1:A:495:LEU:HD13	2.01	0.42
1:A:595:LEU:HA	1:A:598:TYR:CD2	2.55	0.42
1:A:644:LYS:HB3	1:A:644:LYS:HE2	1.86	0.42
1:A:658:ASN:O	1:A:662:ALA:N	2.42	0.42
2:B:105:PHE:HB3	2:B:109:PHE:CD2	2.54	0.42
2:B:358:PRO:HB3	3:C:86:TYR:CZ	2.54	0.42
4:D:274:ASP:H	4:D:277:THR:HB	1.84	0.42
4:D:308:PHE:CE2	4:D:318:MET:HE3	2.54	0.42
8:I:643:PHE:CE2	8:I:663:TYR:HB3	2.54	0.42
9:L:90:ASP:N	9:L:90:ASP:OD1	2.51	0.42
9:L:260:ARG:HH12	10:M:434:ASP:C	2.28	0.42
13:S:847:ASP:OD1	13:S:848:LEU:N	2.52	0.42
13:S:915:ALA:HA	13:S:918:TYR:CD2	2.55	0.42
1:H:558:LYS:HE2	1:H:558:LYS:HB2	1.90	0.42
3:K:459:PHE:HB2	3:K:469:ALA:HB2	2.01	0.42
8:R:466:ALA:HB3	8:R:479:ILE:HD11	2.01	0.42
11:Y:113:LYS:H	11:Y:113:LYS:HD2	1.84	0.42
13:V:947:ASP:O	13:V:950:GLU:HG3	2.20	0.42
1:A:226:ASN:HA	2:B:307:PHE:CE1	2.55	0.42
2:B:400:LEU:HD21	4:D:305:TYR:HE2	1.85	0.42
5:E:33:PHE:HA	5:E:36:LYS:HD3	2.00	0.42
8:I:747:LYS:O	8:I:750:GLU:HG3	2.19	0.42
1:H:192:ALA:N	1:H:208:TYR:OH	2.53	0.42
5:O:266:VAL:HG21	5:O:290:ASN:HD21	1.84	0.42
7:Q:146:LYS:HB3	7:Q:147:ARG:NH2	2.34	0.42
8:R:121:THR:HG22	8:R:131:TRP:CZ3	2.55	0.42
11:Y:62:LEU:HD11	12:Z:436:MET:HB3	2.01	0.42
13:V:919:PHE:HD2	13:V:942:ALA:HB2	1.82	0.42
1:A:124:GLU:O	1:A:127:ARG:HD3	2.20	0.42
1:A:551:TYR:CE2	1:A:556:ASP:HB3	2.55	0.42
3:C:283:ALA:O	3:C:287:MET:HG2	2.20	0.42
3:C:316:LEU:HD13	3:C:319:TYR:HD2	1.85	0.42
5:E:295:HIS:HA	5:E:298:HIS:HD2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:129:LYS:HB2	8:I:131:TRP:CZ3	2.55	0.42
8:I:185:HIS:ND1	8:I:207:ASP:OD2	2.52	0.42
8:I:456:TRP:HE1	8:I:458:HIS:CE1	2.37	0.42
8:I:510:HIS:ND1	8:I:513:THR:OG1	2.52	0.42
10:M:398:LEU:HA	10:M:401:VAL:HG12	2.01	0.42
13:S:137:LYS:HB3	13:S:153:ALA:HA	2.01	0.42
13:S:159:TYR:O	13:S:177:MET:N	2.53	0.42
13:S:727:ASP:OD1	13:S:727:ASP:N	2.53	0.42
13:S:908:GLU:HB2	13:S:938:TYR:CZ	2.55	0.42
1:H:422:LYS:HD2	1:H:422:LYS:HA	1.81	0.42
2:J:205:PRO:HD2	2:J:266:VAL:HG23	2.01	0.42
3:K:40:LEU:HD21	3:K:50:LEU:HG	2.02	0.42
6:P:260:LEU:O	6:P:263:THR:OG1	2.30	0.42
8:R:437:SER:OG	8:R:461:GLU:OE2	2.38	0.42
9:T:114:MET:HE3	12:Z:432:ASP:HB2	2.02	0.42
9:T:145:LYS:HG2	10:U:322:LYS:NZ	2.35	0.42
11:Y:66:LYS:NZ	11:Y:73:ARG:HH22	2.18	0.42
13:V:631:GLN:O	13:V:635:LEU:HG	2.20	0.42
13:V:677:GLU:HB2	13:V:685:ALA:HA	2.01	0.42
13:V:981:LYS:HE3	13:V:985:PHE:CZ	2.55	0.42
1:A:507:VAL:HG13	7:G:201:LYS:HD3	2.02	0.42
3:C:383:ARG:O	3:C:386:LYS:HG3	2.20	0.42
3:C:447:GLU:HB3	3:C:452:LYS:HG3	2.01	0.42
5:E:347:GLN:HG2	5:E:368:CYS:HB2	2.01	0.42
6:F:290:GLN:HA	6:F:293:LEU:HD12	2.01	0.42
8:I:81:ALA:HB1	8:I:107:CYS:HB3	2.01	0.42
8:I:211:LYS:HE2	8:I:222:GLN:HG3	2.01	0.42
8:I:218:ARG:HE	8:I:219:LEU:N	2.17	0.42
8:I:385:PHE:HE2	8:I:399:TYR:HA	1.84	0.42
13:S:323:LYS:HG3	13:S:335:TYR:HB2	2.02	0.42
13:S:487:ASN:OD1	13:S:487:ASN:N	2.53	0.42
13:S:868:LEU:HD22	13:S:873:GLN:HB3	2.00	0.42
13:S:974:MET:N	13:S:974:MET:SD	2.93	0.42
1:H:188:ASP:O	1:H:208:TYR:OH	2.28	0.42
1:H:297:TYR:CZ	1:H:301:MET:HE3	2.55	0.42
1:H:477:VAL:HG13	1:H:496:PHE:CE1	2.55	0.42
1:H:531:LYS:NZ	1:H:547:ILE:HG23	2.34	0.42
4:N:246:ILE:HA	4:N:249:LEU:HD13	2.02	0.42
5:O:439:ILE:HD12	5:O:439:ILE:HA	1.96	0.42
8:R:684:ILE:HD11	8:R:700:ALA:HB2	2.01	0.42
8:R:714:ARG:HE	8:R:727:ILE:HD11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:T:134:LYS:HD3	9:T:134:LYS:HA	1.87	0.42
9:T:193:ARG:NH2	9:T:197:ASN:OD1	2.53	0.42
13:V:37:ASP:OD1	13:V:37:ASP:N	2.52	0.42
13:V:356:SER:OG	13:V:360:TYR:N	2.53	0.42
13:V:774:ILE:O	13:V:778:LEU:HG	2.20	0.42
1:A:496:PHE:HB3	1:A:513:LEU:HB2	2.01	0.41
3:C:508:ALA:HA	3:C:511:LEU:HB2	2.01	0.41
6:F:252:TYR:CE2	7:G:253:ILE:HD12	2.55	0.41
7:G:250:MET:O	7:G:254:GLN:HB2	2.20	0.41
8:I:121:THR:HG22	8:I:131:TRP:CZ3	2.55	0.41
8:I:159:GLN:HA	8:I:172:SER:HA	2.02	0.41
8:I:347:LEU:O	8:I:358:TYR:N	2.51	0.41
8:I:625:LEU:HD11	8:I:653:GLU:HA	2.02	0.41
2:J:432:GLY:H	4:N:254:PRO:HB3	1.85	0.41
3:K:102:LYS:HE2	3:K:102:LYS:HB3	1.90	0.41
5:O:260:ILE:HA	5:O:263:ASN:HD21	1.86	0.41
5:O:477:PHE:HA	5:O:480:ALA:HB3	2.01	0.41
6:P:64:ARG:HD2	6:P:64:ARG:HA	1.73	0.41
7:Q:143:LEU:HG	7:Q:147:ARG:HH11	1.84	0.41
7:Q:288:ARG:O	7:Q:291:GLU:HG2	2.20	0.41
8:R:42:MET:HE2	8:R:42:MET:N	2.35	0.41
10:U:452:ARG:HE	10:U:456:LEU:HG	1.85	0.41
12:Z:406:SER:HB2	12:Z:409:ARG:NH2	2.27	0.41
12:Z:411:LEU:HD13	12:Z:411:LEU:C	2.45	0.41
1:A:574:ASP:OD2	1:A:577:VAL:N	2.47	0.41
1:A:639:GLN:NE2	1:A:641:GLN:HE21	2.18	0.41
1:A:651:SER:O	1:A:654:ARG:NH1	2.53	0.41
2:B:343:LEU:HB3	2:B:344:GLN:H	1.79	0.41
5:E:218:ASP:OD1	5:E:218:ASP:N	2.53	0.41
5:E:477:PHE:HA	5:E:480:ALA:HB3	2.01	0.41
6:F:176:LEU:HD12	7:G:182:SER:HB3	2.02	0.41
7:G:158:LYS:HD2	7:G:158:LYS:HA	1.73	0.41
7:G:288:ARG:O	7:G:291:GLU:HG2	2.20	0.41
10:M:449:LEU:O	10:M:453:ASN:ND2	2.53	0.41
10:M:450:SER:HA	10:M:453:ASN:HD21	1.84	0.41
11:W:111:LEU:HD21	12:X:492:ILE:HG12	2.01	0.41
13:S:807:LEU:HD11	13:S:823:TYR:HE1	1.85	0.41
1:H:318:LYS:HB3	1:H:318:LYS:HE3	1.94	0.41
2:J:141:ARG:HA	2:J:144:ILE:HD12	2.02	0.41
2:J:330:ASN:HD21	3:K:548:LYS:HB2	1.84	0.41
2:J:371:SER:OG	2:J:374:ASN:OD1	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:227:SER:HA	3:K:267:PRO:HB2	2.02	0.41
3:K:383:ARG:O	3:K:386:LYS:HG3	2.21	0.41
3:K:383:ARG:HG3	3:K:386:LYS:HE3	2.02	0.41
3:K:637:MET:HB2	3:K:640:LYS:HZ2	1.84	0.41
6:P:221:SER:O	6:P:224:ILE:HG12	2.20	0.41
8:R:279:ASP:HB2	8:R:281:THR:HG22	2.01	0.41
9:T:32:PHE:HB3	9:T:62:ARG:HG2	2.00	0.41
9:T:168:VAL:HA	9:T:171:HIS:CE1	2.55	0.41
11:Y:66:LYS:HD3	12:Z:443:TRP:CZ3	2.55	0.41
11:Y:83:ARG:NH1	11:Y:87:GLN:HG2	2.35	0.41
13:V:215:ILE:HG23	13:V:227:TYR:HB2	2.02	0.41
13:V:231:GLY:O	13:V:232:ARG:NH1	2.53	0.41
13:V:731:VAL:HA	13:V:734:SER:HB3	2.01	0.41
5:E:11:ALA:HB1	5:E:217:PRO:HB2	2.02	0.41
5:E:197:CYS:SG	5:E:225:LEU:HB3	2.61	0.41
5:E:202:TYR:HE2	5:E:232:ARG:HD2	1.83	0.41
7:G:215:PHE:O	7:G:219:LYS:HB2	2.20	0.41
9:L:186:ALA:HB2	10:M:364:ARG:NH1	2.35	0.41
11:W:83:ARG:CZ	12:X:464:ALA:HB2	2.51	0.41
11:W:113:LYS:H	11:W:113:LYS:HD2	1.85	0.41
13:S:37:ASP:OD1	13:S:37:ASP:N	2.52	0.41
13:S:878:ILE:O	13:S:882:ILE:HG12	2.20	0.41
1:H:183:LEU:HD23	1:H:183:LEU:HA	1.86	0.41
1:H:280:LEU:HD13	1:H:280:LEU:HA	1.91	0.41
1:H:465:ALA:O	1:H:470:ARG:HB3	2.21	0.41
5:O:13:ARG:HB3	5:O:250:SER:HA	2.01	0.41
6:P:203:TYR:OH	7:Q:207:PRO:O	2.26	0.41
9:T:43:VAL:O	9:T:47:TYR:N	2.48	0.41
10:U:309:HIS:CE1	11:Y:38:ILE:HG12	2.50	0.41
10:U:312:GLU:HG2	10:U:316:HIS:HE1	1.85	0.41
11:Y:44:MET:O	11:Y:47:LEU:HG	2.19	0.41
13:V:853:PHE:CD1	13:V:854:PRO:HD2	2.56	0.41
1:A:122:PRO:HB2	1:A:123:GLU:H	1.66	0.41
1:A:362:ILE:O	1:A:366:ILE:HG23	2.20	0.41
3:C:58:TYR:HA	3:C:63:TYR:HE1	1.84	0.41
5:E:283:ILE:HB	5:E:284:PRO:HD3	2.03	0.41
5:E:316:PRO:HA	5:E:319:PHE:HB2	2.01	0.41
6:F:186:LYS:HB3	6:F:186:LYS:HE3	1.82	0.41
8:I:20:VAL:HG12	8:I:30:THR:HG22	2.01	0.41
9:L:78:ARG:HH21	11:W:49:ASP:HB2	1.84	0.41
11:W:117:GLU:HG3	13:V:782:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:415:HIS:HA	13:S:420:LEU:HA	2.02	0.41
1:H:404:ASN:HD21	1:H:433:LYS:HD3	1.85	0.41
1:H:666:TYR:HD2	1:H:683:LEU:HD22	1.85	0.41
2:J:448:PHE:CD1	4:N:312:PRO:HG2	2.55	0.41
3:K:297:LYS:HA	3:K:300:PHE:CD2	2.55	0.41
9:T:74:LEU:O	9:T:78:ARG:HA	2.21	0.41
9:T:106:LYS:HA	11:Y:56:ASP:CG	2.45	0.41
13:V:154:HIS:CE1	13:V:156:GLU:HB2	2.56	0.41
13:V:752:LEU:HA	13:V:757:GLU:HB3	2.02	0.41
13:V:993:GLU:HA	13:V:996:LYS:HB2	2.03	0.41
13:V:1046:GLU:HA	13:V:1054:ALA:HB2	2.00	0.41
1:A:250:GLN:OE1	1:A:250:GLN:N	2.43	0.41
1:A:531:LYS:NZ	1:A:547:ILE:HG23	2.34	0.41
3:C:512:MET:O	3:C:516:GLU:N	2.54	0.41
5:E:15:ASN:ND2	5:E:250:SER:O	2.53	0.41
5:E:34:LEU:HA	5:E:39:TYR:CE1	2.55	0.41
9:L:137:LYS:HE2	10:M:316:HIS:HA	2.01	0.41
11:W:72:LEU:O	11:W:76:VAL:HG13	2.21	0.41
11:W:83:ARG:HA	11:W:83:ARG:HD2	1.89	0.41
1:H:288:ASP:OD1	1:H:288:ASP:N	2.46	0.41
1:H:313:LYS:O	1:H:317:ILE:HG12	2.21	0.41
1:H:452:GLU:OE1	10:U:443:SER:HA	2.21	0.41
2:J:23:HIS:H	2:J:23:HIS:CD2	2.38	0.41
2:J:236:GLU:HB2	2:J:239:LYS:HE3	2.01	0.41
2:J:379:LEU:HD23	2:J:399:ILE:HD11	2.02	0.41
3:K:58:TYR:HA	3:K:63:TYR:HE1	1.86	0.41
4:N:214:LYS:HA	4:N:217:LYS:HD3	2.02	0.41
7:Q:304:GLU:HA	7:Q:307:LEU:HG	2.01	0.41
13:V:579:HIS:CE1	13:V:601:ILE:HG22	2.56	0.41
13:V:868:LEU:HD22	13:V:873:GLN:HB3	2.01	0.41
2:B:309:THR:HG22	2:B:313:PRO:HG2	2.03	0.41
2:B:428:SER:N	4:D:254:PRO:HD2	2.24	0.41
3:C:73:LEU:HA	3:C:76:LEU:HG	2.01	0.41
5:E:138:ASP:OD1	5:E:138:ASP:N	2.52	0.41
6:F:196:LYS:HG3	6:F:198:PRO:HD3	2.01	0.41
9:L:240:GLU:HA	9:L:243:ARG:HB2	2.03	0.41
10:M:394:ILE:HA	10:M:397:THR:HG22	2.03	0.41
13:S:537:PRO:HB2	13:S:576:ARG:HD3	2.01	0.41
13:S:993:GLU:HA	13:S:996:LYS:HB2	2.03	0.41
1:H:546:GLN:NE2	2:J:276:ALA:HB3	2.35	0.41
1:H:578:LEU:HD23	1:H:597:TYR:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:142:ALA:HB1	2:J:255:GLN:HG2	2.03	0.41
3:K:199:HIS:O	3:K:202:GLU:HG3	2.20	0.41
3:K:265:ASP:OD1	3:K:265:ASP:N	2.52	0.41
3:K:473:TYR:HB3	3:K:495:LEU:HD11	2.02	0.41
3:K:538:ASN:HA	3:K:541:ILE:HG22	2.02	0.41
4:N:326:GLY:O	4:N:327:MET:HE2	2.21	0.41
5:O:137:ASP:HA	5:O:140:LEU:HD12	2.02	0.41
5:O:202:TYR:HE2	5:O:232:ARG:HD2	1.85	0.41
5:O:305:PHE:O	5:O:309:LYS:HG2	2.20	0.41
5:O:378:VAL:HG12	5:O:382:LEU:HD23	2.03	0.41
6:P:16:PHE:HE1	6:P:40:VAL:HA	1.85	0.41
6:P:321:ILE:HD11	7:Q:330:LYS:HB2	2.01	0.41
13:V:598:GLU:HA	13:V:601:ILE:HD12	2.03	0.41
13:V:706:LEU:HD21	13:V:719:TYR:HE1	1.86	0.41
13:V:915:ALA:HA	13:V:918:TYR:CD2	2.56	0.41
1:A:191:LEU:HD12	1:A:195:TYR:CZ	2.56	0.41
1:A:444:ASN:OD1	2:B:286:LEU:HD12	2.21	0.41
1:A:618:TYR:O	1:A:622:SER:OG	2.26	0.41
5:E:305:PHE:HA	5:E:308:ILE:HG22	2.01	0.41
8:I:531:SER:O	8:I:531:SER:OG	2.36	0.41
8:I:604:ARG:NH2	8:I:635:ILE:HA	2.36	0.41
9:L:26:ASN:HD22	9:L:34:LEU:HB3	1.85	0.41
13:S:183:LYS:HE3	13:S:197:SER:HB2	2.02	0.41
13:S:254:ASN:OD1	13:S:255:PRO:HD2	2.20	0.41
1:H:496:PHE:HB3	1:H:513:LEU:HB2	2.02	0.41
1:H:618:TYR:O	1:H:622:SER:OG	2.25	0.41
2:J:245:PHE:O	2:J:249:LYS:HB2	2.19	0.41
3:K:73:LEU:HD13	3:K:83:TYR:CE1	2.56	0.41
3:K:200:LEU:HD11	3:K:245:LEU:HG	2.03	0.41
3:K:260:LYS:HA	3:K:285:ILE:HD11	2.02	0.41
3:K:551:TYR:HB2	3:K:595:LEU:HD21	2.03	0.41
4:N:242:ARG:NH1	4:N:243:MET:HG2	2.35	0.41
6:P:212:LYS:HD3	6:P:212:LYS:HA	1.58	0.41
6:P:277:GLU:O	6:P:281:LYS:NZ	2.47	0.41
8:R:651:PRO:O	8:R:763:ARG:NH2	2.51	0.41
8:R:697:LEU:HG	8:R:729:ARG:HD3	2.03	0.41
9:T:110:LYS:HA	9:T:113:ASP:HB2	2.03	0.41
11:Y:83:ARG:CZ	12:Z:464:ALA:HB2	2.51	0.41
13:V:770:TYR:HA	13:V:773:ALA:HB3	2.02	0.41
2:B:249:LYS:NZ	2:B:250:PRO:O	2.36	0.41
2:B:338:THR:HA	2:B:339:PRO:HD3	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:324:HIS:HB3	3:C:326:PHE:CD2	2.56	0.41
8:I:389:ASP:OD1	8:I:389:ASP:N	2.52	0.41
9:L:104:LEU:C	9:L:106:LYS:H	2.29	0.41
13:S:443:LEU:HD13	13:S:495:LEU:HD21	2.02	0.41
13:S:731:VAL:HA	13:S:734:SER:HB3	2.02	0.41
1:H:184:MET:HE2	1:H:184:MET:HB2	1.99	0.41
2:J:24:LYS:HZ3	2:J:24:LYS:HG3	1.64	0.41
2:J:448:PHE:HB3	4:N:316:GLN:HG2	2.03	0.41
3:K:176:GLN:HB2	3:K:179:LEU:HB2	2.03	0.41
3:K:468:GLU:OE1	3:K:471:ARG:NE	2.41	0.41
3:K:550:ASN:OD1	3:K:550:ASN:N	2.53	0.41
3:K:575:TYR:HA	3:K:578:LYS:HB2	2.02	0.41
6:P:16:PHE:HB3	6:P:18:TYR:HD2	1.86	0.41
8:R:95:ARG:NE	8:R:97:GLU:OE2	2.54	0.41
8:R:431:VAL:HB	8:R:442:ARG:HB2	2.01	0.41
10:U:389:GLN:HG3	10:U:393:ARG:NH1	2.36	0.41
13:V:759:GLN:O	13:V:763:VAL:HG23	2.21	0.41
13:V:895:ILE:O	13:V:898:ARG:HG2	2.21	0.41
1:A:297:TYR:HD2	2:B:301:ASP:HB2	1.86	0.41
1:A:575:PRO:HG3	1:A:605:TYR:HB3	2.02	0.41
3:C:70:TYR:HB3	3:C:87:TYR:HB2	2.03	0.41
3:C:364:GLU:O	3:C:368:ARG:HG2	2.21	0.41
4:D:300:VAL:O	4:D:303:THR:OG1	2.29	0.41
5:E:123:GLN:HE22	5:E:127:LEU:HD22	1.85	0.41
5:E:355:GLU:HG2	5:E:360:PRO:HG2	2.03	0.41
6:F:73:LYS:HA	6:F:75:ARG:HH22	1.85	0.41
6:F:261:LEU:HD12	6:F:261:LEU:HA	1.85	0.41
7:G:236:ARG:NH2	6:P:22:LEU:HB3	2.36	0.41
8:I:5:VAL:HG11	8:I:265:LEU:HD22	2.03	0.41
8:I:165:GLY:HA2	8:I:188:VAL:HG13	2.02	0.41
8:I:458:HIS:NE2	8:I:490:LEU:HD11	2.35	0.41
8:I:679:LEU:HG	8:I:681:PHE:H	1.84	0.41
9:L:106:LYS:CA	11:W:56:ASP:HB3	2.44	0.41
9:L:122:ILE:HD13	9:L:122:ILE:HA	1.88	0.41
9:L:145:LYS:HG2	10:M:322:LYS:NZ	2.35	0.41
9:L:179:ARG:NH2	10:M:359:LEU:HD13	2.36	0.41
10:M:389:GLN:HG3	10:M:393:ARG:NH1	2.36	0.41
13:S:67:ILE:H	13:S:85:SER:HB3	1.85	0.41
13:S:712:VAL:HG11	13:S:738:ALA:H	1.85	0.41
13:S:737:HIS:CG	13:S:740:ALA:HB2	2.56	0.41
13:S:1056:LYS:HA	13:S:1059:VAL:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:551:TYR:CE2	1:H:556:ASP:HB3	2.56	0.41
1:H:605:TYR:CE1	1:H:607:VAL:HB	2.55	0.41
2:J:280:ASP:OD1	2:J:280:ASP:N	2.44	0.41
2:J:419:ARG:HB3	4:N:344:LEU:HD13	2.02	0.41
3:K:110:HIS:HB3	3:K:113:ALA:HB3	2.02	0.41
3:K:122:SER:HA	3:K:125:GLN:HG2	2.03	0.41
3:K:430:LEU:HD23	3:K:430:LEU:HA	1.94	0.41
3:K:590:LYS:HD2	3:K:590:LYS:HA	1.72	0.41
5:O:39:TYR:HB2	5:O:70:TYR:CD1	2.56	0.41
6:P:279:TYR:HB2	7:Q:289:PHE:CZ	2.56	0.41
8:R:193:ASP:HB2	8:R:233:VAL:HG23	2.02	0.41
8:R:508:ARG:HH12	8:R:510:HIS:HA	1.85	0.41
8:R:596:TRP:HE1	8:R:627:THR:HB	1.86	0.41
8:R:600:THR:HG22	8:R:635:ILE:HG23	2.02	0.41
8:R:614:THR:O	8:R:618:MET:HG2	2.21	0.41
11:Y:115:LYS:O	12:Z:495:ASN:ND2	2.54	0.41
13:V:267:ARG:HD3	13:V:285:HIS:ND1	2.36	0.41
13:V:500:ARG:NH2	13:V:539:SER:O	2.54	0.41
13:V:581:THR:HG23	13:V:601:ILE:HG12	2.03	0.41
1:A:466:LEU:HD22	1:A:479:LYS:HG2	2.02	0.41
2:B:138:ILE:HG13	2:B:193:LEU:HD23	2.02	0.41
2:B:142:ALA:HB1	2:B:255:GLN:HG2	2.03	0.41
3:C:557:ARG:HB2	3:C:560:LYS:HE3	2.03	0.41
5:E:45:LEU:HA	5:E:48:PHE:CD2	2.57	0.41
5:E:457:ASN:H	5:E:460:SER:HB3	1.86	0.41
6:F:324:ILE:HG22	6:F:327:ARG:CZ	2.51	0.41
11:W:58:GLN:O	11:W:62:LEU:HG	2.21	0.41
13:S:495:LEU:N	13:S:495:LEU:HD23	2.35	0.41
1:H:574:ASP:OD1	2:J:272:LEU:N	2.54	0.41
1:H:653:TYR:HE2	1:H:665:LYS:HG2	1.86	0.41
2:J:23:HIS:CD2	2:J:42:LYS:HG2	2.56	0.41
4:N:226:ASN:O	4:N:229:HIS:NE2	2.54	0.41
5:O:125:ARG:O	5:O:129:HIS:ND1	2.34	0.41
5:O:205:SER:HA	5:O:208:ILE:HG22	2.03	0.41
7:Q:147:ARG:HA	7:Q:150:ILE:HG12	2.02	0.41
7:Q:199:LEU:HA	7:Q:203:GLY:HA3	2.02	0.41
8:R:514:ALA:HB1	8:R:530:PRO:HG3	2.02	0.41
13:V:338:LYS:HA	13:V:338:LYS:HD3	1.88	0.41
13:V:727:ASP:N	13:V:727:ASP:OD1	2.54	0.41
1:A:263:MET:HE1	1:A:282:SER:OG	2.21	0.40
4:D:225:ILE:HD13	4:D:225:ILE:HA	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:213:LEU:HD11	5:E:226:LYS:HE3	2.03	0.40
8:I:599:ALA:O	8:I:602:LEU:HG	2.20	0.40
9:L:110:LYS:HA	9:L:113:ASP:HB2	2.02	0.40
13:S:981:LYS:HE3	13:S:985:PHE:CZ	2.56	0.40
1:H:224:ARG:NH1	1:H:243:MET:O	2.46	0.40
1:H:664:GLY:HA2	1:H:667:LYS:HE3	2.02	0.40
2:J:193:LEU:HB2	2:J:207:GLY:HA3	2.03	0.40
2:J:426:MET:HE1	4:N:287:ASP:H	1.85	0.40
3:K:99:GLU:OE1	3:K:102:LYS:NZ	2.37	0.40
3:K:311:THR:HA	3:K:314:ASN:HD22	1.86	0.40
6:P:324:ILE:HA	6:P:327:ARG:HG2	2.02	0.40
8:R:576:VAL:HG22	11:Y:92:ARG:NH1	2.33	0.40
9:T:5:GLU:H	9:T:5:GLU:HG3	1.68	0.40
13:V:582:GLU:HA	13:V:595:ALA:HA	2.04	0.40
13:V:1028:GLN:H	13:V:1028:GLN:HG2	1.77	0.40
1:A:127:ARG:O	1:A:131:LYS:HG2	2.21	0.40
1:A:181:LEU:HG	1:A:185:TYR:CD2	2.56	0.40
1:A:479:LYS:HD2	1:A:479:LYS:HA	1.79	0.40
2:B:337:GLU:H	2:B:337:GLU:HG3	1.74	0.40
3:C:611:GLU:HB3	3:C:615:LYS:HE2	2.03	0.40
6:F:164:LYS:HD3	6:F:294:SER:HA	2.02	0.40
7:G:199:LEU:HA	7:G:203:GLY:HA3	2.04	0.40
13:S:407:GLU:HB2	13:S:441:PRO:HB3	2.03	0.40
1:H:211:ILE:HA	1:H:214:ASN:HD21	1.86	0.40
1:H:362:ILE:O	1:H:366:ILE:HG23	2.22	0.40
6:P:252:TYR:CE2	7:Q:253:ILE:HD12	2.56	0.40
8:R:138:ARG:HH12	13:V:435:ARG:NH1	2.19	0.40
8:R:154:ALA:HB2	8:R:194:TRP:CZ3	2.55	0.40
8:R:347:LEU:O	8:R:358:TYR:N	2.50	0.40
13:V:56:LYS:H	13:V:56:LYS:HG2	1.73	0.40
13:V:401:SER:HB3	13:V:416:TYR:HD1	1.87	0.40
13:V:542:ILE:O	13:V:552:VAL:HA	2.20	0.40
1:A:131:LYS:HA	1:A:131:LYS:HD3	1.85	0.40
1:A:391:CYS:O	1:A:395:ARG:HG3	2.22	0.40
1:A:562:LYS:HB2	9:T:238:MET:HE1	2.03	0.40
1:A:600:GLU:HG2	1:A:603:ARG:HH21	1.85	0.40
1:A:619:HIS:CG	1:A:628:ALA:HB2	2.57	0.40
2:B:358:PRO:HD2	3:C:59:TYR:HE1	1.86	0.40
4:D:242:ARG:NH2	4:D:245:GLU:HA	2.35	0.40
8:I:7:GLN:HE21	8:I:7:GLN:HB2	1.68	0.40
8:I:64:PRO:HG2	8:I:67:SER:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:527:TRP:HA	8:I:544:ARG:HA	2.04	0.40
9:L:74:LEU:O	9:L:78:ARG:HA	2.21	0.40
9:L:137:LYS:HD2	9:L:137:LYS:HA	1.78	0.40
9:L:214:GLU:HA	9:L:217:LYS:HG2	2.03	0.40
9:L:256:LEU:O	9:L:260:ARG:HG3	2.21	0.40
11:W:24:TYR:CZ	11:W:28:LYS:HD3	2.56	0.40
11:W:122:ILE:HG12	12:X:498:THR:OG1	2.21	0.40
13:S:25:ALA:HB2	13:S:30:ARG:HB3	2.04	0.40
13:S:892:LYS:HA	13:S:895:ILE:HD12	2.02	0.40
1:H:303:ASN:OD1	9:T:299:LEU:CD1	2.70	0.40
2:J:382:LYS:HE3	5:O:23:GLU:HB3	2.04	0.40
3:K:324:HIS:HB3	3:K:326:PHE:CD2	2.57	0.40
5:O:218:ASP:OD1	5:O:218:ASP:N	2.53	0.40
6:P:86:GLN:HE21	6:P:86:GLN:HB2	1.76	0.40
6:P:217:GLU:HG3	7:Q:222:ASN:CG	2.46	0.40
7:Q:172:ASN:HA	7:Q:175:ASP:OD2	2.21	0.40
8:R:129:LYS:HB2	8:R:131:TRP:CZ3	2.56	0.40
8:R:392:ALA:O	8:R:408:ARG:NH1	2.36	0.40
8:R:596:TRP:NE1	12:Z:503:LEU:HD11	2.36	0.40
8:R:712:TRP:HB2	8:R:744:VAL:HG11	2.03	0.40
9:T:137:LYS:HE2	10:U:316:HIS:HA	2.02	0.40
9:T:143:ILE:HG23	11:Y:23:LYS:NZ	2.37	0.40
11:Y:24:TYR:O	11:Y:28:LYS:HG2	2.22	0.40
13:V:80:LEU:HD13	13:V:94:LEU:HB3	2.03	0.40
13:V:161:VAL:HG11	13:V:207:TYR:HA	2.04	0.40
1:A:134:HIS:HA	1:A:137:LEU:HG	2.03	0.40
1:A:161:LYS:HG3	1:A:165:LYS:HE3	2.03	0.40
1:A:306:LEU:HD21	9:L:296:GLU:HG2	2.02	0.40
1:A:468:SER:OG	1:A:469:ASP:N	2.52	0.40
1:A:483:LEU:HD13	1:A:488:ASP:HB3	2.03	0.40
2:B:193:LEU:HB2	2:B:207:GLY:HA3	2.03	0.40
2:B:246:LYS:HB3	2:B:254:ILE:HD11	2.02	0.40
3:C:430:LEU:HD23	3:C:430:LEU:HA	1.94	0.40
3:C:518:GLU:HG2	3:C:521:ARG:CZ	2.52	0.40
5:E:54:ARG:HA	5:E:54:ARG:HD2	1.92	0.40
5:E:94:PHE:HD1	5:E:113:GLN:NE2	2.15	0.40
5:E:134:GLN:OE1	5:E:139:LYS:NZ	2.34	0.40
6:F:328:LYS:O	6:F:331:GLN:NE2	2.54	0.40
8:I:38:HIS:CE1	8:I:46:PRO:HB2	2.56	0.40
8:I:194:TRP:HA	8:I:201:ILE:HA	2.04	0.40
8:I:279:ASP:HB2	8:I:281:THR:HG22	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:427:ASP:OD1	8:I:427:ASP:N	2.53	0.40
8:I:552:PHE:CD1	8:I:568:VAL:HG21	2.56	0.40
8:I:600:THR:HA	8:I:603:CYS:HB2	2.03	0.40
8:I:684:ILE:HD11	8:I:700:ALA:HB2	2.04	0.40
9:L:128:LEU:HD22	12:X:417:HIS:CD2	2.56	0.40
10:M:434:ASP:O	10:M:438:ARG:HD3	2.22	0.40
11:W:117:GLU:O	11:W:121:MET:HG3	2.22	0.40
12:X:412:VAL:HG23	12:X:413:GLN:N	2.36	0.40
13:S:56:LYS:H	13:S:56:LYS:HG2	1.73	0.40
13:S:76:ASP:OD2	13:S:79:LYS:NZ	2.52	0.40
13:S:306:MET:SD	13:S:318:TYR:HB2	2.61	0.40
13:S:337:SER:OG	13:S:338:LYS:N	2.55	0.40
13:S:1051:LEU:HD21	10:U:362:GLN:OE1	2.21	0.40
1:H:201:TYR:CE1	1:H:230:ILE:HD12	2.56	0.40
1:H:352:LYS:HA	3:K:636:ARG:HD3	2.04	0.40
2:J:54:ARG:HD2	2:J:79:PHE:CD1	2.56	0.40
2:J:176:VAL:HG21	2:J:234:LYS:HB3	2.03	0.40
2:J:294:ARG:NH2	2:J:298:SER:O	2.42	0.40
5:O:541:VAL:HA	5:O:544:MET:HG2	2.03	0.40
6:P:139:LYS:HD3	6:P:142:ILE:HD12	2.03	0.40
11:Y:104:LEU:O	11:Y:107:GLU:HG2	2.21	0.40
13:V:145:ASN:OD1	13:V:145:ASN:N	2.55	0.40
13:V:248:PHE:CD1	13:V:262:PHE:HB3	2.57	0.40
13:V:343:VAL:HB	13:V:352:ILE:HG23	2.04	0.40
1:A:139:LYS:HZ1	1:A:151:SER:C	2.29	0.40
2:B:312:ILE:HB	3:C:589:ALA:HB1	2.04	0.40
3:C:311:THR:HA	3:C:314:ASN:HD22	1.85	0.40
3:C:590:LYS:HD2	3:C:590:LYS:HA	1.79	0.40
5:E:106:MET:HE3	5:E:106:MET:HA	2.03	0.40
5:E:258:ASP:HB3	5:E:261:ARG:HB2	2.04	0.40
6:F:173:ILE:HD13	6:F:173:ILE:HA	1.96	0.40
8:I:577:SER:HB2	11:W:97:LYS:NZ	2.36	0.40
9:L:66:LEU:HA	9:L:69:VAL:HG22	2.02	0.40
10:M:452:ARG:HE	10:M:456:LEU:HG	1.87	0.40
11:W:118:GLN:O	11:W:122:ILE:HG13	2.21	0.40
13:S:770:TYR:O	13:S:774:ILE:HG12	2.22	0.40
13:S:851:ARG:HB3	13:S:855:ALA:HB2	2.03	0.40
13:S:947:ASP:O	13:S:950:GLU:HG3	2.22	0.40
1:H:191:LEU:HD12	1:H:195:TYR:CZ	2.56	0.40
3:K:22:THR:HA	3:K:25:LYS:HB2	2.03	0.40
3:K:358:GLY:HA3	3:K:366:ALA:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:485:LEU:HD21	3:K:519:GLU:HA	2.03	0.40
4:N:266:MET:HE2	4:N:271:VAL:HA	2.04	0.40
4:N:283:CYS:SG	4:N:289:PRO:HB3	2.61	0.40
5:O:158:ALA:HB2	5:O:173:ILE:HG21	2.04	0.40
8:R:189:VAL:HA	8:R:205:GLY:HA2	2.04	0.40
8:R:209:LYS:HE2	8:R:209:LYS:HB3	1.85	0.40
8:R:515:MET:SD	8:R:584:PRO:HB2	2.61	0.40
8:R:747:LYS:O	8:R:750:GLU:HG3	2.21	0.40
10:U:367:ARG:HH22	10:U:370:PHE:HD2	1.68	0.40
10:U:372:ASP:O	10:U:376:THR:OG1	2.23	0.40
13:V:709:GLN:OE1	13:V:711:LYS:NZ	2.50	0.40
13:V:900:PHE:O	13:V:903:ALA:N	2.54	0.40
13:V:908:GLU:HB2	13:V:938:TYR:CZ	2.57	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	535/782 (68%)	472 (88%)	61 (11%)	2 (0%)	30	67
1	H	535/782 (68%)	474 (89%)	57 (11%)	4 (1%)	18	56
2	B	452/454 (100%)	391 (86%)	60 (13%)	1 (0%)	43	78
2	J	452/454 (100%)	393 (87%)	58 (13%)	1 (0%)	43	78
3	C	613/647 (95%)	580 (95%)	33 (5%)	0	100	100
3	K	613/647 (95%)	582 (95%)	31 (5%)	0	100	100
4	D	131/344 (38%)	116 (88%)	15 (12%)	0	100	100
4	N	131/344 (38%)	117 (89%)	14 (11%)	0	100	100
5	E	553/555 (100%)	508 (92%)	45 (8%)	0	100	100
5	O	553/555 (100%)	513 (93%)	40 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	333/683 (49%)	324 (97%)	9 (3%)	0	100	100
6	P	333/683 (49%)	323 (97%)	10 (3%)	0	100	100
7	G	203/641 (32%)	192 (95%)	11 (5%)	0	100	100
7	Q	203/641 (32%)	191 (94%)	12 (6%)	0	100	100
8	I	763/765 (100%)	697 (91%)	65 (8%)	1 (0%)	48	83
8	R	763/765 (100%)	704 (92%)	58 (8%)	1 (0%)	48	83
9	L	301/443 (68%)	279 (93%)	22 (7%)	0	100	100
9	T	301/443 (68%)	276 (92%)	25 (8%)	0	100	100
10	M	162/469 (34%)	158 (98%)	4 (2%)	0	100	100
10	U	162/469 (34%)	158 (98%)	4 (2%)	0	100	100
11	W	112/135 (83%)	112 (100%)	0	0	100	100
11	Y	112/135 (83%)	112 (100%)	0	0	100	100
12	X	104/510 (20%)	104 (100%)	0	0	100	100
12	Z	104/510 (20%)	102 (98%)	2 (2%)	0	100	100
13	S	1102/1755 (63%)	1034 (94%)	67 (6%)	1 (0%)	48	83
13	V	1102/1755 (63%)	1030 (94%)	72 (6%)	0	100	100
All	All	10728/16366 (66%)	9942 (93%)	775 (7%)	11 (0%)	49	83

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	629	MET
1	H	629	MET
1	A	431	GLU
1	H	304	TYR
1	H	305	ALA
1	H	431	GLU
2	B	187	LYS
13	S	779	LYS
2	J	187	LYS
8	I	537	LYS
8	R	537	LYS

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	457/627 (73%)	456 (100%)	1 (0%)	87	87
1	H	457/627 (73%)	456 (100%)	1 (0%)	87	87
2	B	388/388 (100%)	388 (100%)	0	100	100
2	J	388/388 (100%)	388 (100%)	0	100	100
3	C	534/558 (96%)	534 (100%)	0	100	100
3	K	534/558 (96%)	534 (100%)	0	100	100
4	D	114/288 (40%)	114 (100%)	0	100	100
4	N	114/288 (40%)	114 (100%)	0	100	100
5	E	469/469 (100%)	469 (100%)	0	100	100
5	O	469/469 (100%)	469 (100%)	0	100	100
6	F	296/581 (51%)	296 (100%)	0	100	100
6	P	296/581 (51%)	295 (100%)	1 (0%)	86	86
7	G	185/526 (35%)	185 (100%)	0	100	100
7	Q	185/526 (35%)	185 (100%)	0	100	100
8	I	648/648 (100%)	647 (100%)	1 (0%)	87	87
8	R	648/648 (100%)	648 (100%)	0	100	100
9	L	261/358 (73%)	261 (100%)	0	100	100
9	T	261/358 (73%)	261 (100%)	0	100	100
10	M	144/380 (38%)	144 (100%)	0	100	100
10	U	144/380 (38%)	144 (100%)	0	100	100
11	W	101/120 (84%)	101 (100%)	0	100	100
11	Y	101/120 (84%)	101 (100%)	0	100	100
12	X	90/401 (22%)	90 (100%)	0	100	100
12	Z	90/401 (22%)	90 (100%)	0	100	100
13	S	915/1431 (64%)	914 (100%)	1 (0%)	88	89
13	V	915/1431 (64%)	914 (100%)	1 (0%)	88	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9204/13550 (68%)	9198 (100%)	6 (0%)	87 89

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	449	TYR
8	I	7	GLN
13	S	495	LEU
1	H	449	TYR
6	P	86	GLN
13	V	495	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (129) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	234	GLN
1	A	294	GLN
1	A	303	ASN
1	A	404	ASN
1	A	457	GLN
1	A	639	GLN
1	A	668	GLN
2	B	23	HIS
2	B	330	ASN
2	B	384	HIS
2	B	405	GLN
3	C	35	HIS
3	C	41	GLN
3	C	167	ASN
3	C	176	GLN
3	C	211	HIS
3	C	244	ASN
3	C	314	ASN
3	C	337	ASN
3	C	405	ASN
3	C	608	ASN
4	D	220	GLN
4	D	310	ASN
4	D	322	ASN
5	E	86	HIS
5	E	113	GLN

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Mol	Chain	Res	Type
5	E	132	GLN
5	E	168	GLN
5	E	224	ASN
5	E	235	ASN
5	E	262	HIS
5	E	275	GLN
5	E	290	ASN
5	E	343	GLN
6	F	214	GLN
6	F	308	GLN
6	F	320	GLN
7	G	310	ASN
8	I	38	HIS
8	I	282	GLN
8	I	354	GLN
8	I	362	ASN
8	I	559	GLN
8	I	594	GLN
8	I	595	GLN
8	I	702	GLN
9	L	126	ASN
9	L	274	GLN
9	L	277	GLN
10	M	309	HIS
10	M	315	GLN
10	M	346	GLN
10	M	355	GLN
10	M	378	ASN
10	M	453	ASN
10	M	458	GLN
13	S	198	GLN
13	S	274	ASN
13	S	408	ASN
13	S	438	HIS
13	S	521	GLN
13	S	549	ASN
13	S	631	GLN
13	S	745	GLN
13	S	746	GLN
1	H	229	ASN
1	H	231	HIS
1	H	234	GLN

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Mol	Chain	Res	Type
1	H	404	ASN
1	H	457	GLN
1	H	546	GLN
1	H	559	ASN
2	J	23	HIS
2	J	330	ASN
2	J	405	GLN
3	K	41	GLN
3	K	182	ASN
3	K	244	ASN
3	K	280	HIS
3	K	314	ASN
3	K	380	GLN
3	K	405	ASN
3	K	480	ASN
3	K	608	ASN
4	N	226	ASN
4	N	310	ASN
4	N	322	ASN
5	O	86	HIS
5	O	168	GLN
5	O	224	ASN
5	O	235	ASN
5	O	290	ASN
5	O	343	GLN
6	P	49	GLN
6	P	86	GLN
6	P	214	GLN
6	P	225	GLN
6	P	231	GLN
6	P	308	GLN
7	Q	168	GLN
7	Q	172	ASN
7	Q	310	ASN
8	R	7	GLN
8	R	26	ASN
8	R	198	ASN
8	R	354	GLN
8	R	448	GLN
8	R	559	GLN
8	R	595	GLN
8	R	732	GLN

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Mol	Chain	Res	Type
9	T	126	ASN
9	T	245	GLN
9	T	274	GLN
9	T	277	GLN
10	U	346	GLN
10	U	378	ASN
10	U	433	HIS
11	Y	58	GLN
13	V	198	GLN
13	V	274	ASN
13	V	278	ASN
13	V	408	ASN
13	V	499	GLN
13	V	521	GLN
13	V	549	ASN
13	V	631	GLN
13	V	694	GLN
13	V	1069	GLN
13	V	1073	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

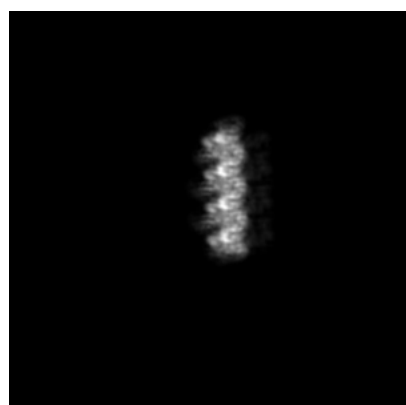
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15977. These allow visual inspection of the internal detail of the map and identification of artifacts.

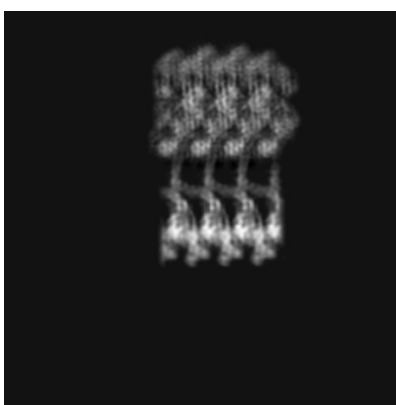
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

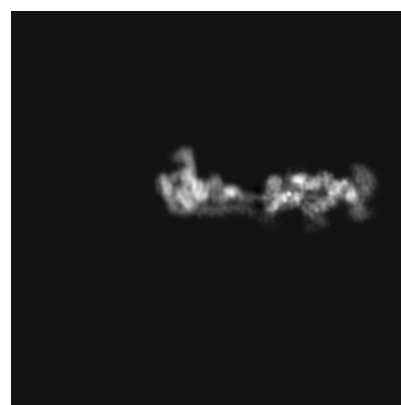
6.1.1 Primary map



X



Y

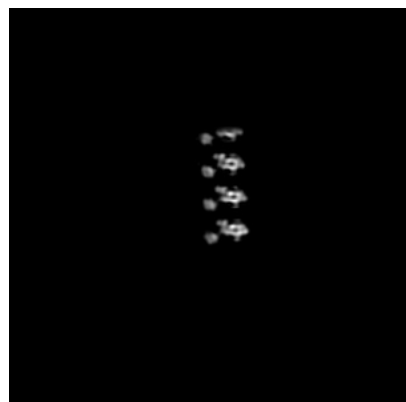


Z

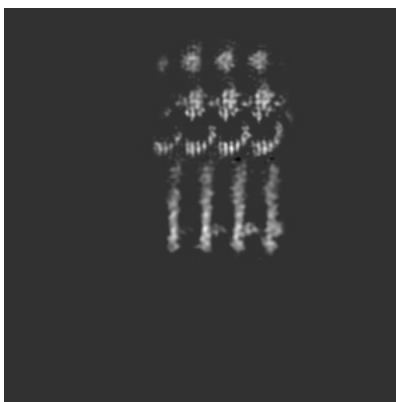
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 128



Y Index: 128

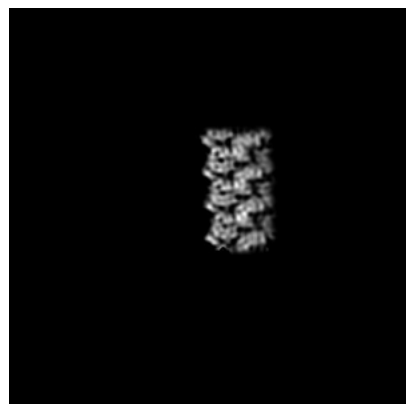


Z Index: 128

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

6.3 Largest variance slices [i](#)

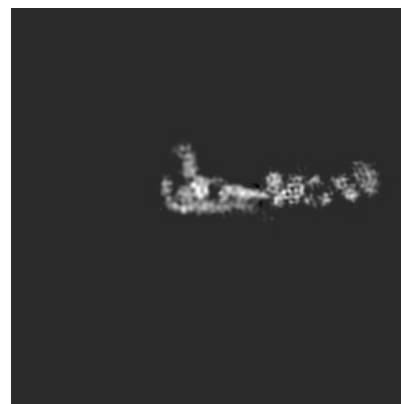
6.3.1 Primary map



X Index: 113



Y Index: 138

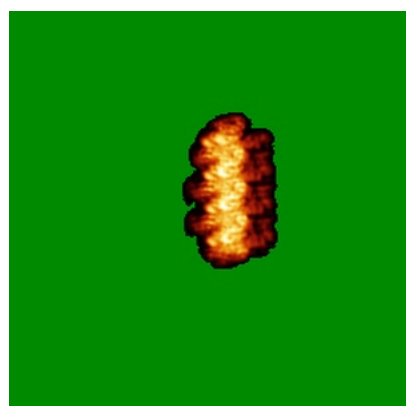


Z Index: 130

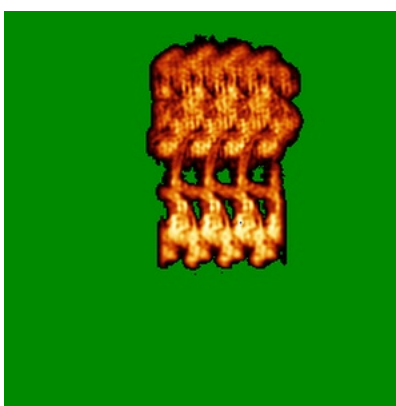
The images above show the largest variance slices of the map in three orthogonal directions.

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

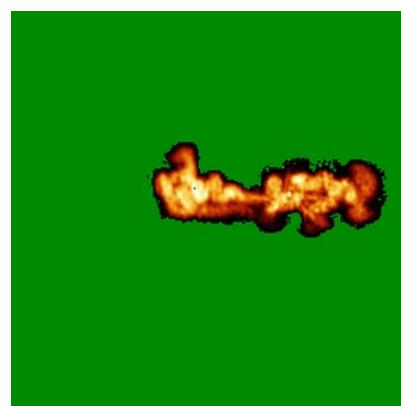
6.4.1 Primary map



X



Y

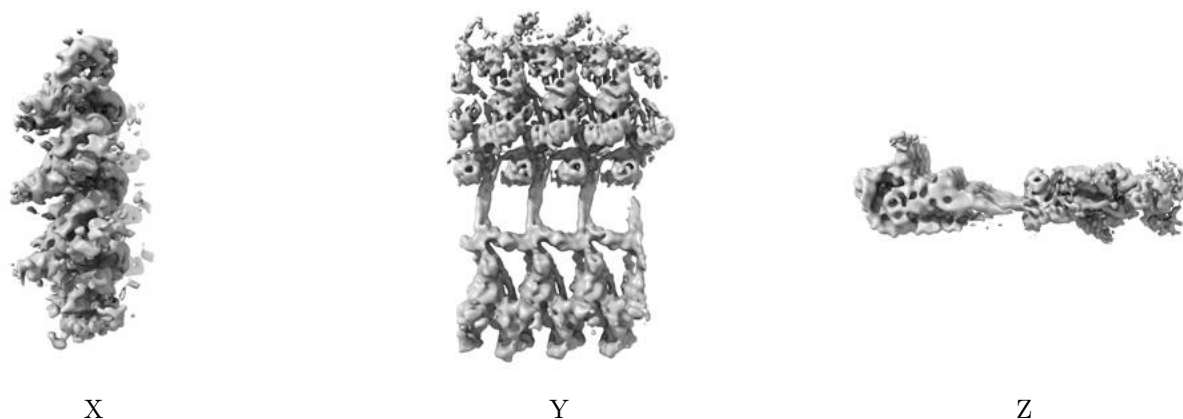


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.466. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

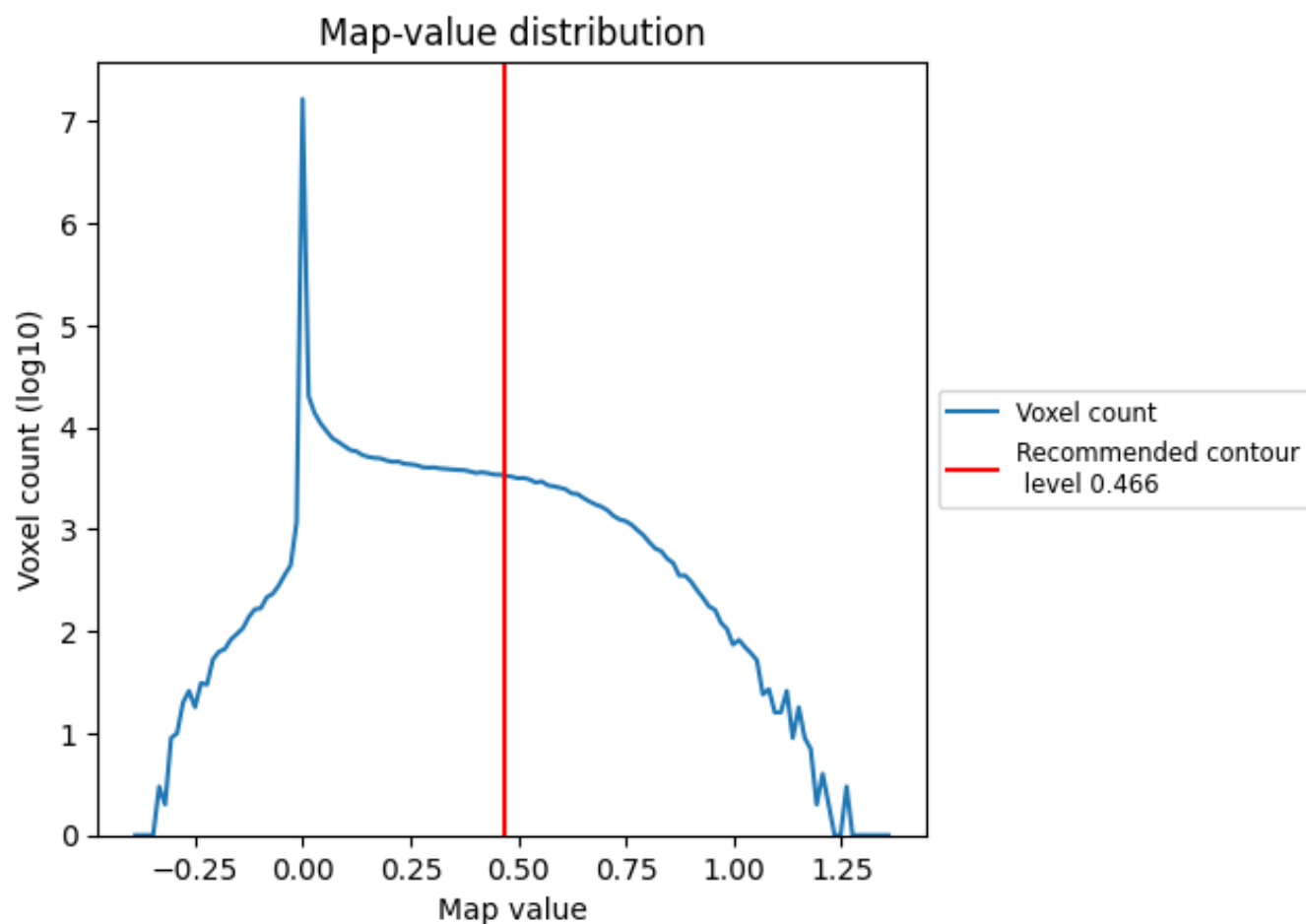
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

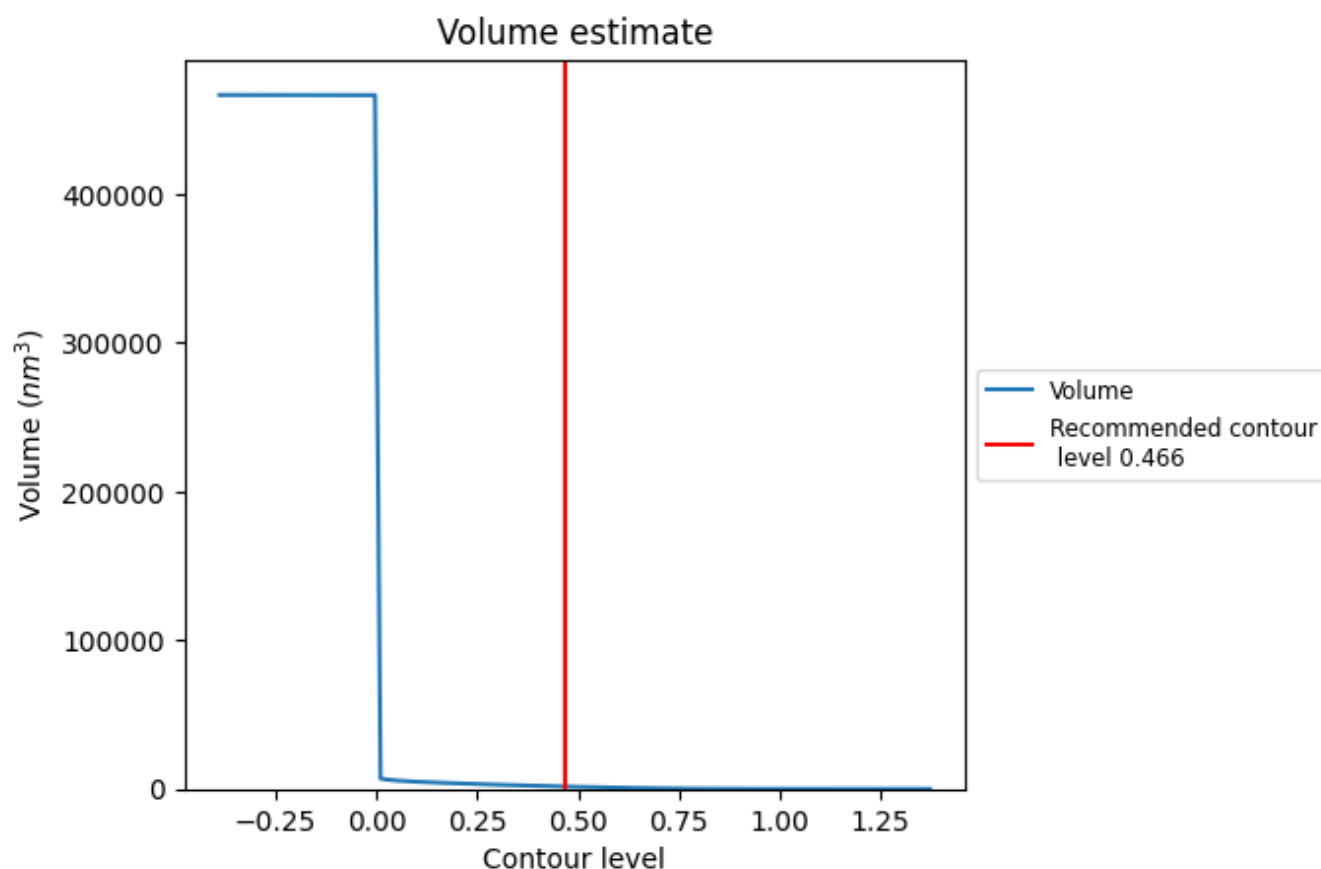
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

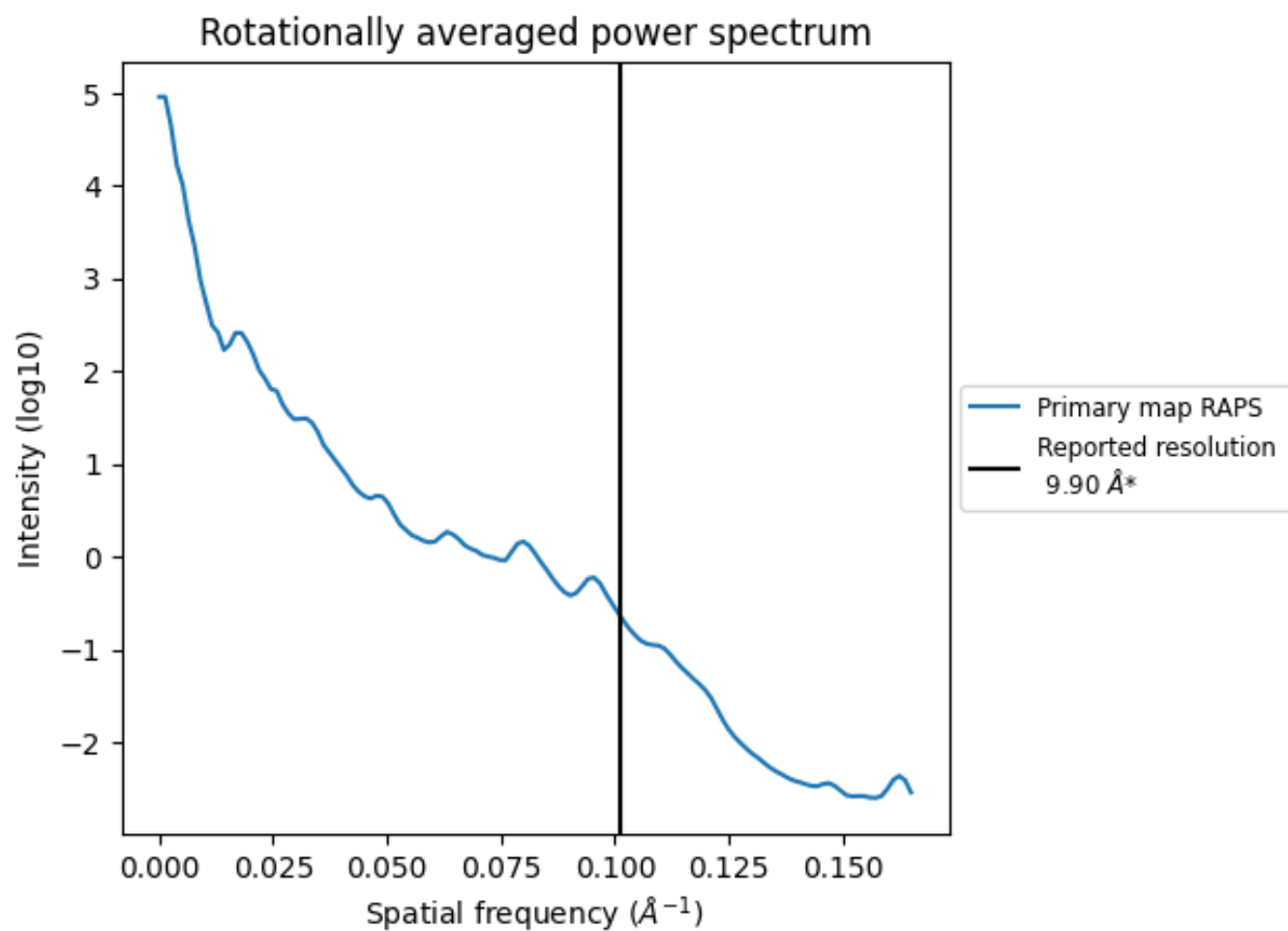
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1645 nm^3 ; this corresponds to an approximate mass of 1486 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 0.101 Å⁻¹

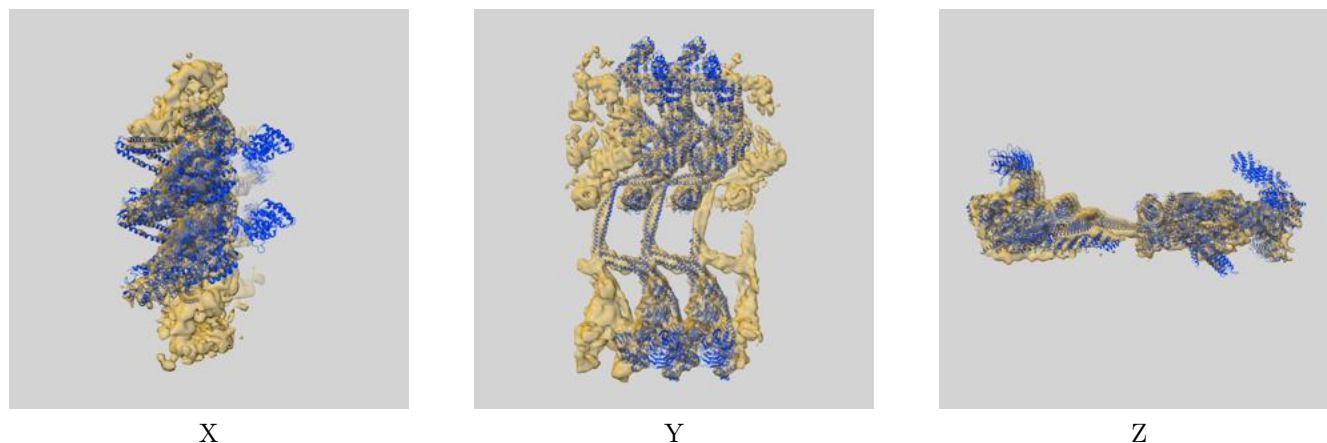
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

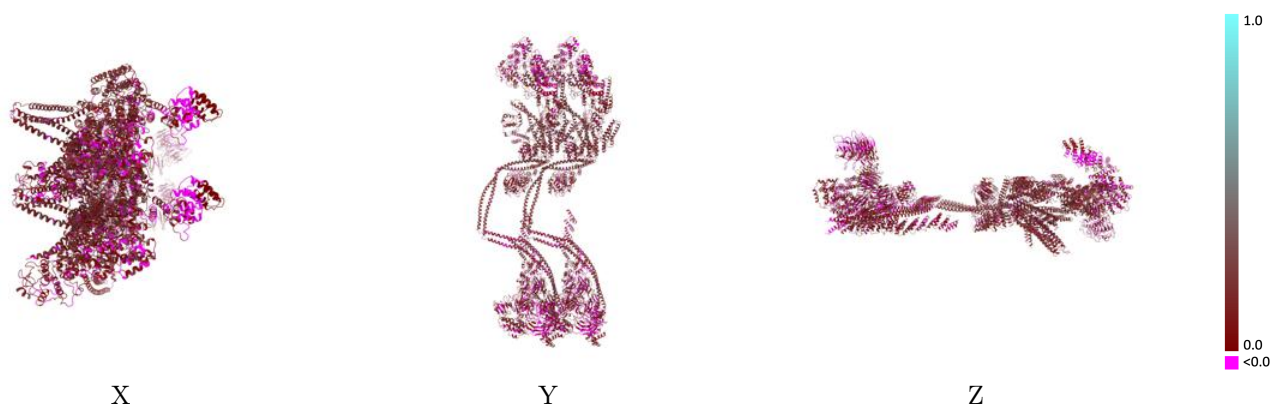
This section contains information regarding the fit between EMDB map EMD-15977 and PDB model 8BD7. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



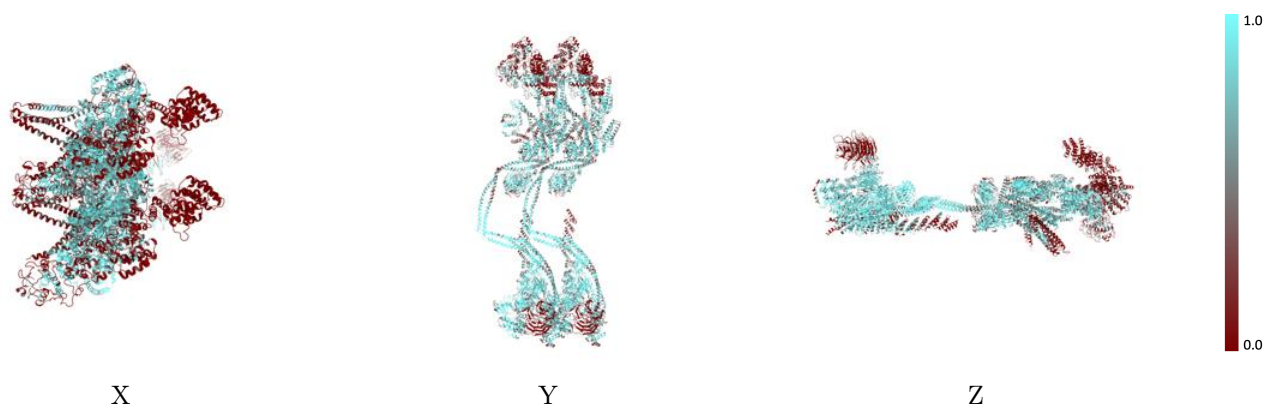
The images above show the 3D surface view of the map at the recommended contour level 0.466 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



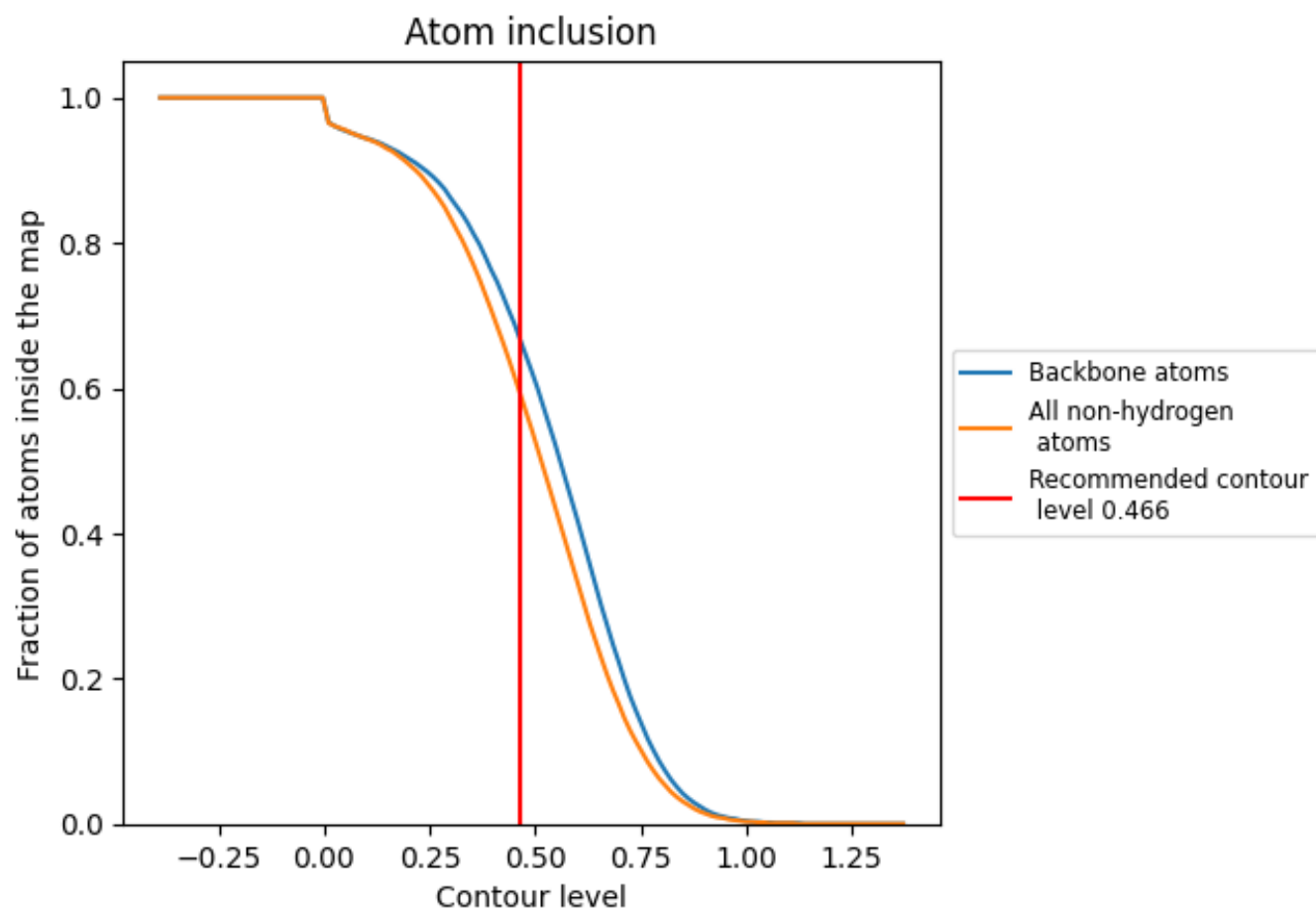
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.466).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 59% 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 (0.466) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5900	 0.1160
A	 0.7580	 0.1590
B	 0.5930	 0.1360
C	 0.7070	 0.1610
D	 0.2980	 0.0960
E	 0.1130	 0.0420
F	 0.5210	 0.1690
G	 0.4670	 0.1840
H	 0.7500	 0.1580
I	 0.8760	 0.1030
J	 0.5710	 0.1220
K	 0.6770	 0.1590
L	 0.8300	 0.1370
M	 0.7730	 0.1540
N	 0.2730	 0.0760
O	 0.0990	 0.0400
P	 0.5200	 0.1620
Q	 0.4430	 0.1720
R	 0.8590	 0.0980
S	 0.4670	 0.0810
T	 0.8340	 0.1350
U	 0.7860	 0.1600
V	 0.4690	 0.0790
W	 0.7630	 0.1070
X	 0.6990	 0.1260
Y	 0.7600	 0.1010
Z	 0.7260	 0.1260

