



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 01:08 PM UTC

PDB ID : 5V5S / pdb_00005v5s
EMDB ID : EMD-8636
Title : multi-drug efflux; membrane transport; RND superfamily; Drug resistance
Authors : wang, Z.; fan, G.; Hryc, C.F.; Blaza, J.N.; Serysheva, I.I.; Schmid, M.F.; Chiu, W.; Luisi, B.F.; Du, D.
Deposited on : 2017-03-15
Resolution : 6.50 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:

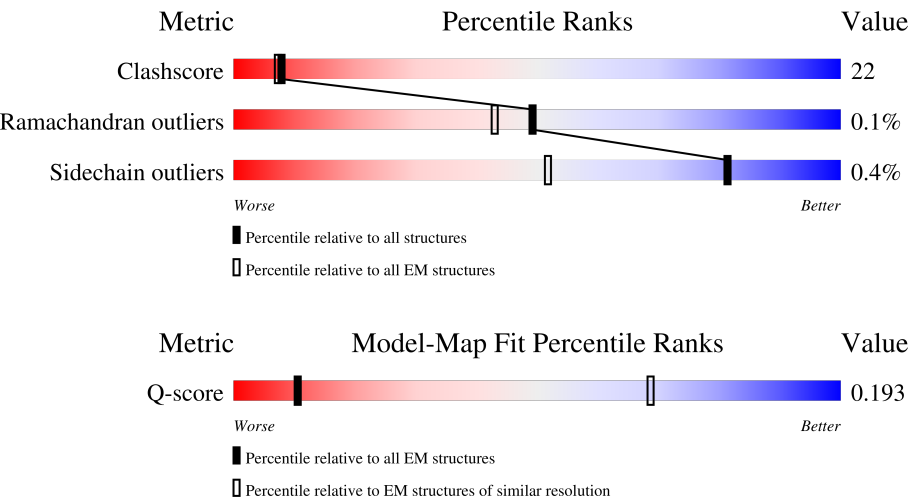
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.50 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	556 (6.00 - 7.00)

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	442	
1	B	442	
1	C	442	
2	D	397	

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Mol	Chain	Length	Quality of chain
2	E	397	
2	F	397	
2	G	397	
2	H	397	
2	I	397	
3	J	1049	
3	K	1049	
3	L	1049	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 48705 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 Outer membrane protein TolC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	428	Total	C	N	O	Se	0	0
			3304	2037	586	676	5		
1	B	428	Total	C	N	O	Se	0	0
			3304	2037	586	676	5		
1	C	428	Total	C	N	O	Se	0	0
			3304	2037	586	676	5		

- Molecule 2 is a protein called Multidrug efflux pump subunit AcrA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	340	Total	C	N	O	S	0	0
			2556	1598	451	505	2		
2	E	340	Total	C	N	O	S	0	0
			2556	1598	451	505	2		
2	F	340	Total	C	N	O	S	0	0
			2556	1598	451	505	2		
2	G	340	Total	C	N	O	S	0	0
			2556	1598	451	505	2		
2	H	340	Total	C	N	O	S	0	0
			2556	1598	451	505	2		
2	I	340	Total	C	N	O	S	0	0
			2556	1598	451	505	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	273	CYS	SER	conflict	UNP P0AE07
E	273	CYS	SER	conflict	UNP P0AE07
F	273	CYS	SER	conflict	UNP P0AE07
G	273	CYS	SER	conflict	UNP P0AE07
H	273	CYS	SER	conflict	UNP P0AE07
I	273	CYS	SER	conflict	UNP P0AE07

- Molecule 3 is a protein called Multidrug efflux pump subunit AcrB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	1037	Total	C	N	O	S	0	0
			7819	5032	1290	1452	45		
3	K	1037	Total	C	N	O	S	0	0
			7819	5032	1290	1452	45		
3	L	1037	Total	C	N	O	S	0	0
			7819	5032	1290	1452	45		

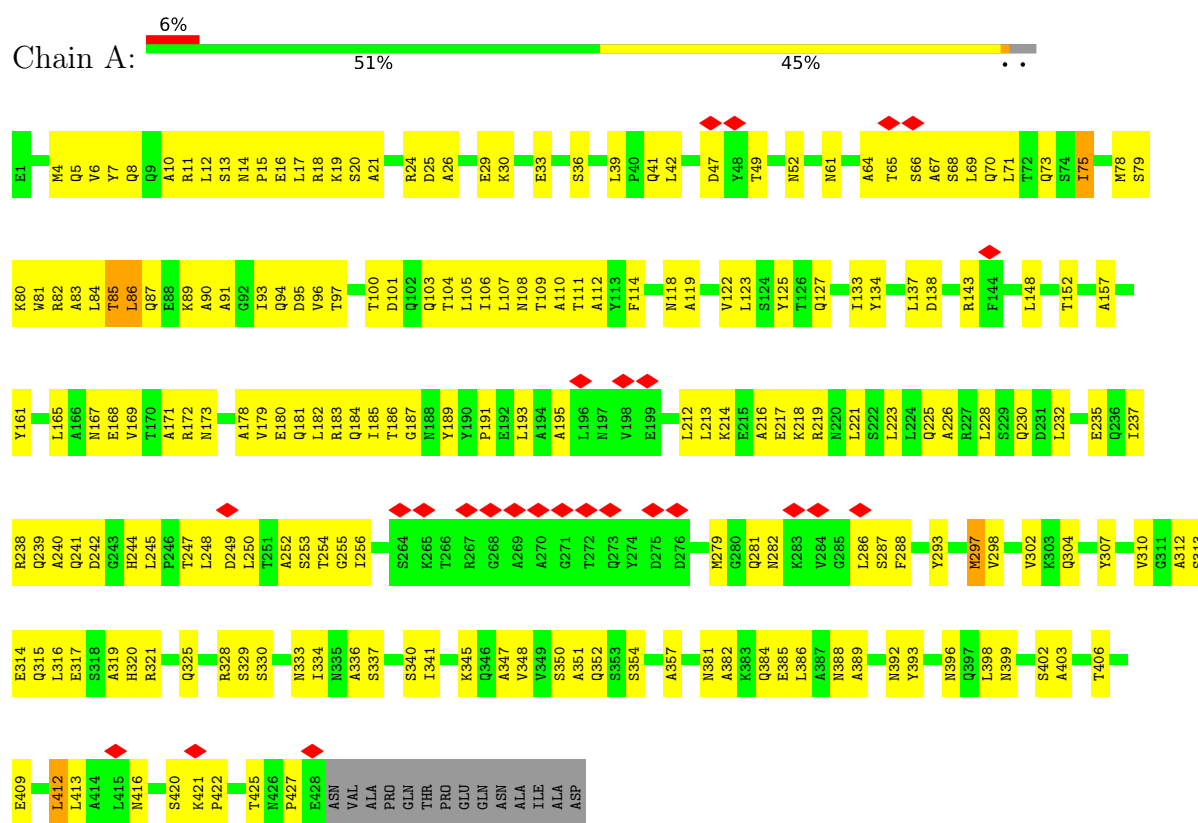
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	258	CYS	SER	conflict	UNP P31224
K	258	CYS	SER	conflict	UNP P31224
L	258	CYS	SER	conflict	UNP P31224

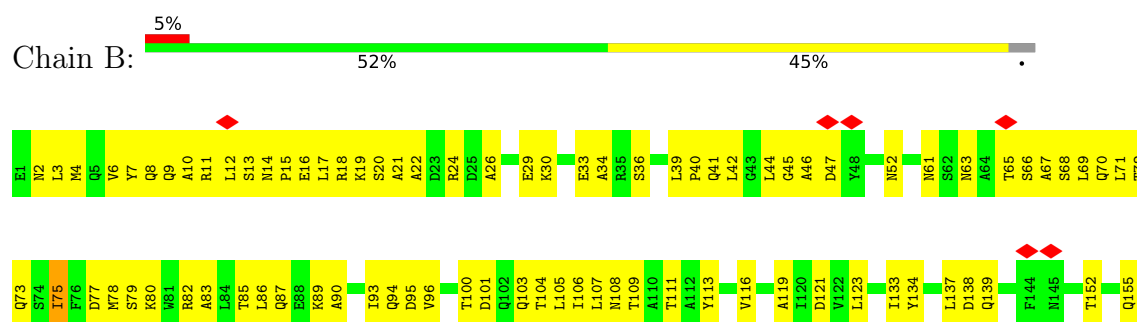
3 Residue-property plots

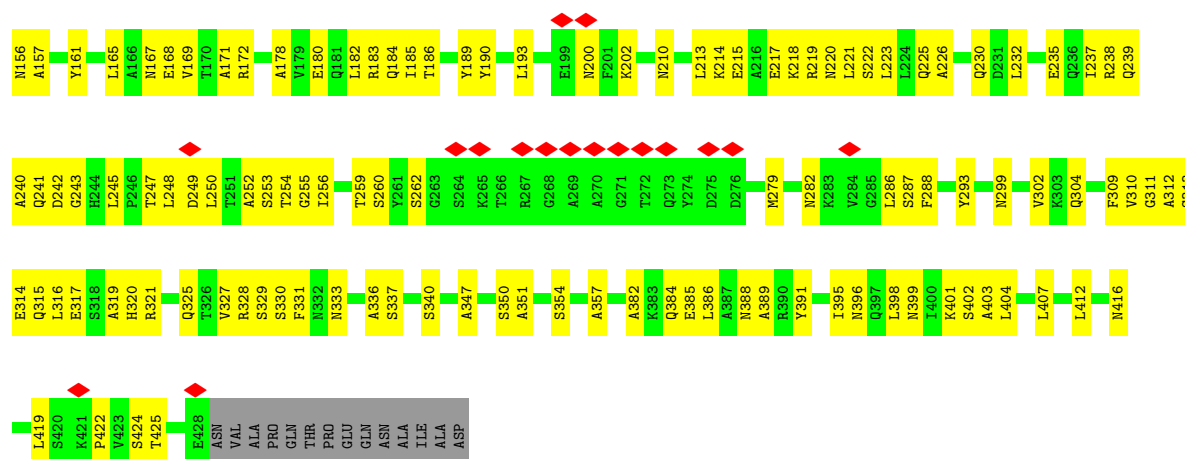
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

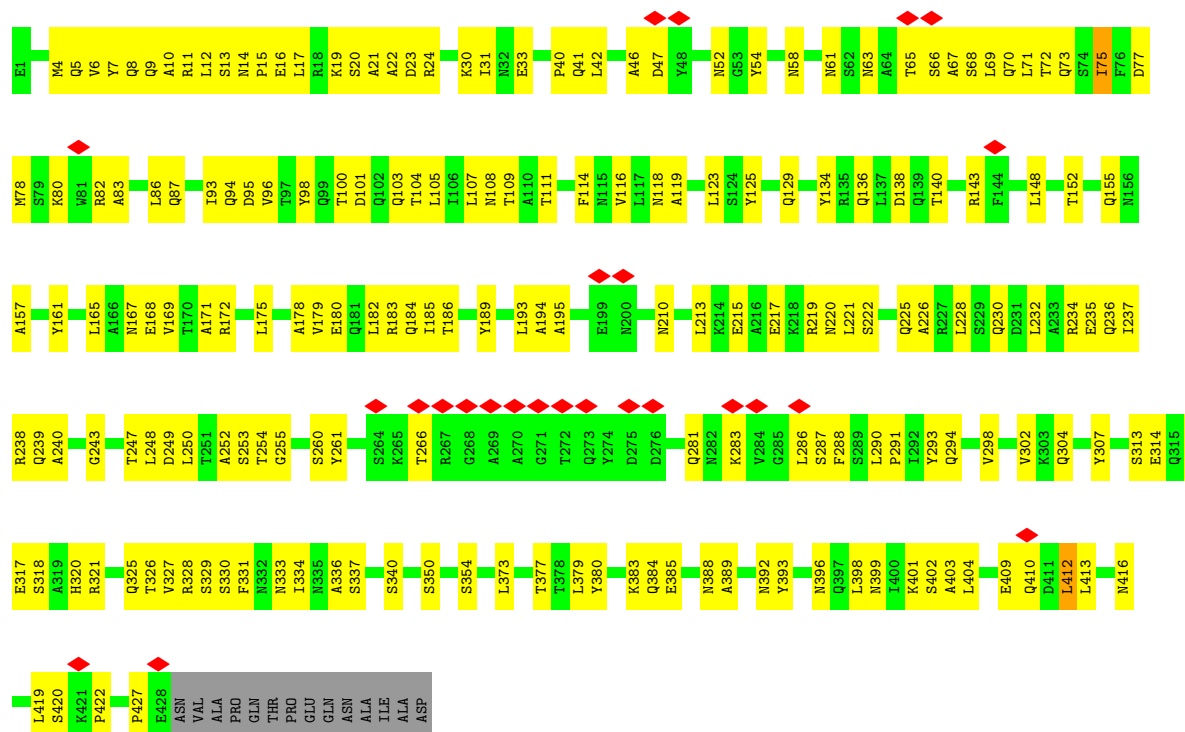


• Molecule 1: Outer membrane protein TolC

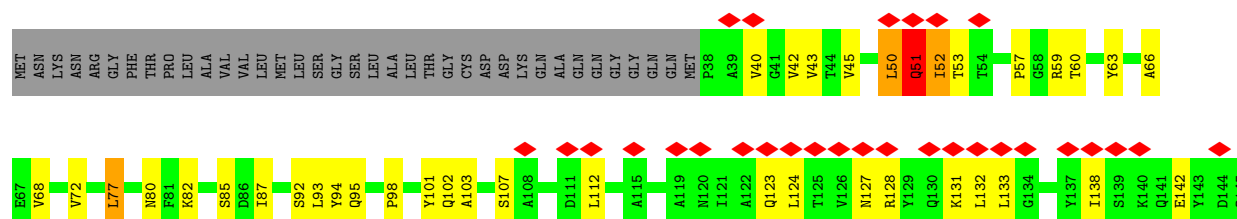


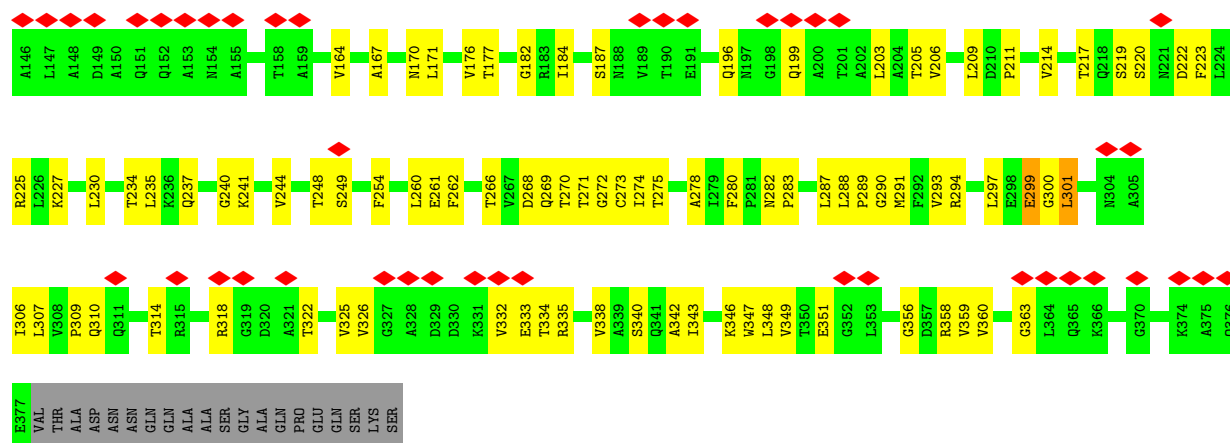


• Molecule 1: Outer membrane protein TolC

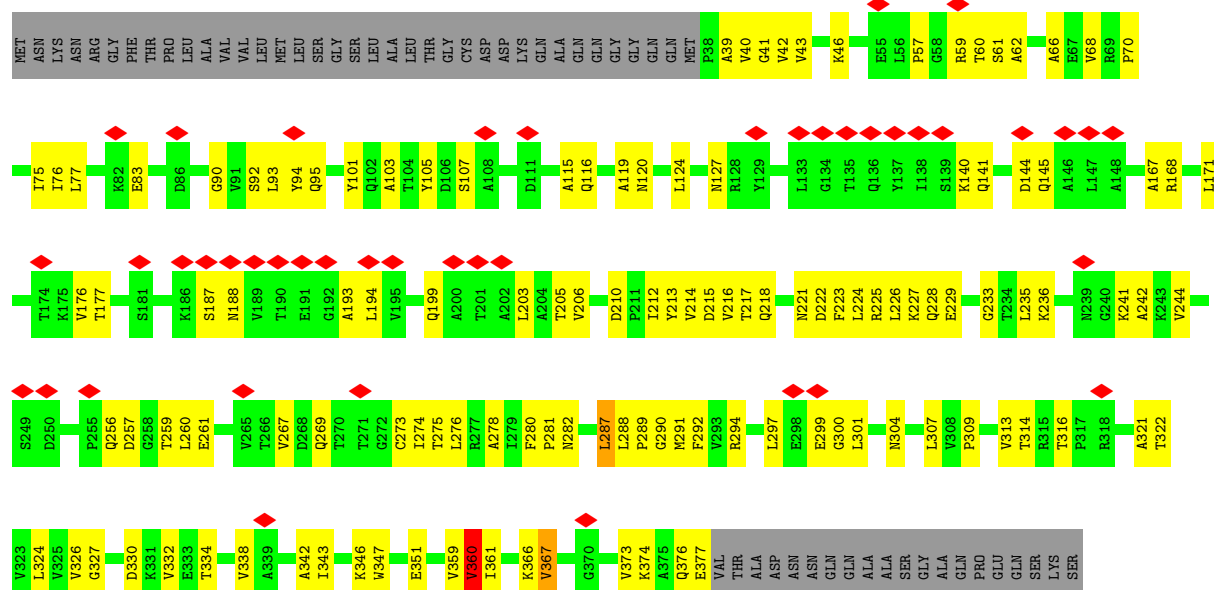


• Molecule 2: Multidrug efflux pump subunit AcrA

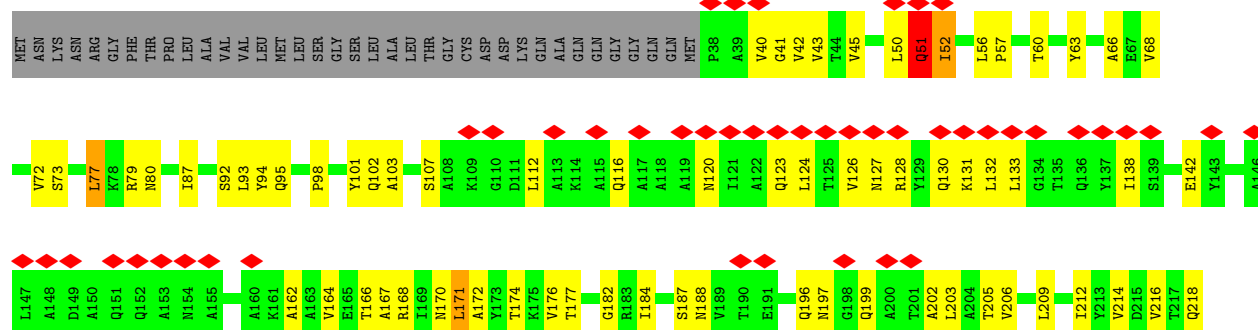




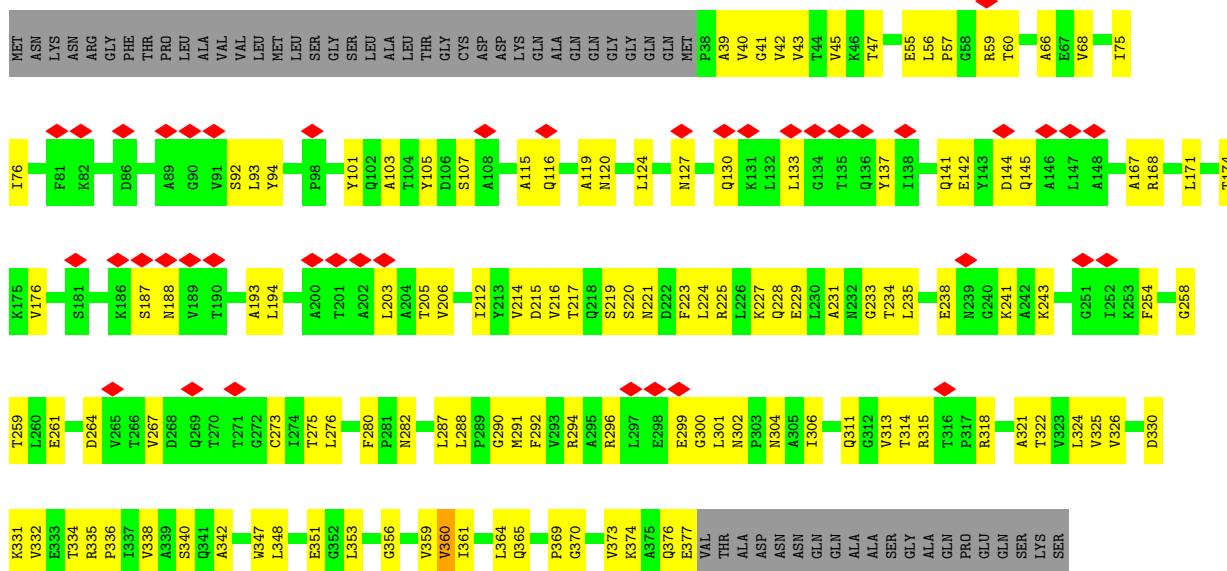
• Molecule 2: Multidrug efflux pump subunit AcrA



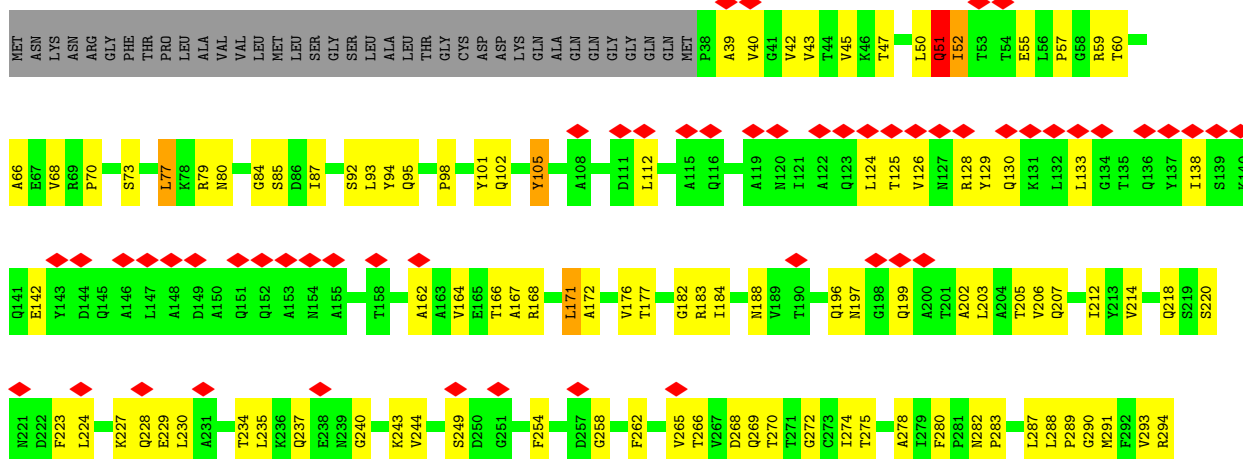
• Molecule 2: Multidrug efflux pump subunit AcrA

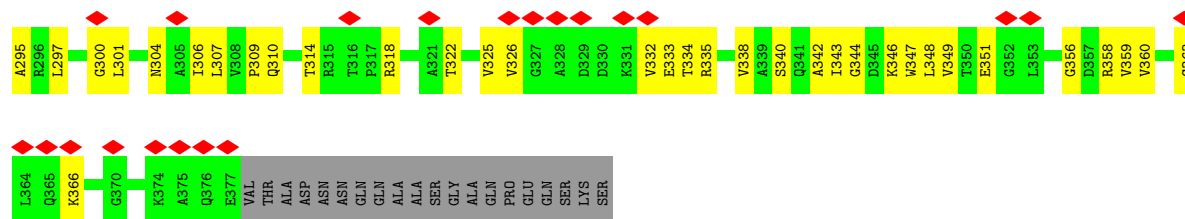


- Molecule 2: Multidrug efflux pump subunit AcrA

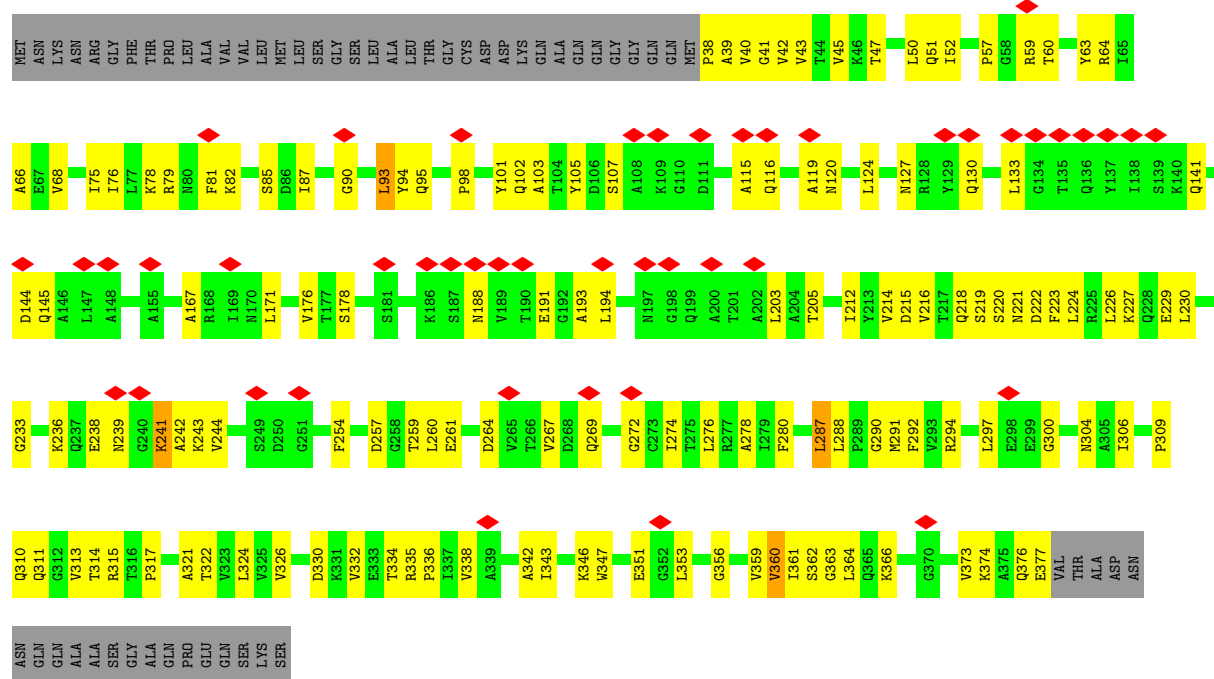


- Molecule 2: Multidrug efflux pump subunit AcrA

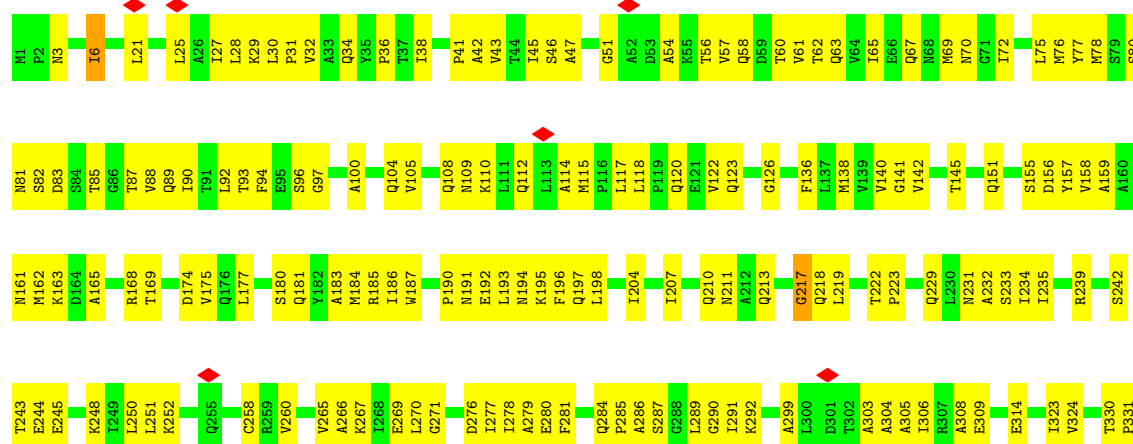


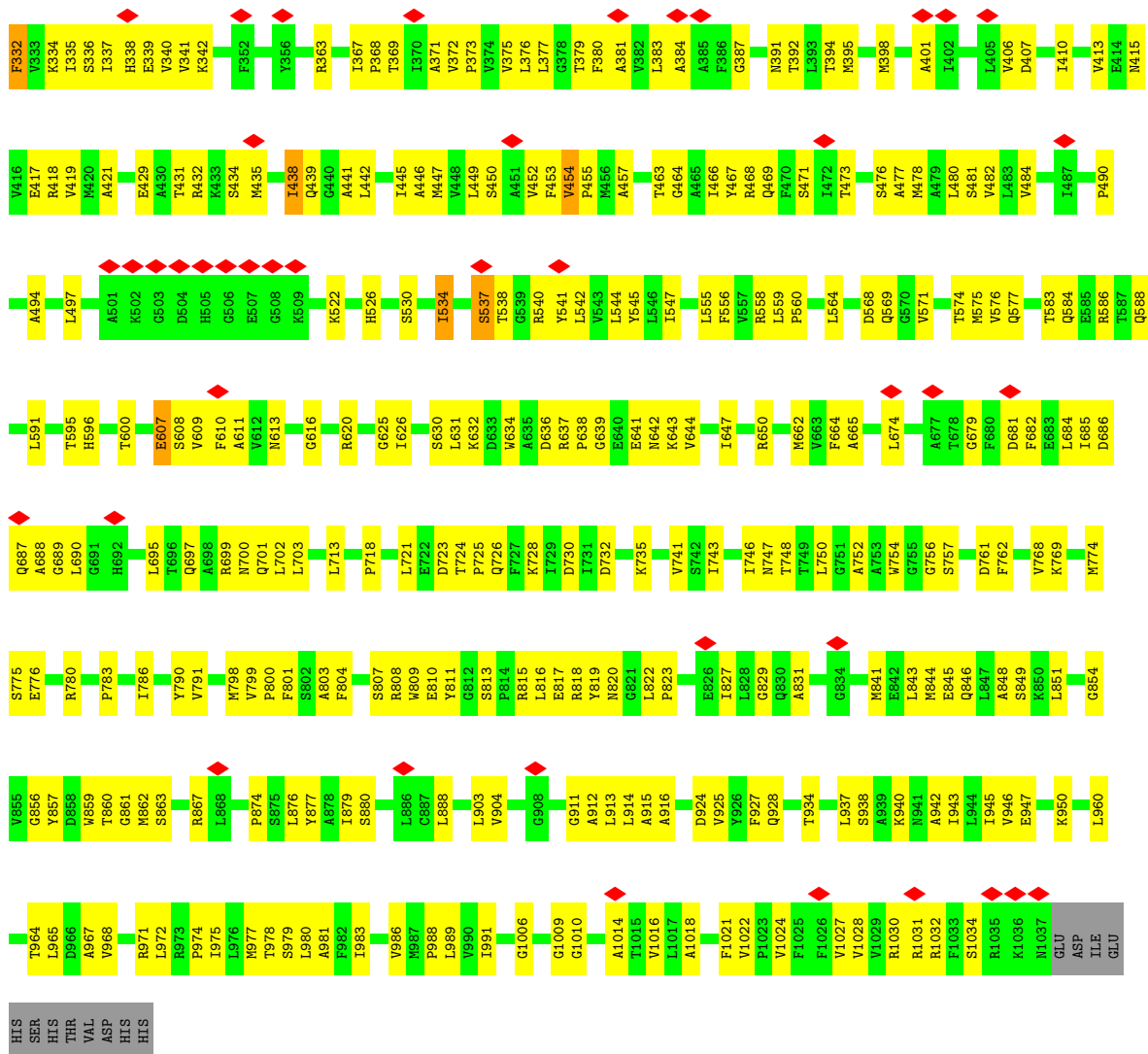


• Molecule 2: Multidrug efflux pump subunit AcrA



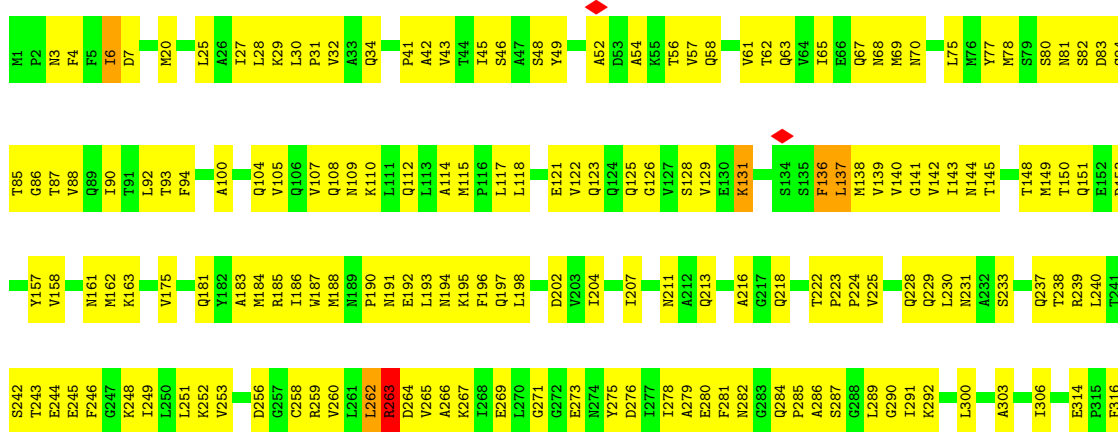
• Molecule 3: Multidrug efflux pump subunit AcrB

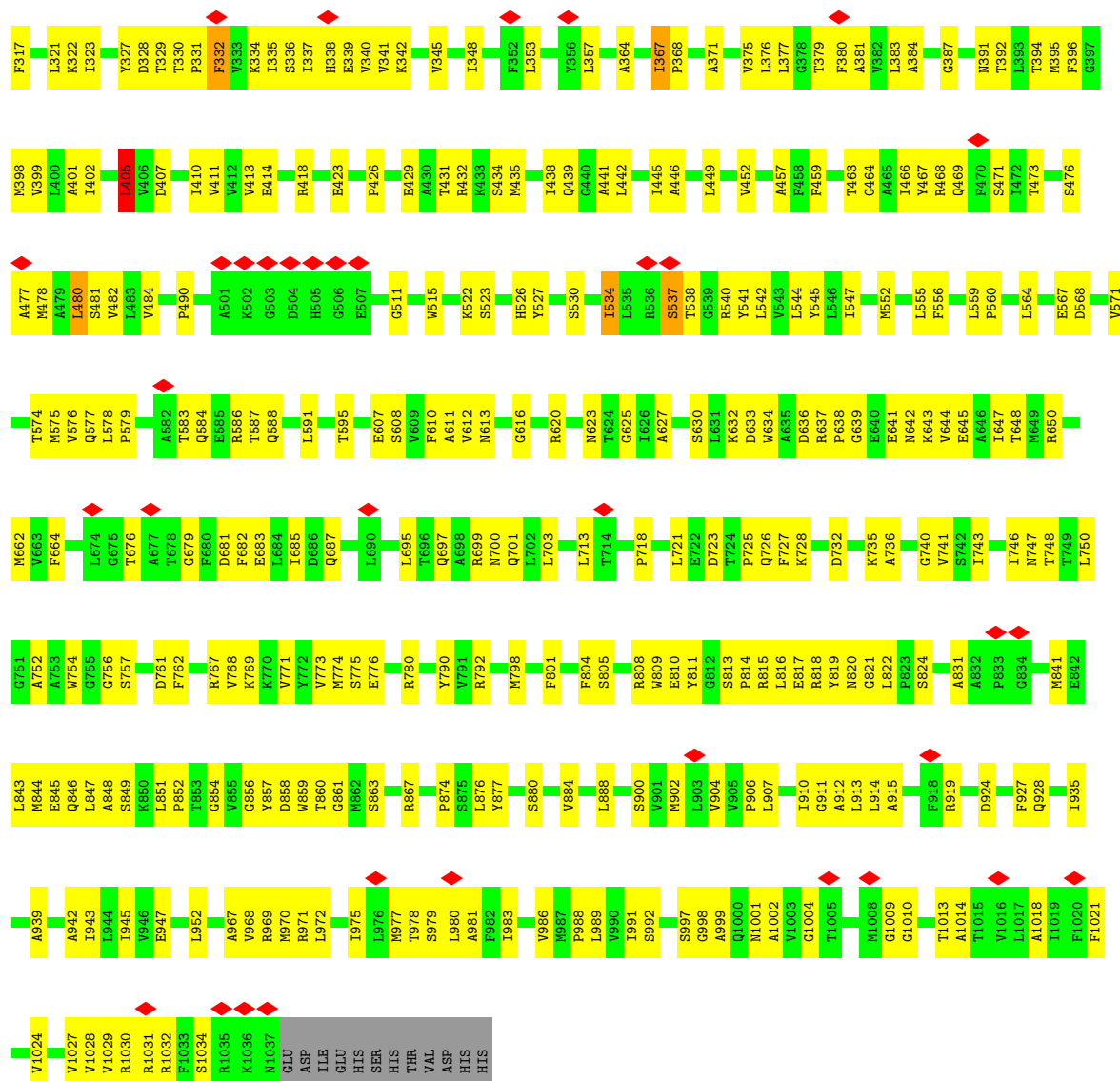




• Molecule 3: Multidrug efflux pump subunit AcrB

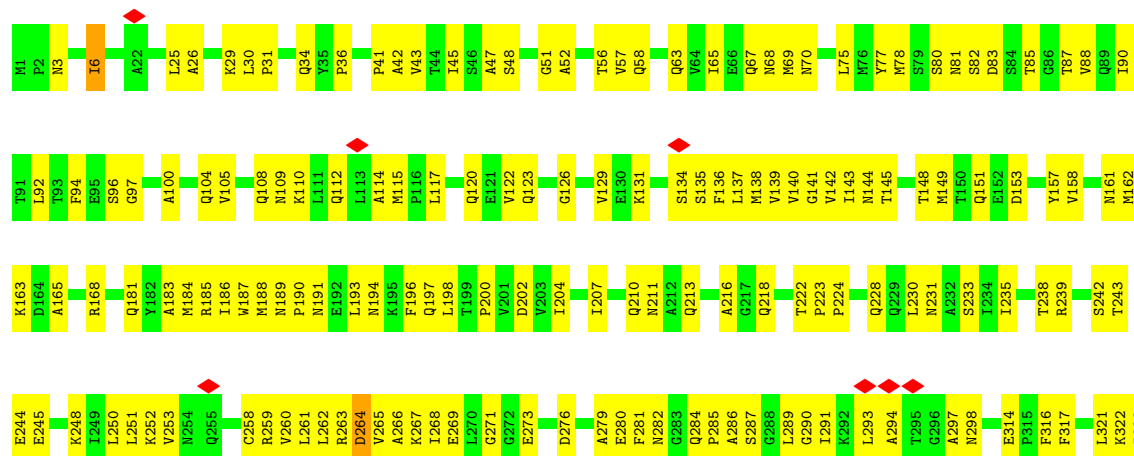
Chain K: 54% 44%





• Molecule 3: Multidrug efflux pump subunit AcrB

Chain L: 54% 44% ::



V1027	V1028	V1029	R1030	R1031	R1032	F1033	S1034	R1035	K1036	N1037	GLU	ASP	ILE	GLU	HIS	SER	HIS	THR	VAL	ASP	HIS	HIS																																
G936	L937	S938	A939	K940	N941	A942	I943	L944	I945	V946	E947	F948	L952	A963	T964	D965	D966	A967	V968	R971	L972	M977	L980	A981	F982	I983	V986	L989	S997	G998	A999	Q1000	N1001	A1002	V1003	G1009	G1010	M1011	V1012	T1013	A1014	A1018	I1019	F1020	F1021	V1024	F1025	F1026						
A848	L851	P852	K769	T770	L771	V772	W773	M774	S775	E776	A777	R780	Y790	W791	R792	G796	Q797	M798	V799	P800	F801	F804	S805	S806	S807	R808	W809	E810	Y811	P814	R815	L816	E817	R818	V819	N820	G821	L822	P823	L914	A915	F918	R919	D924	V925	Y926	F927	Q928	V929	L932	T933	T934	I935	
D681	F682	E683	L684	I685	D686	Q687	A688	G689	L690	L695	T696	Q697	A698	R699	N700	Q701	L702	L703	L713	T714	P718	L721	E722	D723	T724	P725	Q726	F727	K728	I729	D730	I731	D732	K735	L739	G740	V741	S742	I743	N744	D745	I746	N747	T748	T749	A752	G756	S757	D761					
V576	Q577	T583	Q584	E585	R586	T587	Q588	L591	T595	S608	V609	F610	A611	V612	G625	I626	A627	F628	V629	S630	L631	K632	D633	W634	R637	P638	G639	E640	E641	N642	K643	V644	S650	I653	S657	T538	G539	R540	Y541	L542	V543	L544	L555	R558	L559	P560	F563	V564	D568	Q569	G570	V571	T574	M575
I402	L405	D407	I410	V413	E417	R418	V419	M420	A421	G424	K502	G503	D504	H505	G506	E507	G508	K509	M510	G511	W515	Y527	S530	I534	S537	T538	R540	Y541	L542	V543	F458	F459	T463	G464	A465	I466	Y467	R468	T473	S476	A477	M478	A479											
V324	T325	P326	Y327	T330	P331	F332	V333	K334	I335	S336	I337	H338	E339	V340	V341	K342	V345	I348	Y356	F362	R363	S434	A364	I367	P368	A371	V372	P373	V375	L376	L377	G378	T379	F380	A381	V382	L383	A384	A385	F386	G387	N391	T392	M395	F396	G397	M398	V399	L400	A401				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	13544	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.092	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0266	Depositor
Map size ($\text{\AA}$)	402.8, 402.8, 402.8	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	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	0.33	0/3340	0.69	2/4529 (0.0%)
1	B	0.33	0/3340	0.68	2/4529 (0.0%)
1	C	0.33	0/3340	0.66	0/4529
2	D	0.33	0/2589	0.69	3/3521 (0.1%)
2	E	0.34	1/2589 (0.0%)	0.74	4/3521 (0.1%)
2	F	0.32	0/2589	0.67	3/3521 (0.1%)
2	G	0.33	0/2589	0.71	2/3521 (0.1%)
2	H	2.20	7/2589 (0.3%)	0.72	6/3521 (0.2%)
2	I	0.34	1/2589 (0.0%)	0.71	2/3521 (0.1%)
3	J	0.43	0/7968	0.78	7/10826 (0.1%)
3	K	0.43	0/7968	0.79	6/10826 (0.1%)
3	L	0.43	0/7968	0.79	8/10826 (0.1%)
All	All	0.63	9/49458 (0.0%)	0.74	45/67191 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	1
2	D	0	5
2	E	0	3
2	F	0	3
2	G	0	3
2	H	0	2
2	I	0	4
3	J	0	7
3	K	0	9
3	L	0	8
All	All	0	51

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	171	LEU	CG-CD2	100.38	4.83	1.52
2	H	105	TYR	CD2-CE2	23.86	2.10	1.38
2	H	105	TYR	CD1-CE1	21.90	2.04	1.38
2	H	105	TYR	CE2-CZ	18.03	1.81	1.38
2	H	105	TYR	CE1-CZ	17.66	1.80	1.38
2	H	105	TYR	CG-CD1	15.94	1.72	1.39
2	H	105	TYR	CG-CD2	15.63	1.72	1.39
2	I	287	LEU	C-N	-5.55	1.24	1.33
2	E	287	LEU	C-N	-5.38	1.25	1.33

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	367	VAL	CA-C-N	8.86	142.90	123.15
2	E	367	VAL	C-N-CA	8.86	142.90	123.15
2	H	300	GLY	N-CA-C	-7.94	103.56	115.00
2	D	52	ILE	N-CA-C	7.08	124.08	109.34
2	F	52	ILE	N-CA-C	6.94	123.78	109.34
2	H	52	ILE	N-CA-C	6.69	123.26	109.34
2	E	291	MET	CA-C-N	6.39	133.20	121.70
2	E	291	MET	C-N-CA	6.39	133.20	121.70
3	J	332	PHE	CA-C-N	-6.37	114.83	122.35
3	J	332	PHE	C-N-CA	-6.37	114.83	122.35
2	G	291	MET	CA-C-N	6.28	133.01	121.70
2	G	291	MET	C-N-CA	6.28	133.01	121.70
1	A	297	MSE	N-CA-C	-6.17	104.46	112.23
2	I	291	MET	CA-C-N	6.13	132.74	121.70
2	I	291	MET	C-N-CA	6.13	132.74	121.70
3	K	405	LEU	CA-CB-CG	6.02	137.38	116.30
3	K	452	VAL	CA-C-N	-5.98	111.62	122.50
3	K	452	VAL	C-N-CA	-5.98	111.62	122.50
2	H	51	GLN	CA-C-N	5.84	132.48	121.97
2	H	51	GLN	C-N-CA	5.84	132.48	121.97
3	L	405	LEU	CA-CB-CG	5.82	136.66	116.30
2	H	105	TYR	CA-CB-CG	5.67	124.11	113.90
3	L	332	PHE	CA-C-N	-5.65	115.68	122.35
3	L	332	PHE	C-N-CA	-5.65	115.68	122.35
3	L	534	ILE	N-CA-C	-5.62	107.01	112.29
1	B	279	MSE	N-CA-C	5.60	117.77	110.43
3	L	452	VAL	CA-C-N	-5.51	112.94	122.14
3	L	452	VAL	C-N-CA	-5.51	112.94	122.14
2	F	51	GLN	CA-C-N	5.51	131.88	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	51	GLN	C-N-CA	5.51	131.88	121.97
3	L	406	VAL	CA-C-N	-5.42	111.66	121.14
3	L	406	VAL	C-N-CA	-5.42	111.66	121.14
3	K	534	ILE	N-CA-C	-5.39	107.22	112.29
3	K	332	PHE	CA-C-N	-5.39	115.75	121.84
3	K	332	PHE	C-N-CA	-5.39	115.75	121.84
3	J	534	ILE	N-CA-C	-5.36	107.26	112.29
2	D	51	GLN	CA-C-N	5.31	131.53	121.97
2	D	51	GLN	C-N-CA	5.31	131.53	121.97
2	H	171	LEU	CD1-CG-CD2	5.20	122.24	110.80
1	A	279	MSE	N-CA-C	5.19	118.00	110.42
3	J	452	VAL	CA-C-N	-5.15	113.13	122.50
3	J	452	VAL	C-N-CA	-5.15	113.13	122.50
1	B	78	MSE	N-CA-C	-5.12	108.05	114.56
3	J	406	VAL	CA-C-N	-5.01	112.37	121.14
3	J	406	VAL	C-N-CA	-5.01	112.37	121.14

There are no chirality outliers.

All (51) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	297	MSE	Peptide
1	A	75	ILE	Peptide
1	A	85	THR	Peptide
1	B	2	ASN	Peptide
1	B	75	ILE	Peptide
1	B	85	THR	Peptide
1	C	75	ILE	Peptide
2	D	209	LEU	Peptide
2	D	299	GLU	Peptide
2	D	50	LEU	Peptide
2	D	51	GLN	Peptide
2	D	77	LEU	Peptide
2	E	360	VAL	Peptide
2	E	361	ILE	Peptide
2	E	93	LEU	Peptide
2	F	209	LEU	Peptide
2	F	51	GLN	Peptide
2	F	77	LEU	Peptide
2	G	238	GLU	Peptide
2	G	360	VAL	Peptide
2	G	93	LEU	Peptide

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Mol	Chain	Res	Type	Group
2	H	51	GLN	Peptide
2	H	77	LEU	Peptide
2	I	238	GLU	Peptide
2	I	241	LYS	Peptide
2	I	360	VAL	Peptide
2	I	93	LEU	Peptide
3	J	1016	VAL	Peptide
3	J	217	GLY	Peptide
3	J	36	PRO	Peptide
3	J	438	ILE	Peptide
3	J	537	SER	Peptide
3	J	607	GLU	Peptide
3	J	609	VAL	Peptide
3	K	131	LYS	Peptide
3	K	136	PHE	Peptide
3	K	137	LEU	Peptide
3	K	262	LEU	Peptide
3	K	263	ARG	Peptide
3	K	273	GLU	Peptide
3	K	426	PRO	Peptide
3	K	537	SER	Peptide
3	K	906	PRO	Peptide
3	L	136	PHE	Peptide
3	L	262	LEU	Peptide
3	L	273	GLU	Peptide
3	L	298	ASN	Peptide
3	L	36	PRO	Peptide
3	L	426	PRO	Peptide
3	L	438	ILE	Peptide
3	L	537	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3304	0	3254	194	0
1	B	3304	0	3254	179	0
1	C	3304	0	3254	179	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2556	0	2616	122	0
2	E	2556	0	2616	102	0
2	F	2556	0	2615	125	0
2	G	2556	0	2616	116	0
2	H	2556	0	2616	122	0
2	I	2556	0	2616	113	0
3	J	7819	0	7919	330	0
3	K	7819	0	7919	366	0
3	L	7819	0	7919	357	0
All	All	48705	0	49214	2187	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 22.

All (2187) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:105:TYR:CZ	2:H:105:TYR:CE2	1.81	1.63
2:D:217:THR:HG23	2:D:273:CYS:SG	1.40	1.60
2:H:105:TYR:CZ	2:H:105:TYR:CE1	1.80	1.60
2:H:220:SER:HA	2:H:223:PHE:CE1	1.36	1.60
2:G:217:THR:HG23	2:G:273:CYS:SG	1.43	1.56
2:D:288:LEU:CD2	2:E:267:VAL:HG21	1.44	1.47
2:H:105:TYR:CE1	2:H:105:TYR:CD1	2.04	1.43
2:G:217:THR:CG2	2:G:273:CYS:SG	2.06	1.39
2:H:105:TYR:CE2	2:H:105:TYR:CD2	2.10	1.38
3:L:141:GLY:HA2	3:L:287:SER:O	1.21	1.32
2:D:223:PHE:CE2	2:D:274:ILE:HG12	1.64	1.31
3:K:141:GLY:HA2	3:K:287:SER:O	1.26	1.31
2:D:223:PHE:HE2	2:D:274:ILE:CG1	1.44	1.31
3:K:139:VAL:HA	3:K:289:LEU:O	1.25	1.31
3:J:611:ALA:HA	3:J:626:ILE:O	1.11	1.28
2:F:223:PHE:CZ	2:F:274:ILE:HB	1.71	1.25
2:F:223:PHE:CE2	2:F:274:ILE:HB	1.72	1.24
2:H:220:SER:CA	2:H:223:PHE:CE1	2.22	1.21
3:L:139:VAL:HA	3:L:289:LEU:O	1.37	1.20
2:E:217:THR:HG23	2:E:273:CYS:SG	1.83	1.19
2:D:288:LEU:HD22	2:E:267:VAL:CG2	1.73	1.17
2:E:288:LEU:HD13	2:F:269:GLN:OE1	1.39	1.17
2:E:223:PHE:CE2	2:E:227:LYS:HE3	1.80	1.16
2:D:217:THR:CG2	2:D:273:CYS:SG	2.34	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:223:PHE:CD2	2:G:227:LYS:NZ	2.14	1.15
2:F:249:SER:OG	2:G:224:LEU:CD1	1.96	1.14
2:F:220:SER:HA	2:F:223:PHE:HD1	1.04	1.11
2:F:288:LEU:HD22	2:G:267:VAL:HG22	1.26	1.11
2:H:220:SER:HA	2:H:223:PHE:CD1	1.84	1.11
2:H:288:LEU:CD2	2:I:267:VAL:HG21	1.82	1.09
2:D:220:SER:HA	2:D:223:PHE:HD1	1.11	1.09
3:J:611:ALA:CA	3:J:626:ILE:O	2.02	1.07
2:F:220:SER:HA	2:F:223:PHE:CD1	1.90	1.06
2:H:288:LEU:HD22	2:I:267:VAL:HG21	1.33	1.06
2:G:223:PHE:CE2	2:G:227:LYS:NZ	2.24	1.05
2:H:220:SER:O	2:H:223:PHE:HD1	1.36	1.05
1:A:165:LEU:O	1:A:169:VAL:HG23	1.58	1.04
2:H:288:LEU:HD22	2:I:267:VAL:CG2	1.87	1.04
2:D:223:PHE:HE2	2:D:274:ILE:HG12	0.93	1.04
1:B:235:GLU:O	1:B:239:GLN:HB2	1.57	1.02
2:D:223:PHE:CE2	2:D:274:ILE:CG1	2.32	1.02
3:J:330:THR:O	3:J:334:LYS:HB3	1.57	1.02
1:B:165:LEU:O	1:B:169:VAL:HG23	1.60	1.01
3:K:137:LEU:HB3	3:K:291:ILE:O	1.58	1.01
2:D:220:SER:HA	2:D:223:PHE:CD1	1.95	1.00
3:L:968:VAL:O	3:L:972:LEU:HB2	1.59	1.00
2:F:77:LEU:HB3	2:F:95:GLN:O	1.61	1.00
2:F:219:SER:C	2:F:223:PHE:CE1	2.40	1.00
3:L:729:ILE:HA	3:L:806:SER:O	1.62	1.00
3:L:537:SER:O	3:L:541:TYR:HB2	1.60	0.99
2:H:77:LEU:HB3	2:H:95:GLN:O	1.60	0.99
3:L:330:THR:O	3:L:334:LYS:HB2	1.60	0.99
2:F:219:SER:O	2:F:223:PHE:CD1	2.16	0.98
3:K:537:SER:O	3:K:541:TYR:HB2	1.62	0.98
3:L:186:ILE:HA	3:L:267:LYS:O	1.63	0.98
3:L:137:LEU:HB3	3:L:291:ILE:O	1.62	0.98
2:D:77:LEU:HB3	2:D:95:GLN:O	1.64	0.98
2:D:288:LEU:CD2	2:E:267:VAL:CG2	2.38	0.98
3:J:607:GLU:O	3:J:630:SER:HB3	1.61	0.98
3:J:141:GLY:O	3:J:323:ILE:HA	1.64	0.97
2:D:220:SER:CA	2:D:223:PHE:HD1	1.77	0.97
2:F:220:SER:CA	2:F:223:PHE:HD1	1.78	0.97
3:L:332:PHE:O	3:L:336:SER:HB3	1.65	0.97
3:L:725:PRO:HA	3:L:810:GLU:O	1.65	0.97
2:H:101:TYR:O	2:H:105:TYR:HB2	1.65	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:537:SER:O	3:J:541:TYR:HB2	1.64	0.96
2:F:288:LEU:CD2	2:G:267:VAL:HG22	1.96	0.96
3:K:139:VAL:CA	3:K:289:LEU:O	2.14	0.96
3:K:175:VAL:HA	3:K:290:GLY:O	1.64	0.96
3:K:577:GLN:HB3	3:K:662:MET:O	1.66	0.96
1:A:249:ASP:O	1:A:286:LEU:HA	1.65	0.95
3:J:332:PHE:O	3:J:336:SER:HB3	1.66	0.95
2:E:61:SER:O	2:E:213:TYR:HB2	1.66	0.95
3:J:968:VAL:O	3:J:972:LEU:HB2	1.65	0.95
1:A:235:GLU:O	1:A:239:GLN:HB2	1.66	0.95
2:G:66:ALA:O	2:G:205:THR:HA	1.67	0.94
3:K:968:VAL:O	3:K:972:LEU:HB2	1.67	0.94
2:E:223:PHE:HE2	2:E:227:LYS:HE3	1.25	0.94
3:K:575:MET:HB3	3:K:664:PHE:O	1.68	0.94
1:B:41:GLN:O	1:B:71:LEU:HA	1.66	0.93
2:E:59:ARG:HB3	2:E:215:ASP:O	1.67	0.93
3:L:141:GLY:CA	3:L:287:SER:O	2.16	0.93
2:G:217:THR:HG23	2:G:273:CYS:HG	1.15	0.92
3:J:538:THR:O	3:J:542:LEU:HB2	1.69	0.92
2:I:93:LEU:O	2:I:176:VAL:HB	1.70	0.92
1:C:249:ASP:O	1:C:286:LEU:HA	1.70	0.92
2:H:220:SER:O	2:H:223:PHE:CD1	2.21	0.92
3:K:337:ILE:O	3:K:341:VAL:HB	1.69	0.92
1:C:41:GLN:O	1:C:71:LEU:HA	1.69	0.91
2:F:219:SER:C	2:F:223:PHE:CD1	2.48	0.91
2:D:271:THR:HB	3:L:258:CYS:SG	2.10	0.91
2:D:219:SER:C	2:D:223:PHE:CD1	2.49	0.91
3:K:538:THR:O	3:K:542:LEU:HB2	1.71	0.90
2:H:42:VAL:HA	2:H:359:VAL:O	1.71	0.90
3:K:1027:VAL:O	3:K:1031:ARG:HB2	1.70	0.90
3:L:1027:VAL:O	3:L:1031:ARG:HB2	1.70	0.90
3:J:1027:VAL:O	3:J:1031:ARG:HB2	1.72	0.90
3:J:724:THR:O	3:J:811:TYR:HA	1.72	0.90
3:K:576:VAL:HB	3:K:625:GLY:O	1.72	0.89
3:J:679:GLY:HA2	3:J:829:GLY:O	1.72	0.89
2:F:223:PHE:CZ	2:F:274:ILE:CB	2.54	0.89
3:L:576:VAL:HB	3:L:625:GLY:O	1.71	0.89
3:L:538:THR:O	3:L:542:LEU:HB2	1.73	0.89
3:L:762:PHE:O	3:L:768:VAL:HA	1.70	0.89
1:B:182:LEU:O	1:B:186:THR:HB	1.73	0.89
3:J:682:PHE:O	3:J:827:ILE:HB	1.73	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:ASP:O	1:B:286:LEU:HA	1.72	0.88
2:F:249:SER:HG	2:G:224:LEU:CD1	1.82	0.88
2:E:66:ALA:O	2:E:205:THR:HA	1.73	0.88
3:K:336:SER:O	3:K:340:VAL:HB	1.73	0.88
3:L:726:GLN:O	3:L:809:TRP:HA	1.74	0.88
2:D:254:PHE:CE1	2:D:287:LEU:HD11	2.08	0.88
2:H:220:SER:CB	2:H:223:PHE:HE1	1.86	0.88
2:I:223:PHE:CE2	2:I:227:LYS:HE3	2.09	0.88
1:B:67:ALA:O	1:B:255:GLY:HA3	1.74	0.88
3:K:750:LEU:O	3:K:754:TRP:HB2	1.72	0.87
1:A:41:GLN:O	1:A:71:LEU:HA	1.73	0.87
3:L:139:VAL:HA	3:L:289:LEU:C	1.99	0.87
1:C:69:LEU:O	1:C:253:SER:HA	1.73	0.87
2:D:288:LEU:HD22	2:E:267:VAL:HG21	0.88	0.87
1:C:193:LEU:O	1:C:422:PRO:HA	1.75	0.87
1:A:16:GLU:O	1:A:20:SER:HB3	1.74	0.87
2:F:249:SER:OG	2:G:224:LEU:HD11	1.75	0.87
2:D:42:VAL:HA	2:D:359:VAL:O	1.74	0.86
3:J:47:ALA:O	3:J:87:THR:HA	1.75	0.86
3:K:332:PHE:O	3:K:336:SER:HB3	1.75	0.86
1:B:46:ALA:HA	1:B:66:SER:O	1.75	0.86
1:B:69:LEU:O	1:B:253:SER:HA	1.75	0.86
2:F:325:VAL:HB	2:F:333:GLU:O	1.75	0.86
1:A:182:LEU:O	1:A:186:THR:HB	1.74	0.86
1:B:247:THR:O	1:B:288:PHE:HA	1.75	0.86
2:E:217:THR:CG2	2:E:273:CYS:SG	2.64	0.86
2:F:42:VAL:HA	2:F:359:VAL:O	1.75	0.86
2:F:288:LEU:HD22	2:G:267:VAL:CG2	2.06	0.86
3:K:141:GLY:CA	3:K:287:SER:O	2.19	0.85
3:J:142:VAL:O	3:J:287:SER:HB3	1.76	0.85
3:L:139:VAL:CA	3:L:289:LEU:O	2.23	0.85
2:F:288:LEU:CD2	2:G:267:VAL:CG2	2.55	0.85
1:B:42:LEU:HA	1:B:70:GLN:O	1.76	0.84
2:G:223:PHE:HD2	2:G:227:LYS:NZ	1.73	0.84
3:L:142:VAL:HA	3:L:322:LYS:O	1.75	0.84
2:G:221:ASN:O	2:G:224:LEU:HB2	1.78	0.84
1:A:69:LEU:O	1:A:253:SER:HA	1.78	0.84
2:D:325:VAL:HB	2:D:333:GLU:O	1.78	0.84
2:F:223:PHE:CE2	2:F:274:ILE:CB	2.60	0.83
3:J:337:ILE:O	3:J:341:VAL:HB	1.77	0.83
1:B:157:ALA:O	1:B:161:TYR:HB2	1.78	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:220:SER:CA	2:H:223:PHE:CD1	2.57	0.83
3:L:331:PRO:O	3:L:335:ILE:HB	1.78	0.83
2:D:167:ALA:O	2:D:171:LEU:HB2	1.77	0.82
3:J:576:VAL:HB	3:J:625:GLY:O	1.79	0.82
3:K:683:GLU:O	3:K:857:TYR:HA	1.78	0.82
3:J:577:GLN:HB3	3:J:662:MET:O	1.78	0.82
3:L:584:GLN:O	3:L:588:GLN:HB2	1.79	0.82
1:B:169:VAL:HG12	1:C:336:ALA:HB1	1.61	0.82
2:H:288:LEU:CD2	2:I:267:VAL:CG2	2.52	0.82
3:J:783:PRO:O	3:J:786:ILE:HB	1.80	0.81
2:H:325:VAL:HB	2:H:333:GLU:O	1.80	0.81
3:K:726:GLN:O	3:K:809:TRP:HA	1.80	0.81
2:E:223:PHE:HE2	2:E:227:LYS:CE	1.94	0.81
2:G:92:SER:HA	2:G:176:VAL:O	1.81	0.81
2:F:254:PHE:CE1	2:F:287:LEU:HD11	2.15	0.81
3:J:338:HIS:O	3:J:342:LYS:HB2	1.80	0.81
3:K:584:GLN:O	3:K:588:GLN:HB2	1.81	0.81
3:K:725:PRO:HA	3:K:810:GLU:O	1.81	0.81
3:K:100:ALA:O	3:K:104:GLN:HB2	1.81	0.81
2:G:59:ARG:HB3	2:G:215:ASP:O	1.80	0.80
3:J:376:LEU:O	3:J:379:THR:HB	1.80	0.80
3:L:575:MET:HB3	3:L:664:PHE:O	1.81	0.80
2:H:268:ASP:HB3	2:H:272:GLY:H	1.47	0.80
3:L:337:ILE:O	3:L:341:VAL:HB	1.81	0.80
1:C:398:LEU:O	1:C:402:SER:HB3	1.82	0.80
1:A:82:ARG:O	1:A:86:LEU:HB2	1.80	0.80
3:L:997:SER:O	3:L:1001:ASN:HB2	1.83	0.79
2:E:223:PHE:CE2	2:E:227:LYS:CE	2.64	0.79
2:I:221:ASN:O	2:I:224:LEU:HB2	1.82	0.79
3:J:762:PHE:O	3:J:768:VAL:HA	1.82	0.79
2:I:66:ALA:O	2:I:205:THR:HA	1.82	0.79
1:C:157:ALA:O	1:C:161:TYR:HB2	1.83	0.79
2:E:221:ASN:O	2:E:224:LEU:HB2	1.82	0.79
2:H:223:PHE:HE2	2:H:274:ILE:HD11	1.49	0.78
1:B:68:SER:HA	1:B:254:THR:O	1.83	0.78
2:H:126:VAL:O	2:H:130:GLN:HB2	1.83	0.78
1:A:68:SER:HA	1:A:254:THR:O	1.83	0.78
2:H:220:SER:HA	2:H:223:PHE:HE1	1.31	0.78
3:K:376:LEU:O	3:K:379:THR:HB	1.82	0.78
1:C:182:LEU:O	1:C:186:THR:HB	1.82	0.78
2:H:254:PHE:CE1	2:H:287:LEU:HD11	2.19	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:187:TRP:O	3:K:266:ALA:HA	1.82	0.78
1:A:169:VAL:HG12	1:B:336:ALA:HB1	1.65	0.78
3:J:175:VAL:HA	3:J:290:GLY:O	1.83	0.78
3:J:911:GLY:O	3:J:915:ALA:HB3	1.83	0.78
3:J:277:ILE:HA	3:J:613:ASN:O	1.84	0.78
1:C:253:SER:O	1:C:283:LYS:HB2	1.82	0.77
3:L:338:HIS:O	3:L:342:LYS:HB2	1.83	0.77
2:F:219:SER:C	2:F:223:PHE:HE1	1.92	0.77
1:A:226:ALA:O	1:A:230:GLN:HB2	1.85	0.76
3:J:790:TYR:HA	3:J:799:VAL:O	1.84	0.76
1:A:316:LEU:O	1:A:320:HIS:HB2	1.86	0.76
1:A:398:LEU:O	1:A:402:SER:HB3	1.84	0.76
3:J:186:ILE:HA	3:J:267:LYS:O	1.85	0.76
2:D:271:THR:CB	3:L:258:CYS:SG	2.74	0.76
1:B:316:LEU:O	1:B:320:HIS:HB2	1.85	0.76
3:L:157:TYR:O	3:L:161:ASN:HB2	1.86	0.76
1:C:183:ARG:HH21	1:C:189:TYR:HB2	1.51	0.76
1:A:385:GLU:O	1:A:389:ALA:HB2	1.86	0.75
2:G:224:LEU:HD23	2:G:227:LYS:HD2	1.67	0.75
2:D:223:PHE:CZ	2:D:274:ILE:HG12	2.20	0.75
1:B:66:SER:HA	1:B:256:ILE:O	1.86	0.75
3:J:46:SER:HA	3:J:88:VAL:O	1.87	0.75
3:K:139:VAL:HA	3:K:289:LEU:C	2.10	0.75
1:B:16:GLU:O	1:B:20:SER:HB3	1.87	0.75
3:K:338:HIS:O	3:K:342:LYS:HB2	1.85	0.75
2:D:269:GLN:OE1	2:I:288:LEU:HD13	1.87	0.74
2:F:40:VAL:HG13	2:F:363:GLY:H	1.52	0.74
3:K:142:VAL:HA	3:K:322:LYS:O	1.87	0.74
3:L:376:LEU:O	3:L:379:THR:HB	1.87	0.74
1:B:248:LEU:HA	1:B:287:SER:O	1.86	0.74
1:C:248:LEU:HA	1:C:287:SER:O	1.87	0.74
1:B:63:ASN:O	1:B:259:THR:HA	1.88	0.74
2:D:271:THR:CG2	3:L:258:CYS:SG	2.75	0.74
2:I:116:GLN:O	2:I:120:ASN:HB2	1.87	0.74
3:J:336:SER:O	3:J:340:VAL:HB	1.87	0.74
3:J:946:VAL:O	3:J:950:LYS:HB2	1.88	0.74
2:E:167:ALA:O	2:E:171:LEU:HB2	1.88	0.74
2:G:288:LEU:HD13	2:H:269:GLN:OE1	1.88	0.74
3:K:42:ALA:HA	3:K:92:LEU:O	1.87	0.74
2:G:217:THR:HG21	2:G:273:CYS:SG	2.27	0.73
2:H:167:ALA:O	2:H:171:LEU:HB3	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:218:GLN:HA	3:J:232:ALA:O	1.87	0.73
3:K:256:ASP:OD2	3:K:258:CYS:SG	2.47	0.73
3:L:42:ALA:HA	3:L:92:LEU:O	1.89	0.73
2:D:271:THR:HG21	3:L:258:CYS:SG	2.29	0.73
2:G:221:ASN:HA	2:G:224:LEU:HD12	1.69	0.73
1:B:14:ASN:HD22	1:B:17:LEU:HG	1.52	0.73
3:K:330:THR:O	3:K:334:LYS:HB2	1.89	0.73
2:D:219:SER:O	2:D:223:PHE:CD1	2.42	0.73
3:K:4:PHE:O	3:K:7:ASP:HB2	1.89	0.73
2:G:217:THR:HG22	2:G:273:CYS:SG	2.25	0.72
1:A:321:ARG:O	1:A:325:GLN:HB2	1.89	0.72
1:C:316:LEU:O	1:C:320:HIS:HB2	1.89	0.72
2:D:223:PHE:HE2	2:D:274:ILE:HG13	1.47	0.72
3:J:331:PRO:O	3:J:335:ILE:HB	1.89	0.72
3:L:683:GLU:O	3:L:857:TYR:HA	1.89	0.72
3:J:100:ALA:O	3:J:104:GLN:HB2	1.88	0.72
3:J:575:MET:HB3	3:J:664:PHE:O	1.89	0.72
3:K:141:GLY:HA2	3:K:287:SER:C	2.12	0.72
1:A:157:ALA:O	1:A:161:TYR:HB2	1.89	0.71
2:E:116:GLN:O	2:E:120:ASN:HB2	1.90	0.71
3:J:42:ALA:HA	3:J:92:LEU:O	1.90	0.71
3:J:761:ASP:HA	3:J:769:LYS:O	1.90	0.71
1:A:73:GLN:O	1:A:250:LEU:HB3	1.90	0.71
2:D:50:LEU:HB2	2:D:301:LEU:HB3	1.71	0.71
2:H:288:LEU:HD23	2:I:267:VAL:HG21	1.70	0.71
2:E:60:THR:HG23	2:E:290:GLY:H	1.56	0.71
2:I:224:LEU:HD23	2:I:227:LYS:HD2	1.71	0.71
1:C:384:GLN:O	1:C:388:ASN:HB3	1.90	0.71
2:I:254:PHE:CD1	2:I:287:LEU:HD11	2.25	0.71
1:A:101:ASP:O	1:A:105:LEU:HB2	1.91	0.71
3:L:100:ALA:O	3:L:104:GLN:HB2	1.91	0.71
3:L:999:ALA:O	3:L:1003:VAL:HB	1.91	0.71
1:B:398:LEU:O	1:B:402:SER:HB3	1.91	0.71
1:B:215:GLU:O	1:B:219:ARG:HB2	1.91	0.71
2:H:223:PHE:HE2	2:H:274:ILE:CD1	2.04	0.70
3:K:186:ILE:HA	3:K:267:LYS:O	1.92	0.70
2:E:366:LYS:HG3	2:E:367:VAL:HG23	1.73	0.70
2:G:330:ASP:HB3	2:G:373:VAL:H	1.55	0.70
3:K:139:VAL:C	3:K:289:LEU:H	2.00	0.70
1:B:193:LEU:O	1:B:422:PRO:HA	1.91	0.70
2:D:219:SER:C	2:D:223:PHE:CE1	2.69	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:943:ILE:O	3:K:947:GLU:HB2	1.92	0.70
2:F:249:SER:OG	2:G:224:LEU:HD13	1.90	0.70
3:J:305:ALA:O	3:J:309:GLU:HB2	1.92	0.70
3:J:555:LEU:HD22	3:J:913:LEU:HB3	1.74	0.70
2:H:220:SER:C	2:H:223:PHE:CD1	2.69	0.70
3:L:141:GLY:HA2	3:L:287:SER:C	2.12	0.70
3:L:577:GLN:HB3	3:L:662:MET:O	1.92	0.70
1:B:61:ASN:HB2	1:B:262:SER:O	1.92	0.69
2:E:216:VAL:HB	2:E:276:LEU:HB2	1.74	0.69
3:J:120:GLN:HA	3:J:123:GLN:HE21	1.57	0.69
3:K:157:TYR:O	3:K:161:ASN:HB2	1.92	0.69
2:I:330:ASP:HB3	2:I:373:VAL:H	1.58	0.69
1:B:183:ARG:HH21	1:B:189:TYR:HB2	1.57	0.69
3:L:187:TRP:O	3:L:266:ALA:HA	1.91	0.69
1:A:96:VAL:HG13	1:A:221:LEU:HB3	1.75	0.69
2:G:60:THR:HG23	2:G:290:GLY:H	1.58	0.69
3:J:140:VAL:HB	3:J:289:LEU:HB2	1.74	0.69
2:H:105:TYR:CZ	2:H:171:LEU:HG	2.28	0.69
2:I:244:VAL:HG22	2:I:297:LEU:HA	1.73	0.69
3:J:219:LEU:O	3:J:231:ASN:HA	1.93	0.69
3:J:723:ASP:HB3	3:J:811:TYR:HB3	1.74	0.69
2:I:223:PHE:HE2	2:I:227:LYS:HE3	1.56	0.68
1:A:83:ALA:O	1:A:87:GLN:HB2	1.92	0.68
1:B:168:GLU:O	1:B:172:ARG:HB2	1.93	0.68
2:D:45:VAL:O	2:D:356:GLY:HA2	1.92	0.68
3:L:530:SER:O	3:L:534:ILE:HB	1.93	0.68
2:F:218:GLN:HB3	2:F:223:PHE:CZ	2.27	0.68
1:B:180:GLU:O	1:B:184:GLN:HB2	1.92	0.68
1:B:237:ILE:HG23	1:B:302:VAL:HG13	1.75	0.68
3:L:43:VAL:O	3:L:92:LEU:HB2	1.94	0.68
1:A:168:GLU:O	1:A:172:ARG:HB2	1.94	0.68
1:C:165:LEU:O	1:C:169:VAL:HG23	1.92	0.68
3:K:368:PRO:O	3:K:371:ALA:HB3	1.94	0.68
1:A:193:LEU:O	1:A:422:PRO:HA	1.93	0.68
2:H:288:LEU:HD22	2:I:267:VAL:HG22	1.73	0.68
3:L:729:ILE:HG23	3:L:806:SER:H	1.59	0.68
1:C:168:GLU:O	1:C:172:ARG:HB2	1.93	0.68
2:E:223:PHE:CD2	2:E:227:LYS:HE3	2.29	0.68
2:F:219:SER:O	2:F:223:PHE:CE1	2.41	0.68
3:K:140:VAL:N	3:K:289:LEU:H	1.92	0.68
3:L:632:LYS:O	3:L:637:ARG:NH1	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:VAL:O	1:B:331:PHE:HB2	1.93	0.67
3:L:145:THR:HA	3:L:284:GLN:HE22	1.59	0.67
1:C:134:TYR:O	1:C:138:ASP:HB2	1.95	0.67
2:E:224:LEU:HD23	2:E:227:LYS:HD2	1.76	0.67
1:A:169:VAL:HG12	1:B:336:ALA:CB	2.25	0.67
3:K:6:ILE:HD11	3:K:490:PRO:HB2	1.75	0.67
3:L:761:ASP:HA	3:L:769:LYS:O	1.95	0.67
2:F:288:LEU:HD23	2:G:267:VAL:CG2	2.23	0.67
2:H:42:VAL:HG12	2:H:358:ARG:HB3	1.77	0.67
2:F:365:GLN:HG2	3:K:852:PRO:HB3	1.77	0.67
2:E:41:GLY:HA2	2:E:376:GLN:HB2	1.75	0.67
2:F:50:LEU:HB2	2:F:301:LEU:HB3	1.76	0.67
2:F:244:VAL:HG22	2:F:297:LEU:HA	1.77	0.67
2:H:249:SER:OG	2:I:224:LEU:HD12	1.94	0.67
3:K:48:SER:HA	3:K:87:THR:HA	1.78	0.66
3:L:120:GLN:HA	3:L:123:GLN:HE21	1.60	0.66
3:J:158:VAL:HG13	3:J:162:MET:HB2	1.77	0.66
3:K:158:VAL:HG13	3:K:162:MET:HB2	1.77	0.66
1:A:26:ALA:O	1:A:30:LYS:HB2	1.96	0.66
2:F:249:SER:HG	2:G:224:LEU:HD12	1.60	0.66
1:A:214:LYS:O	1:A:218:LYS:HB2	1.95	0.66
3:L:263:ARG:HH11	3:L:268:ILE:H	1.43	0.66
3:K:848:ALA:HA	3:K:851:LEU:HD13	1.78	0.66
1:C:42:LEU:HA	1:C:70:GLN:O	1.96	0.66
2:G:216:VAL:HB	2:G:276:LEU:HB2	1.76	0.66
1:B:82:ARG:O	1:B:86:LEU:HB2	1.96	0.66
1:B:4:MSE:O	1:B:7:TYR:HB3	1.96	0.66
1:C:70:GLN:HA	1:C:252:ALA:O	1.96	0.66
3:J:191:ASN:O	3:J:195:LYS:HB2	1.96	0.66
1:B:226:ALA:O	1:B:230:GLN:HB2	1.96	0.65
1:C:73:GLN:O	1:C:250:LEU:HB3	1.95	0.65
3:K:253:VAL:HG12	3:K:259:ARG:HA	1.77	0.65
1:C:125:TYR:HB2	1:C:384:GLN:HE21	1.61	0.65
2:H:265:VAL:HB	2:H:274:ILE:HD12	1.78	0.65
2:G:41:GLY:HA2	2:G:376:GLN:HB2	1.77	0.65
3:K:571:VAL:HG12	3:K:630:SER:HA	1.78	0.65
3:L:140:VAL:N	3:L:289:LEU:H	1.95	0.65
1:C:235:GLU:O	1:C:239:GLN:HB2	1.96	0.65
3:K:756:GLY:HA2	3:K:774:MET:HB2	1.79	0.65
3:L:681:ASP:HB3	3:L:860:THR:O	1.96	0.65
2:E:92:SER:HA	2:E:176:VAL:O	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:318:ARG:NH2	3:K:244:GLU:OE1	2.30	0.65
3:K:402:ILE:HA	3:K:405:LEU:HD13	1.78	0.65
3:K:723:ASP:HB3	3:K:811:TYR:HB3	1.78	0.65
1:B:42:LEU:HB3	1:C:293:TYR:HB3	1.79	0.65
2:I:241:LYS:HG2	2:I:261:GLU:HA	1.78	0.65
1:B:16:GLU:HA	1:B:19:LYS:HB3	1.78	0.65
1:A:42:LEU:HA	1:A:70:GLN:O	1.97	0.65
2:E:244:VAL:HG22	2:E:297:LEU:HA	1.79	0.65
3:J:32:VAL:HB	3:J:299:ALA:H	1.62	0.65
3:L:197:GLN:O	3:L:792:ARG:NH1	2.30	0.65
3:J:185:ARG:NH2	3:J:774:MET:O	2.30	0.64
2:D:269:GLN:HE22	2:I:288:LEU:HB3	1.61	0.64
2:G:224:LEU:O	2:G:227:LYS:HB2	1.97	0.64
2:G:332:VAL:HG23	2:G:369:PRO:HA	1.78	0.64
3:K:338:HIS:O	3:K:342:LYS:CB	2.44	0.64
2:D:219:SER:C	2:D:223:PHE:HD1	2.05	0.64
3:J:136:PHE:HA	3:J:292:LYS:HG2	1.80	0.64
3:J:632:LYS:O	3:J:637:ARG:NH1	2.31	0.64
3:L:139:VAL:C	3:L:289:LEU:H	2.05	0.64
1:C:114:PHE:O	1:C:118:ASN:HB2	1.96	0.64
3:K:136:PHE:HA	3:K:292:LYS:HG2	1.78	0.64
1:A:71:LEU:O	1:A:252:ALA:HB3	1.98	0.64
3:J:756:GLY:HA2	3:J:774:MET:HB2	1.78	0.64
1:B:26:ALA:O	1:B:30:LYS:HB2	1.96	0.64
2:D:220:SER:N	2:D:223:PHE:HD1	1.95	0.64
3:J:183:ALA:O	3:J:270:LEU:HA	1.98	0.64
3:J:338:HIS:O	3:J:342:LYS:CB	2.46	0.64
3:J:637:ARG:HB2	3:J:642:ASN:HB3	1.79	0.64
3:K:538:THR:O	3:K:542:LEU:CB	2.46	0.64
3:K:695:LEU:O	3:K:699:ARG:HB2	1.98	0.64
1:C:180:GLU:O	1:C:184:GLN:HB2	1.97	0.64
2:G:235:LEU:HD23	2:G:301:LEU:HD23	1.80	0.64
1:C:83:ALA:O	1:C:87:GLN:HB2	1.98	0.63
2:I:167:ALA:O	2:I:171:LEU:HB2	1.98	0.63
3:K:639:GLY:O	3:K:643:LYS:NZ	2.29	0.63
2:H:45:VAL:O	2:H:356:GLY:HA2	1.98	0.63
3:K:534:ILE:HA	3:K:537:SER:HB2	1.81	0.63
2:H:249:SER:OG	2:I:224:LEU:CD1	2.47	0.63
2:D:60:THR:HA	2:D:214:VAL:HA	1.80	0.63
2:E:141:GLN:O	2:E:145:GLN:HB2	1.99	0.63
2:F:42:VAL:HG12	2:F:358:ARG:HB3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:335:ARG:HE	2:G:353:LEU:HD21	1.64	0.63
3:K:198:LEU:HD21	3:K:252:LYS:HD3	1.79	0.63
3:L:158:VAL:HG13	3:L:162:MET:HB2	1.81	0.63
2:D:42:VAL:HG12	2:D:358:ARG:HB3	1.81	0.63
3:J:196:PHE:HB3	3:J:252:LYS:HD3	1.80	0.63
3:L:207:ILE:O	3:L:211:ASN:HB2	1.99	0.63
2:D:244:VAL:HG22	2:D:297:LEU:HA	1.80	0.62
2:D:306:ILE:HB	2:D:349:VAL:HB	1.80	0.62
2:G:141:GLN:O	2:G:145:GLN:HB2	1.99	0.62
3:L:998:GLY:O	3:L:1002:ALA:HB3	1.99	0.62
1:A:237:ILE:HG23	1:A:302:VAL:HG13	1.81	0.62
1:C:93:ILE:HG12	1:C:225:GLN:HG3	1.80	0.62
3:K:82:SER:HB2	3:K:816:LEU:HB2	1.82	0.62
2:I:101:TYR:O	2:I:105:TYR:HB2	2.00	0.62
3:J:534:ILE:HA	3:J:537:SER:HB2	1.82	0.62
3:K:967:ALA:O	3:K:971:ARG:HB2	1.98	0.62
1:A:7:TYR:O	1:A:11:ARG:N	2.32	0.62
1:C:16:GLU:HA	1:C:19:LYS:HB3	1.80	0.62
3:J:607:GLU:O	3:J:630:SER:CB	2.43	0.62
3:K:1028:VAL:O	3:K:1032:ARG:HB3	1.99	0.62
2:I:60:THR:HG23	2:I:290:GLY:H	1.65	0.62
3:K:638:PRO:O	3:K:642:ASN:ND2	2.32	0.62
1:A:114:PHE:O	1:A:118:ASN:HB2	2.00	0.62
1:C:247:THR:O	1:C:288:PHE:HA	1.99	0.62
3:J:417:GLU:O	3:J:421:ALA:HB2	2.00	0.62
3:K:632:LYS:O	3:K:637:ARG:NH1	2.32	0.62
1:B:7:TYR:O	1:B:11:ARG:N	2.32	0.62
1:B:103:GLN:NE2	1:B:402:SER:O	2.33	0.62
2:H:43:VAL:O	2:H:358:ARG:HA	2.00	0.62
3:J:383:LEU:O	3:J:387:GLY:N	2.33	0.62
1:B:169:VAL:HG12	1:C:336:ALA:CB	2.27	0.62
2:D:288:LEU:HD21	2:E:267:VAL:HG21	1.71	0.62
3:J:142:VAL:HG12	3:J:323:ILE:HG12	1.81	0.62
1:B:310:VAL:HA	1:B:313:SER:HB2	1.82	0.61
2:F:45:VAL:O	2:F:356:GLY:HA2	2.00	0.61
3:J:174:ASP:H	3:J:292:LYS:HB2	1.64	0.61
3:J:904:VAL:HG11	3:J:1022:VAL:HG22	1.82	0.61
2:F:249:SER:OG	2:G:224:LEU:HD12	1.98	0.61
2:F:306:ILE:HB	2:F:349:VAL:HB	1.83	0.61
2:G:167:ALA:O	2:G:171:LEU:HB2	2.00	0.61
1:A:180:GLU:O	1:A:184:GLN:CB	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:249:SER:HG	2:G:224:LEU:HD11	1.54	0.61
2:G:243:LYS:HA	2:G:258:GLY:O	2.00	0.61
2:I:236:LYS:HG2	2:I:239:ASN:HD22	1.64	0.61
2:D:318:ARG:NH2	3:L:244:GLU:OE1	2.33	0.61
2:E:316:THR:H	2:E:321:ALA:HA	1.66	0.61
2:H:59:ARG:NH2	2:I:269:GLN:O	2.33	0.61
3:K:57:VAL:HG13	3:K:88:VAL:HG22	1.81	0.61
1:A:42:LEU:HB3	1:B:293:TYR:HB3	1.83	0.61
1:A:325:GLN:HG3	1:C:180:GLU:HB3	1.83	0.61
1:B:30:LYS:HA	1:B:33:GLU:HG2	1.81	0.61
2:G:68:VAL:O	2:G:203:LEU:N	2.32	0.61
2:G:223:PHE:HE2	2:G:227:LYS:HZ1	1.42	0.61
3:J:538:THR:O	3:J:542:LEU:CB	2.45	0.61
3:L:538:THR:O	3:L:542:LEU:CB	2.46	0.61
1:B:45:GLY:O	1:B:67:ALA:HA	1.99	0.61
1:C:215:GLU:O	1:C:219:ARG:HB2	2.01	0.61
2:E:324:LEU:HA	2:E:334:THR:HA	1.83	0.61
2:F:318:ARG:NH2	3:J:244:GLU:OE1	2.34	0.61
1:C:6:VAL:O	1:C:10:ALA:N	2.34	0.61
2:F:72:VAL:HG11	2:F:174:THR:HG22	1.82	0.61
3:J:684:LEU:HD11	3:J:851:LEU:HD21	1.83	0.61
3:L:190:PRO:O	3:L:194:ASN:HB2	2.00	0.61
1:C:237:ILE:HG23	1:C:302:VAL:HG13	1.82	0.61
2:G:288:LEU:HB3	2:H:269:GLN:HE22	1.65	0.61
3:J:911:GLY:HA2	3:J:914:LEU:HG	1.83	0.61
3:L:58:GLN:HE21	3:L:818:ARG:HH11	1.46	0.61
3:J:639:GLY:O	3:J:643:LYS:NZ	2.32	0.61
3:L:383:LEU:O	3:L:387:GLY:N	2.34	0.61
1:A:52:ASN:HB3	1:B:282:ASN:HD22	1.66	0.60
1:B:36:SER:HA	1:B:39:LEU:HD13	1.83	0.60
1:B:230:GLN:NE2	1:B:313:SER:OG	2.34	0.60
2:H:59:ARG:HE	2:H:290:GLY:HA2	1.66	0.60
3:J:151:GLN:NE2	3:J:286:ALA:O	2.34	0.60
3:K:383:LEU:O	3:K:387:GLY:N	2.34	0.60
3:K:541:TYR:HA	3:K:544:LEU:HB3	1.83	0.60
3:L:459:PHE:O	3:L:468:ARG:NH2	2.34	0.60
3:L:1009:GLY:O	3:L:1013:THR:OG1	2.19	0.60
1:C:19:LYS:NZ	1:C:23:ASP:OD1	2.35	0.60
3:J:986:VAL:HA	3:J:989:LEU:HD13	1.82	0.60
3:K:282:ASN:HD21	3:K:608:SER:HB2	1.65	0.60
3:L:6:ILE:HD11	3:L:490:PRO:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:368:PRO:O	3:L:371:ALA:HB3	2.00	0.60
1:A:75:ILE:O	1:A:248:LEU:HB3	2.01	0.60
1:B:96:VAL:HG13	1:B:221:LEU:HB3	1.83	0.60
1:C:327:VAL:O	1:C:331:PHE:HB2	2.01	0.60
2:F:219:SER:CA	2:F:223:PHE:HE1	2.13	0.60
3:L:185:ARG:NH2	3:L:774:MET:O	2.35	0.60
1:B:180:GLU:HB3	1:C:325:GLN:HG3	1.84	0.60
1:B:384:GLN:O	1:B:388:ASN:HB3	2.00	0.60
2:I:41:GLY:HA2	2:I:376:GLN:HB2	1.83	0.60
2:I:93:LEU:HB2	2:I:176:VAL:O	2.01	0.60
3:J:568:ASP:OD2	3:J:634:TRP:NE1	2.34	0.60
1:B:165:LEU:O	1:B:169:VAL:CG2	2.44	0.60
3:L:417:GLU:O	3:L:421:ALA:HB2	2.02	0.60
1:B:24:ARG:NH1	1:B:95:ASP:OD1	2.34	0.60
2:F:219:SER:HA	2:F:273:CYS:HA	1.81	0.60
2:F:338:VAL:HB	2:F:351:GLU:HB3	1.83	0.60
2:G:324:LEU:HA	2:G:334:THR:HA	1.83	0.60
2:I:60:THR:HA	2:I:214:VAL:HA	1.84	0.60
3:K:78:MET:HG3	3:K:92:LEU:HG	1.83	0.60
3:L:555:LEU:HB3	3:L:913:LEU:HD13	1.82	0.60
1:A:42:LEU:HB2	1:A:71:LEU:HD12	1.84	0.60
1:A:49:THR:HB	1:A:64:ALA:HB3	1.83	0.60
2:D:241:LYS:HA	2:D:260:LEU:O	2.01	0.60
2:E:217:THR:HG23	2:E:273:CYS:HG	1.61	0.60
2:G:43:VAL:O	2:G:359:VAL:C	2.45	0.60
3:J:223:PRO:O	3:K:780:ARG:NH2	2.34	0.60
3:K:145:THR:HA	3:K:284:GLN:HE22	1.66	0.60
3:L:731:ILE:HD12	3:L:804:PHE:HD2	1.67	0.60
1:A:180:GLU:O	1:A:184:GLN:HB3	2.01	0.60
2:D:68:VAL:O	2:D:203:LEU:N	2.34	0.60
2:E:124:LEU:HD23	2:E:127:ASN:HD22	1.67	0.60
2:E:229:GLU:O	2:E:233:GLY:N	2.35	0.60
3:K:75:LEU:HA	3:K:94:PHE:HA	1.83	0.60
3:K:762:PHE:O	3:K:768:VAL:HA	2.01	0.60
2:D:184:ILE:HA	2:D:206:VAL:HA	1.83	0.60
2:E:68:VAL:O	2:E:203:LEU:N	2.31	0.60
1:A:24:ARG:NH1	1:A:95:ASP:OD1	2.35	0.59
1:A:183:ARG:HH21	1:A:189:TYR:HB2	1.67	0.59
1:B:200:ASN:O	1:B:202:LYS:NZ	2.35	0.59
2:H:68:VAL:O	2:H:203:LEU:N	2.35	0.59
2:I:218:GLN:HB3	2:I:274:ILE:HB	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:407:ASP:HA	3:J:410:ILE:HG12	1.84	0.59
3:J:583:THR:HG23	3:J:586:ARG:H	1.67	0.59
3:J:780:ARG:NH2	3:L:223:PRO:O	2.34	0.59
3:L:202:ASP:OD2	3:L:792:ARG:NH2	2.36	0.59
1:A:30:LYS:HA	1:A:33:GLU:HG2	1.82	0.59
1:A:384:GLN:O	1:A:388:ASN:CB	2.50	0.59
1:C:16:GLU:O	1:C:20:SER:HB3	2.02	0.59
2:D:249:SER:OG	2:E:224:LEU:CD1	2.50	0.59
3:J:157:TYR:O	3:J:161:ASN:HB2	2.03	0.59
3:K:25:LEU:O	3:K:29:LYS:HB2	2.02	0.59
3:K:191:ASN:O	3:K:195:LYS:HB2	2.03	0.59
1:A:67:ALA:O	1:A:255:GLY:HA2	2.02	0.59
2:E:241:LYS:HG2	2:E:261:GLU:HA	1.83	0.59
3:L:210:GLN:HE22	3:L:250:LEU:HB3	1.67	0.59
3:L:534:ILE:HA	3:L:537:SER:HB2	1.84	0.59
3:J:65:ILE:O	3:J:69:MET:N	2.35	0.59
3:K:353:LEU:O	3:K:357:LEU:HB2	2.02	0.59
1:B:93:ILE:HG12	1:B:225:GLN:HG3	1.84	0.59
1:C:401:LYS:HD3	1:C:404:LEU:HD12	1.83	0.59
2:D:59:ARG:HE	2:D:290:GLY:HA2	1.68	0.59
2:H:218:GLN:HB3	2:H:274:ILE:HB	1.83	0.59
2:I:75:ILE:HA	2:I:194:LEU:HA	1.84	0.59
3:J:541:TYR:HA	3:J:544:LEU:HB3	1.83	0.59
3:J:1024:VAL:HA	3:J:1027:VAL:HG22	1.84	0.59
3:J:280:GLU:HA	3:J:285:PRO:HA	1.83	0.59
3:K:418:ARG:HD2	3:K:970:MET:HB3	1.84	0.59
3:K:845:GLU:OE2	3:K:859:TRP:NE1	2.36	0.59
3:L:818:ARG:HA	3:L:823:PRO:HA	1.83	0.59
1:C:17:LEU:O	1:C:21:ALA:HB2	2.03	0.59
2:F:326:VAL:HA	2:F:332:VAL:HG12	1.84	0.59
2:H:244:VAL:HG22	2:H:297:LEU:HA	1.84	0.59
3:J:181:GLN:NE2	3:J:768:VAL:O	2.36	0.59
3:J:608:SER:OG	3:J:630:SER:N	2.35	0.59
3:K:202:ASP:OD2	3:K:792:ARG:NH2	2.36	0.59
3:K:511:GLY:O	3:K:515:TRP:HB3	2.02	0.59
1:A:93:ILE:HG12	1:A:225:GLN:HG3	1.84	0.59
1:C:384:GLN:O	1:C:388:ASN:CB	2.50	0.59
2:H:128:ARG:NH2	2:I:144:ASP:OD2	2.36	0.59
3:J:25:LEU:O	3:J:29:LYS:HB2	2.03	0.59
3:J:183:ALA:H	3:J:271:GLY:H	1.50	0.59
3:K:398:MET:HA	3:K:401:ALA:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:564:LEU:HD23	3:K:924:ASP:HB2	1.84	0.59
1:A:384:GLN:O	1:A:388:ASN:HB2	2.03	0.59
1:B:107:LEU:O	1:B:111:THR:OG1	2.17	0.59
3:J:368:PRO:O	3:J:371:ALA:HB3	2.03	0.59
3:K:327:TYR:HH	3:K:329:THR:HG1	1.48	0.59
3:L:184:MET:HE1	3:L:243:THR:HG22	1.85	0.59
1:C:172:ARG:HH12	1:C:427:PRO:HD2	1.68	0.58
2:F:288:LEU:HD23	2:G:267:VAL:HG21	1.85	0.58
3:J:198:LEU:HD21	3:J:252:LYS:HD2	1.85	0.58
3:L:193:LEU:HA	3:L:198:LEU:HD12	1.83	0.58
3:L:407:ASP:HA	3:L:410:ILE:HG12	1.85	0.58
1:C:103:GLN:NE2	1:C:402:SER:O	2.36	0.58
2:H:234:THR:O	2:H:237:GLN:NE2	2.36	0.58
1:A:240:ALA:O	1:A:244:HIS:ND1	2.37	0.58
1:B:384:GLN:O	1:B:388:ASN:CB	2.51	0.58
2:D:266:THR:HB	2:D:275:THR:H	1.68	0.58
2:E:70:PRO:HG3	2:E:199:GLN:HE21	1.69	0.58
2:I:43:VAL:O	2:I:359:VAL:C	2.46	0.58
3:J:967:ALA:O	3:J:971:ARG:HB2	2.03	0.58
3:K:144:ASN:ND2	3:K:148:THR:OG1	2.36	0.58
3:L:75:LEU:HA	3:L:94:PHE:HA	1.84	0.58
3:L:294:ALA:HB3	3:L:297:ALA:HB2	1.84	0.58
3:L:748:THR:O	3:L:752:ALA:HB2	2.04	0.58
3:L:756:GLY:HA2	3:L:774:MET:HB2	1.85	0.58
1:B:47:ASP:O	1:B:65:THR:HA	2.02	0.58
2:E:43:VAL:O	2:E:359:VAL:C	2.46	0.58
2:E:330:ASP:HB3	2:E:373:VAL:H	1.68	0.58
3:L:684:LEU:HD11	3:L:851:LEU:HD11	1.86	0.58
1:A:17:LEU:O	1:A:21:ALA:HB2	2.02	0.58
1:A:119:ALA:O	1:A:123:LEU:HB3	2.03	0.58
1:A:337:SER:OG	1:A:396:ASN:ND2	2.37	0.58
3:L:25:LEU:O	3:L:29:LYS:HB2	2.02	0.58
1:A:347:ALA:O	1:A:351:ALA:HB3	2.03	0.58
2:F:128:ARG:NH2	2:G:144:ASP:OD2	2.36	0.58
3:J:848:ALA:HA	3:J:851:LEU:HD13	1.85	0.58
3:K:583:THR:HG23	3:K:586:ARG:H	1.68	0.58
1:B:52:ASN:H	1:C:281:GLN:HE22	1.50	0.58
3:K:335:ILE:O	3:K:339:GLU:CB	2.52	0.58
3:K:1024:VAL:HA	3:K:1027:VAL:HG22	1.85	0.58
3:L:723:ASP:HB3	3:L:811:TYR:HB3	1.86	0.58
1:C:100:THR:O	1:C:104:THR:OG1	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:223:PHE:O	2:E:227:LYS:N	2.34	0.58
2:E:288:LEU:HB3	2:F:269:GLN:HE22	1.67	0.58
2:G:124:LEU:HD23	2:G:127:ASN:HD22	1.68	0.58
3:J:686:ASP:HB2	3:J:695:LEU:HD13	1.85	0.58
3:L:82:SER:HB2	3:L:816:LEU:HB2	1.85	0.58
1:C:228:LEU:O	1:C:232:LEU:HB2	2.04	0.58
2:F:214:VAL:HB	2:F:278:ALA:HB3	1.86	0.58
3:K:190:PRO:O	3:K:194:ASN:HB2	2.03	0.58
3:L:105:VAL:HA	3:L:108:GLN:HG2	1.85	0.58
3:L:151:GLN:HE22	3:L:279:ALA:HB3	1.69	0.58
3:L:986:VAL:HA	3:L:989:LEU:HD13	1.85	0.58
1:A:80:LYS:O	1:A:84:LEU:HB2	2.04	0.58
1:A:228:LEU:O	1:A:232:LEU:HB2	2.04	0.58
2:E:282:ASN:HD21	2:E:287:LEU:H	1.52	0.58
2:H:138:ILE:HD11	2:H:142:GLU:HB2	1.84	0.58
2:I:124:LEU:HD23	2:I:127:ASN:HD22	1.68	0.58
3:J:122:VAL:O	3:J:126:GLY:N	2.36	0.58
3:J:685:ILE:HG21	3:J:822:LEU:HB3	1.86	0.58
3:K:223:PRO:O	3:L:780:ARG:NH2	2.37	0.58
3:L:845:GLU:OE2	3:L:859:TRP:NE1	2.37	0.58
1:B:89:LYS:O	1:B:93:ILE:HB	2.04	0.57
1:C:167:ASN:O	1:C:171:ALA:HB3	2.04	0.57
2:I:229:GLU:O	2:I:233:GLY:N	2.35	0.57
1:B:100:THR:O	1:B:104:THR:OG1	2.22	0.57
2:F:184:ILE:HA	2:F:206:VAL:HA	1.86	0.57
2:G:223:PHE:HE2	2:G:227:LYS:NZ	1.92	0.57
2:H:84:GLY:O	2:H:183:ARG:NH1	2.37	0.57
2:H:243:LYS:HA	2:H:258:GLY:O	2.03	0.57
2:I:223:PHE:O	2:I:227:LYS:N	2.36	0.57
3:J:641:GLU:O	3:J:650:ARG:NH2	2.37	0.57
3:K:335:ILE:O	3:K:339:GLU:HB2	2.04	0.57
3:L:137:LEU:CB	3:L:291:ILE:O	2.46	0.57
1:A:167:ASN:O	1:A:171:ALA:HB3	2.03	0.57
1:A:168:GLU:O	1:A:172:ARG:CB	2.52	0.57
1:B:385:GLU:O	1:B:389:ALA:CB	2.52	0.57
2:D:342:ALA:HA	2:D:347:TRP:HA	1.86	0.57
3:J:112:GLN:HA	3:J:115:MET:HG2	1.87	0.57
3:K:368:PRO:HG3	3:K:413:VAL:HG21	1.85	0.57
1:A:230:GLN:NE2	1:A:313:SER:OG	2.37	0.57
2:D:220:SER:N	2:D:223:PHE:CD1	2.70	0.57
2:H:47:THR:HB	2:H:304:ASN:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:438:ILE:O	3:J:442:LEU:HB2	2.04	0.57
3:J:743:ILE:HA	3:J:746:ILE:HD12	1.87	0.57
3:K:137:LEU:HD23	3:K:138:MET:HG2	1.87	0.57
3:K:743:ILE:HG22	3:K:747:ASN:HD21	1.69	0.57
3:K:863:SER:O	3:K:867:ARG:CB	2.53	0.57
3:L:338:HIS:O	3:L:342:LYS:CB	2.51	0.57
1:A:100:THR:O	1:A:104:THR:OG1	2.22	0.57
1:A:127:GLN:HE22	1:A:427:PRO:HG2	1.70	0.57
1:C:4:MSE:O	1:C:7:TYR:HB3	2.04	0.57
2:D:128:ARG:NH2	2:E:144:ASP:OD2	2.36	0.57
2:I:57:PRO:HA	2:I:294:ARG:HA	1.85	0.57
3:J:555:LEU:HB3	3:J:913:LEU:HD13	1.86	0.57
3:J:687:GLN:N	3:J:854:GLY:O	2.37	0.57
3:K:185:ARG:HH22	3:K:774:MET:HB3	1.70	0.57
3:K:245:GLU:HA	3:K:248:LYS:HE2	1.86	0.57
3:L:641:GLU:O	3:L:650:ARG:NH2	2.33	0.57
3:L:884:VAL:HG12	3:L:902:MET:HE1	1.86	0.57
2:H:77:LEU:CB	2:H:95:GLN:O	2.47	0.57
2:I:314:THR:OG1	2:I:322:THR:O	2.22	0.57
3:J:571:VAL:HA	3:J:630:SER:HA	1.84	0.57
3:K:218:GLN:OE1	3:K:231:ASN:ND2	2.36	0.57
3:L:919:ARG:HH12	3:L:998:GLY:HA2	1.69	0.57
1:A:100:THR:O	1:A:104:THR:CB	2.52	0.57
1:B:101:ASP:O	1:B:105:LEU:HB2	2.05	0.57
2:E:288:LEU:CD1	2:F:269:GLN:OE1	2.33	0.57
2:F:227:LYS:O	2:F:231:ALA:HB2	2.05	0.57
3:L:48:SER:HA	3:L:87:THR:HA	1.85	0.57
1:A:399:ASN:O	1:A:403:ALA:CB	2.53	0.57
2:H:218:GLN:O	2:H:274:ILE:N	2.38	0.57
3:J:684:LEU:HA	3:J:857:TYR:HA	1.86	0.57
3:J:790:TYR:HB3	3:J:798:MET:HB3	1.87	0.57
3:J:845:GLU:OE2	3:J:859:TRP:NE1	2.38	0.57
3:L:402:ILE:HA	3:L:405:LEU:HD13	1.86	0.57
3:L:741:VAL:HG13	3:L:746:ILE:HD11	1.86	0.57
1:B:6:VAL:O	1:B:10:ALA:N	2.38	0.57
1:A:247:THR:O	1:A:288:PHE:HA	2.04	0.57
1:C:168:GLU:O	1:C:172:ARG:CB	2.52	0.57
2:F:68:VAL:O	2:F:203:LEU:N	2.36	0.57
2:F:342:ALA:HA	2:F:347:TRP:HA	1.86	0.57
2:G:229:GLU:O	2:G:233:GLY:N	2.34	0.57
2:H:224:LEU:O	2:H:228:GLN:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:919:ARG:HH12	3:K:1001:ASN:HB3	1.70	0.57
2:E:40:VAL:HB	2:E:373:VAL:HG13	1.87	0.56
2:E:326:VAL:HG23	2:E:332:VAL:HG12	1.86	0.56
2:G:225:ARG:O	2:G:228:GLN:HB3	2.04	0.56
3:K:641:GLU:O	3:K:650:ARG:NH2	2.35	0.56
3:K:676:THR:HG1	3:K:679:GLY:H	1.50	0.56
1:B:83:ALA:O	1:B:87:GLN:HB2	2.05	0.56
2:F:168:ARG:O	2:F:172:ALA:HB2	2.04	0.56
3:K:567:GLU:OE2	3:K:999:ALA:N	2.38	0.56
1:A:381:ASN:O	1:A:385:GLU:HB2	2.06	0.56
1:B:77:ASP:OD2	1:B:80:LYS:N	2.34	0.56
2:H:220:SER:HB3	2:H:223:PHE:HE1	1.67	0.56
2:I:324:LEU:HA	2:I:334:THR:HA	1.86	0.56
3:J:3:ASN:HA	3:J:6:ILE:HB	1.86	0.56
3:J:983:ILE:HA	3:J:986:VAL:HG22	1.87	0.56
3:L:876:LEU:O	3:L:880:SER:OG	2.21	0.56
3:L:880:SER:HA	3:L:883:VAL:HG12	1.88	0.56
2:D:338:VAL:HB	2:D:351:GLU:HB3	1.86	0.56
1:B:17:LEU:O	1:B:21:ALA:CB	2.54	0.56
2:E:288:LEU:HD13	2:F:269:GLN:CD	2.24	0.56
2:I:338:VAL:H	2:I:351:GLU:HB3	1.69	0.56
3:J:977:MET:O	3:J:981:ALA:CB	2.54	0.56
3:K:20:MET:HA	3:K:377:LEU:HD11	1.87	0.56
3:K:197:GLN:O	3:K:792:ARG:NH1	2.38	0.56
3:K:228:GLN:NE2	3:K:230:LEU:O	2.37	0.56
3:L:245:GLU:HA	3:L:248:LYS:HE2	1.88	0.56
1:B:18:ARG:NH1	1:C:314:GLU:OE2	2.38	0.56
2:G:188:ASN:ND2	2:G:203:LEU:O	2.39	0.56
2:G:234:THR:HG21	2:G:302:ASN:HD21	1.70	0.56
3:K:394:THR:HG22	3:K:469:GLN:HB3	1.87	0.56
3:L:139:VAL:HG22	3:L:290:GLY:HA2	1.87	0.56
1:C:6:VAL:HA	1:C:9:GLN:HB2	1.87	0.56
2:I:242:ALA:O	2:I:260:LEU:HB3	2.06	0.56
3:J:863:SER:O	3:J:867:ARG:CB	2.53	0.56
3:J:1030:ARG:O	3:J:1034:SER:N	2.38	0.56
3:K:743:ILE:HA	3:K:746:ILE:HD12	1.87	0.56
3:K:884:VAL:HG12	3:K:902:MET:HE1	1.87	0.56
3:K:910:ILE:O	3:K:913:LEU:HB2	2.06	0.56
2:F:43:VAL:O	2:F:358:ARG:HA	2.06	0.56
3:J:78:MET:HG3	3:J:92:LEU:HG	1.88	0.56
3:L:137:LEU:HD23	3:L:138:MET:HG2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:282:ASN:HD21	3:L:608:SER:HB2	1.69	0.56
2:E:60:THR:HA	2:E:214:VAL:HA	1.87	0.56
2:H:214:VAL:HB	2:H:278:ALA:HB3	1.87	0.56
3:K:637:ARG:HB2	3:K:642:ASN:HB3	1.88	0.56
3:L:438:ILE:O	3:L:442:LEU:HB2	2.05	0.56
1:A:213:LEU:HD21	1:A:328:ARG:HE	1.71	0.56
3:K:975:ILE:O	3:K:979:SER:OG	2.22	0.56
3:L:473:THR:O	3:L:476:SER:OG	2.23	0.56
3:L:1010:GLY:O	3:L:1014:ALA:HB3	2.05	0.56
3:L:1024:VAL:HA	3:L:1027:VAL:HG22	1.87	0.56
3:L:1028:VAL:O	3:L:1032:ARG:HB3	2.06	0.56
1:C:107:LEU:HD12	1:C:398:LEU:HD23	1.88	0.55
3:K:969:ARG:HH12	3:K:970:MET:HE2	1.71	0.55
1:B:190:TYR:HD2	1:B:193:LEU:HD21	1.71	0.55
2:F:138:ILE:HD11	2:F:142:GLU:HB2	1.89	0.55
2:H:196:GLN:HB2	2:H:199:GLN:HB3	1.89	0.55
3:K:457:ALA:O	3:K:468:ARG:NH1	2.39	0.55
3:K:683:GLU:HB2	3:K:858:ASP:HB3	1.87	0.55
3:L:541:TYR:HA	3:L:544:LEU:HB3	1.88	0.55
1:C:9:GLN:O	1:C:13:SER:OG	2.24	0.55
1:C:15:PRO:O	1:C:19:LYS:CB	2.55	0.55
3:K:46:SER:O	3:K:128:SER:OG	2.21	0.55
3:K:1030:ARG:O	3:K:1034:SER:N	2.38	0.55
3:L:790:TYR:HB3	3:L:798:MET:HB3	1.88	0.55
1:A:67:ALA:O	1:A:255:GLY:CA	2.55	0.55
1:B:391:TYR:O	1:B:395:ILE:HB	2.05	0.55
2:D:234:THR:HB	2:D:301:LEU:HD12	1.87	0.55
2:H:326:VAL:HA	2:H:332:VAL:HG12	1.87	0.55
3:J:70:ASN:O	3:J:110:LYS:NZ	2.37	0.55
3:J:75:LEU:HA	3:J:94:PHE:HA	1.87	0.55
3:J:743:ILE:HG22	3:J:747:ASN:HD21	1.71	0.55
1:C:42:LEU:HD13	1:C:71:LEU:HB2	1.89	0.55
3:J:924:ASP:H	3:J:927:PHE:HB3	1.71	0.55
3:J:943:ILE:O	3:J:947:GLU:HB2	2.07	0.55
3:K:555:LEU:HD22	3:K:913:LEU:HB3	1.88	0.55
3:K:681:ASP:O	3:K:859:TRP:HA	2.07	0.55
3:L:144:ASN:ND2	3:L:148:THR:OG1	2.40	0.55
1:B:180:GLU:O	1:B:184:GLN:CB	2.54	0.55
1:C:325:GLN:O	1:C:329:SER:OG	2.23	0.55
3:J:190:PRO:O	3:J:194:ASN:HB2	2.06	0.55
3:J:877:TYR:OH	3:J:928:GLN:OE1	2.25	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:15:PRO:O	1:B:19:LYS:CB	2.55	0.55
1:C:399:ASN:O	1:C:403:ALA:HB2	2.07	0.55
2:G:311:GLN:HE21	3:J:229:GLN:HE21	1.55	0.55
2:H:57:PRO:HA	2:H:294:ARG:HA	1.87	0.55
3:J:105:VAL:HA	3:J:108:GLN:HG2	1.88	0.55
3:K:977:MET:O	3:K:981:ALA:HB2	2.07	0.55
3:L:80:SER:HB2	3:L:90:ILE:HG23	1.88	0.55
3:L:640:GLU:HA	3:L:643:LYS:HD3	1.87	0.55
1:A:79:SER:O	1:A:83:ALA:N	2.35	0.55
2:E:66:ALA:HB3	2:E:206:VAL:HG22	1.89	0.55
2:H:184:ILE:HA	2:H:206:VAL:HA	1.89	0.55
2:H:306:ILE:O	2:H:349:VAL:N	2.39	0.55
2:H:342:ALA:HA	2:H:347:TRP:HA	1.87	0.55
3:J:596:HIS:O	3:J:600:THR:OG1	2.22	0.55
3:J:876:LEU:O	3:J:880:SER:OG	2.21	0.55
1:A:122:VAL:O	1:A:384:GLN:NE2	2.40	0.55
1:B:40:PRO:HA	1:B:72:THR:O	2.07	0.55
1:C:100:THR:O	1:C:104:THR:CB	2.55	0.55
2:D:326:VAL:HA	2:D:332:VAL:HG12	1.87	0.55
2:I:78:LYS:H	2:I:95:GLN:HB3	1.72	0.55
3:J:713:LEU:HA	3:J:831:ALA:HA	1.89	0.55
3:J:732:ASP:OD2	3:J:735:LYS:N	2.36	0.55
3:L:3:ASN:HA	3:L:6:ILE:HB	1.89	0.55
2:D:43:VAL:O	2:D:358:ARG:HA	2.07	0.54
2:D:325:VAL:H	2:D:334:THR:HA	1.72	0.54
2:F:306:ILE:O	2:F:349:VAL:N	2.40	0.54
3:J:30:LEU:HD12	3:J:31:PRO:HD2	1.88	0.54
3:L:83:ASP:OD2	3:L:85:THR:OG1	2.24	0.54
3:L:242:SER:OG	3:L:244:GLU:OE1	2.26	0.54
3:L:1030:ARG:O	3:L:1034:SER:N	2.39	0.54
1:A:6:VAL:O	1:A:10:ALA:N	2.39	0.54
1:A:10:ALA:HB1	1:A:105:LEU:HD11	1.89	0.54
1:A:348:VAL:O	1:A:352:GLN:HB2	2.07	0.54
2:I:45:VAL:O	2:I:356:GLY:N	2.40	0.54
3:L:45:ILE:O	3:L:90:ILE:HB	2.07	0.54
3:L:112:GLN:HA	3:L:115:MET:HG2	1.89	0.54
1:B:89:LYS:HD3	1:B:232:LEU:HB2	1.89	0.54
1:B:399:ASN:O	1:B:403:ALA:HB2	2.07	0.54
1:C:399:ASN:O	1:C:403:ALA:CB	2.55	0.54
2:D:223:PHE:HZ	2:D:273:CYS:HA	1.72	0.54
2:G:66:ALA:HB3	2:G:206:VAL:HG22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:98:PRO:O	2:H:102:GLN:N	2.40	0.54
2:H:282:ASN:HD21	2:H:287:LEU:H	1.55	0.54
3:J:185:ARG:HH22	3:J:774:MET:HB3	1.70	0.54
3:J:687:GLN:HE21	3:J:856:GLY:H	1.55	0.54
3:J:728:LYS:O	3:J:807:SER:HA	2.08	0.54
2:E:242:ALA:O	2:E:260:LEU:HB3	2.07	0.54
3:L:382:VAL:O	3:L:385:ALA:HB3	2.07	0.54
1:A:100:THR:HA	1:A:103:GLN:HB3	1.88	0.54
1:C:243:GLY:O	1:C:294:GLN:NE2	2.38	0.54
2:D:77:LEU:CB	2:D:95:GLN:O	2.49	0.54
2:I:360:VAL:HG11	2:I:364:LEU:HD21	1.88	0.54
3:J:187:TRP:O	3:J:266:ALA:HA	2.07	0.54
3:J:187:TRP:HB2	3:J:267:LYS:HB3	1.88	0.54
3:J:303:ALA:HA	3:J:306:ILE:HD12	1.90	0.54
3:J:394:THR:HG22	3:J:469:GLN:HB3	1.89	0.54
1:B:26:ALA:O	1:C:304:GLN:NE2	2.41	0.54
1:B:213:LEU:HD11	1:B:328:ARG:HH21	1.71	0.54
3:J:377:LEU:HA	3:J:380:PHE:HD2	1.70	0.54
3:K:907:LEU:O	3:K:910:ILE:HB	2.08	0.54
3:K:1027:VAL:HB	3:K:1031:ARG:HD3	1.90	0.54
1:A:26:ALA:O	1:B:304:GLN:NE2	2.40	0.54
1:B:312:ALA:HA	1:B:315:GLN:HB2	1.88	0.54
2:D:291:MET:HB3	2:D:293:VAL:HG13	1.90	0.54
2:E:218:GLN:HB3	2:E:274:ILE:HB	1.90	0.54
3:J:6:ILE:HD11	3:J:490:PRO:HB2	1.89	0.54
3:J:145:THR:HA	3:J:284:GLN:HE22	1.73	0.54
3:K:138:MET:HG3	3:K:291:ILE:HD12	1.89	0.54
3:K:986:VAL:HA	3:K:989:LEU:HD13	1.89	0.54
3:L:844:MET:O	3:L:848:ALA:N	2.41	0.54
3:L:914:LEU:O	3:L:918:PHE:N	2.40	0.54
3:L:983:ILE:HA	3:L:986:VAL:HG22	1.90	0.54
1:B:24:ARG:HG3	1:B:94:GLN:HG3	1.88	0.54
2:D:59:ARG:NH2	2:E:269:GLN:O	2.33	0.54
2:F:77:LEU:CB	2:F:95:GLN:O	2.47	0.54
2:F:218:GLN:HB3	2:F:223:PHE:CE2	2.42	0.54
2:F:220:SER:N	2:F:223:PHE:CD1	2.76	0.54
2:I:311:GLN:HE21	3:K:229:GLN:HE21	1.56	0.54
3:J:165:ALA:HA	3:J:168:ARG:HB2	1.90	0.54
3:J:276:ASP:O	3:J:584:GLN:NE2	2.41	0.54
3:J:574:THR:HG23	3:J:665:ALA:HB2	1.90	0.54
3:K:473:THR:O	3:K:476:SER:OG	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:741:VAL:HG13	3:K:746:ILE:HD11	1.89	0.54
3:L:279:ALA:HA	3:L:612:VAL:HA	1.90	0.54
3:L:638:PRO:O	3:L:642:ASN:ND2	2.30	0.54
3:K:511:GLY:O	3:K:515:TRP:CB	2.55	0.54
3:L:583:THR:HG23	3:L:586:ARG:H	1.72	0.54
1:A:4:MSE:O	1:A:8:GLN:N	2.41	0.54
1:B:152:THR:O	1:B:156:ASN:HB2	2.08	0.54
1:C:226:ALA:O	1:C:230:GLN:HB2	2.08	0.54
2:D:94:TYR:HH	2:D:187:SER:HG	1.49	0.54
2:I:221:ASN:HA	2:I:224:LEU:HD12	1.88	0.54
3:L:743:ILE:HG22	3:L:747:ASN:HD21	1.73	0.54
1:A:185:ILE:O	1:B:321:ARG:NH1	2.41	0.53
2:E:43:VAL:HG22	2:E:377:GLU:HG2	1.89	0.53
2:F:98:PRO:O	2:F:102:GLN:N	2.41	0.53
2:G:47:THR:HG21	2:G:306:ILE:HA	1.90	0.53
2:I:68:VAL:O	2:I:203:LEU:N	2.36	0.53
3:J:51:GLY:O	3:L:216:ALA:N	2.41	0.53
3:K:279:ALA:HA	3:K:612:VAL:HA	1.89	0.53
1:B:223:LEU:HB2	1:B:316:LEU:HG	1.91	0.53
3:J:83:ASP:OD2	3:J:85:THR:OG1	2.25	0.53
3:J:335:ILE:O	3:J:339:GLU:HB2	2.07	0.53
3:K:65:ILE:O	3:K:69:MET:N	2.40	0.53
3:K:336:SER:HA	3:K:339:GLU:HB3	1.88	0.53
3:K:697:GLN:O	3:K:701:GLN:HB2	2.08	0.53
3:L:490:PRO:O	3:L:494:ALA:HB2	2.09	0.53
3:L:511:GLY:O	3:L:515:TRP:CB	2.56	0.53
1:A:103:GLN:NE2	1:A:402:SER:O	2.41	0.53
1:A:119:ALA:O	1:A:123:LEU:CB	2.56	0.53
1:A:325:GLN:O	1:A:329:SER:OG	2.26	0.53
2:G:241:LYS:HG2	2:G:261:GLU:HA	1.89	0.53
2:I:59:ARG:HB3	2:I:215:ASP:O	2.08	0.53
3:K:545:TYR:HE1	3:K:907:LEU:HD21	1.73	0.53
1:A:4:MSE:O	1:A:7:TYR:HB3	2.08	0.53
1:B:100:THR:O	1:B:104:THR:CB	2.56	0.53
1:B:325:GLN:O	1:B:329:SER:OG	2.23	0.53
1:C:101:ASP:O	1:C:105:LEU:HB2	2.08	0.53
2:D:45:VAL:O	2:D:356:GLY:CA	2.57	0.53
2:D:227:LYS:HA	2:D:230:LEU:HB2	1.90	0.53
2:G:322:THR:HA	2:G:336:PRO:HA	1.90	0.53
2:H:291:MET:HB3	2:H:293:VAL:HG13	1.90	0.53
3:L:187:TRP:HB2	3:L:267:LYS:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:LEU:O	1:A:21:ALA:CB	2.56	0.53
3:J:818:ARG:HG2	3:J:823:PRO:HA	1.89	0.53
3:K:190:PRO:O	3:K:194:ASN:CB	2.57	0.53
3:K:703:LEU:HD21	3:K:718:PRO:HG3	1.90	0.53
3:L:135:SER:HB3	3:L:293:LEU:HD12	1.90	0.53
3:L:207:ILE:O	3:L:211:ASN:CB	2.55	0.53
3:L:743:ILE:HA	3:L:746:ILE:HD12	1.90	0.53
1:B:16:GLU:O	1:B:20:SER:CB	2.56	0.53
1:B:317:GLU:OE2	1:B:321:ARG:NE	2.42	0.53
3:K:137:LEU:CB	3:K:291:ILE:O	2.46	0.53
3:L:688:ALA:HB2	3:L:854:GLY:HA3	1.91	0.53
1:C:42:LEU:HB2	1:C:71:LEU:HD12	1.90	0.53
1:C:334:ILE:HG12	1:C:396:ASN:HB3	1.89	0.53
2:D:340:SER:N	2:D:348:LEU:O	2.42	0.53
2:E:43:VAL:O	2:E:359:VAL:O	2.26	0.53
2:E:188:ASN:ND2	2:E:203:LEU:O	2.38	0.53
3:J:968:VAL:HA	3:J:971:ARG:HB3	1.90	0.53
3:K:151:GLN:NE2	3:K:286:ALA:O	2.41	0.53
3:K:687:GLN:N	3:K:854:GLY:O	2.40	0.53
3:L:336:SER:O	3:L:340:VAL:HB	2.08	0.53
3:L:368:PRO:HB3	3:L:413:VAL:HG11	1.90	0.53
1:A:333:ASN:O	1:A:337:SER:OG	2.21	0.53
1:B:316:LEU:O	1:B:320:HIS:CB	2.56	0.53
2:F:325:VAL:H	2:F:334:THR:HA	1.72	0.53
3:J:158:VAL:HG11	3:J:289:LEU:HD11	1.90	0.53
3:J:638:PRO:O	3:J:642:ASN:ND2	2.31	0.53
3:K:34:GLN:O	3:K:392:THR:N	2.39	0.53
3:K:112:GLN:HA	3:K:115:MET:HG2	1.90	0.53
3:L:863:SER:O	3:L:867:ARG:CB	2.57	0.53
1:A:235:GLU:HA	1:A:238:ARG:HB2	1.91	0.53
2:H:223:PHE:O	2:H:227:LYS:HB2	2.07	0.53
2:I:94:TYR:HE2	2:I:203:LEU:HD13	1.74	0.53
3:J:81:ASN:HA	3:J:817:GLU:HA	1.90	0.53
3:K:685:ILE:O	3:K:856:GLY:N	2.36	0.53
3:L:700:ASN:HA	3:L:703:LEU:HB2	1.90	0.53
3:L:910:ILE:HD13	3:L:913:LEU:HD12	1.91	0.53
3:L:935:ILE:O	3:L:939:ALA:HB3	2.09	0.53
1:B:47:ASP:OD1	1:B:66:SER:OG	2.22	0.53
1:B:350:SER:O	1:B:354:SER:HB2	2.09	0.53
2:E:314:THR:OG1	2:E:322:THR:O	2.26	0.53
2:F:218:GLN:O	2:F:274:ILE:N	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:340:SER:N	2:H:348:LEU:O	2.42	0.53
2:I:326:VAL:HA	2:I:332:VAL:HA	1.89	0.53
3:J:56:THR:O	3:J:60:THR:OG1	2.26	0.53
3:K:30:LEU:HD12	3:K:31:PRO:HD2	1.89	0.53
3:L:134:SER:HB3	3:L:673:GLU:HG3	1.91	0.53
3:L:695:LEU:O	3:L:699:ARG:HB2	2.09	0.53
3:L:936:GLY:O	3:L:940:LYS:HB2	2.09	0.53
1:A:350:SER:O	1:A:354:SER:CB	2.57	0.52
1:C:16:GLU:O	1:C:20:SER:CB	2.57	0.52
2:E:309:PRO:HA	2:E:346:LYS:HA	1.89	0.52
2:I:219:SER:OG	2:I:220:SER:N	2.41	0.52
3:J:537:SER:HA	3:J:540:ARG:HG2	1.92	0.52
3:J:911:GLY:O	3:J:915:ALA:CB	2.56	0.52
3:L:431:THR:HA	3:L:434:SER:HB3	1.92	0.52
1:A:42:LEU:HD13	1:A:71:LEU:HB2	1.91	0.52
3:K:844:MET:O	3:K:848:ALA:N	2.42	0.52
3:L:748:THR:O	3:L:752:ALA:CB	2.57	0.52
3:L:924:ASP:H	3:L:927:PHE:HB3	1.73	0.52
1:B:168:GLU:O	1:B:172:ARG:CB	2.57	0.52
2:F:45:VAL:O	2:F:356:GLY:CA	2.56	0.52
2:G:338:VAL:H	2:G:351:GLU:HB3	1.73	0.52
3:K:83:ASP:OD2	3:K:85:THR:OG1	2.27	0.52
3:K:121:GLU:O	3:K:125:GLN:N	2.42	0.52
3:K:149:MET:HB3	3:K:153:ASP:HB2	1.92	0.52
3:K:242:SER:OG	3:K:244:GLU:OE1	2.27	0.52
3:K:713:LEU:HA	3:K:831:ALA:HA	1.91	0.52
1:A:336:ALA:O	1:A:340:SER:OG	2.27	0.52
2:G:101:TYR:O	2:G:105:TYR:HB2	2.10	0.52
3:J:435:MET:O	3:J:439:GLN:HB3	2.10	0.52
3:J:445:ILE:O	3:J:449:LEU:HB2	2.10	0.52
3:J:726:GLN:NE2	3:J:811:TYR:O	2.43	0.52
3:K:407:ASP:HA	3:K:410:ILE:HG12	1.91	0.52
3:K:1010:GLY:O	3:K:1014:ALA:CB	2.57	0.52
3:L:185:ARG:HH22	3:L:774:MET:HB3	1.75	0.52
3:L:391:ASN:O	3:L:395:MET:N	2.34	0.52
3:L:697:GLN:O	3:L:701:GLN:HB2	2.09	0.52
3:L:936:GLY:O	3:L:940:LYS:CB	2.58	0.52
1:A:19:LYS:HG3	1:B:311:GLY:HA2	1.92	0.52
1:A:317:GLU:OE2	1:A:321:ARG:NE	2.42	0.52
2:F:330:ASP:HB3	2:F:373:VAL:H	1.75	0.52
2:I:243:LYS:HD2	2:I:259:THR:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:251:LEU:HD12	3:J:260:VAL:HG12	1.91	0.52
3:K:537:SER:HA	3:K:540:ARG:HG2	1.92	0.52
3:K:818:ARG:NH2	3:K:821:GLY:O	2.32	0.52
3:K:967:ALA:O	3:K:971:ARG:CB	2.57	0.52
3:L:43:VAL:HG13	3:L:131:LYS:HA	1.91	0.52
3:L:188:MET:H	3:L:775:SER:HA	1.74	0.52
3:L:410:ILE:HA	3:L:413:VAL:HG22	1.91	0.52
1:A:4:MSE:HG2	1:A:416:ASN:HD22	1.75	0.52
1:C:321:ARG:O	1:C:325:GLN:HB2	2.10	0.52
2:D:223:PHE:CE2	2:D:274:ILE:CD1	2.91	0.52
2:F:218:GLN:CB	2:F:223:PHE:CZ	2.93	0.52
2:I:47:THR:HG21	2:I:306:ILE:HA	1.91	0.52
3:J:457:ALA:HA	3:J:468:ARG:HG2	1.91	0.52
3:J:473:THR:O	3:J:476:SER:OG	2.28	0.52
3:K:998:GLY:O	3:K:1002:ALA:HB2	2.10	0.52
1:A:106:ILE:O	1:A:110:ALA:HB3	2.10	0.52
1:B:333:ASN:O	1:B:337:SER:OG	2.22	0.52
3:J:276:ASP:OD1	3:L:222:THR:OG1	2.27	0.52
3:L:967:ALA:O	3:L:971:ARG:CB	2.58	0.52
1:B:44:LEU:HB3	1:C:290:LEU:HB3	1.92	0.52
2:G:313:VAL:HG21	2:G:347:TRP:CD1	2.44	0.52
2:H:223:PHE:CE2	2:H:274:ILE:HD11	2.37	0.52
2:H:240:GLY:HA2	2:H:262:PHE:HB2	1.92	0.52
3:J:721:LEU:HD13	3:J:815:ARG:HD3	1.92	0.52
3:K:158:VAL:O	3:K:162:MET:N	2.43	0.52
3:K:682:PHE:HA	3:K:858:ASP:O	2.10	0.52
3:K:924:ASP:H	3:K:927:PHE:HB3	1.73	0.52
3:L:248:LYS:HA	3:L:261:LEU:HD23	1.92	0.52
3:L:945:ILE:HG12	3:L:971:ARG:HG2	1.92	0.52
1:B:9:GLN:O	1:B:13:SER:OG	2.28	0.52
2:I:214:VAL:N	2:I:278:ALA:O	2.42	0.52
3:J:75:LEU:HD13	3:J:77:TYR:HA	1.91	0.52
3:L:591:LEU:O	3:L:595:THR:OG1	2.24	0.52
3:L:952:LEU:HD12	3:L:967:ALA:HB2	1.91	0.52
1:A:293:TYR:HB3	1:C:42:LEU:HB3	1.92	0.52
1:B:350:SER:O	1:B:354:SER:CB	2.57	0.52
3:J:616:GLY:H	3:J:620:ARG:HA	1.73	0.52
3:K:184:MET:HB3	3:K:771:VAL:HA	1.92	0.52
3:L:57:VAL:HG13	3:L:88:VAL:HG22	1.92	0.52
3:L:1010:GLY:O	3:L:1014:ALA:CB	2.58	0.52
3:L:1027:VAL:HB	3:L:1031:ARG:HD3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:PRO:O	1:A:19:LYS:CB	2.58	0.51
1:A:334:ILE:HG12	1:A:396:ASN:HB3	1.91	0.51
1:B:73:GLN:O	1:B:250:LEU:HB3	2.10	0.51
1:B:90:ALA:O	1:B:94:GLN:CB	2.58	0.51
1:B:347:ALA:O	1:B:351:ALA:HB3	2.10	0.51
2:D:57:PRO:HA	2:D:294:ARG:HA	1.91	0.51
2:F:220:SER:N	2:F:223:PHE:HD1	2.06	0.51
2:H:45:VAL:O	2:H:356:GLY:CA	2.58	0.51
2:H:60:THR:HG23	2:H:289:PRO:HA	1.92	0.51
3:L:96:SER:OG	3:L:97:GLY:N	2.43	0.51
3:L:848:ALA:HA	3:L:851:LEU:HD13	1.91	0.51
3:L:967:ALA:O	3:L:971:ARG:HB2	2.09	0.51
1:A:101:ASP:O	1:A:105:LEU:CB	2.58	0.51
1:A:152:THR:HB	1:B:357:ALA:HB3	1.92	0.51
1:B:119:ALA:O	1:B:123:LEU:HB2	2.10	0.51
1:C:316:LEU:O	1:C:320:HIS:CB	2.56	0.51
2:G:223:PHE:O	2:G:227:LYS:N	2.41	0.51
2:I:43:VAL:HG22	2:I:377:GLU:HG2	1.92	0.51
3:K:732:ASP:OD2	3:K:735:LYS:N	2.38	0.51
3:K:877:TYR:OH	3:K:928:GLN:OE1	2.29	0.51
3:L:263:ARG:HB2	3:L:266:ALA:HB3	1.93	0.51
1:A:100:THR:O	1:A:104:THR:HB	2.10	0.51
1:B:100:THR:HA	1:B:103:GLN:HB3	1.92	0.51
1:C:7:TYR:O	1:C:11:ARG:N	2.37	0.51
3:J:222:THR:OG1	3:K:276:ASP:OD1	2.27	0.51
3:J:591:LEU:O	3:J:595:THR:OG1	2.24	0.51
3:J:681:ASP:HB3	3:J:860:THR:O	2.10	0.51
3:L:860:THR:OG1	3:L:861:GLY:N	2.43	0.51
1:B:107:LEU:HD12	1:B:398:LEU:HD23	1.91	0.51
1:C:226:ALA:O	1:C:230:GLN:CB	2.58	0.51
2:F:227:LYS:O	2:F:231:ALA:CB	2.58	0.51
2:I:188:ASN:ND2	2:I:203:LEU:O	2.38	0.51
3:J:431:THR:HA	3:J:434:SER:HB3	1.92	0.51
1:A:178:ALA:HA	1:A:181:GLN:HG2	1.93	0.51
1:A:393:TYR:HA	1:A:396:ASN:HD22	1.74	0.51
1:B:46:ALA:HB3	1:C:288:PHE:HB3	1.92	0.51
2:F:42:VAL:HG22	2:F:360:VAL:HA	1.93	0.51
2:I:141:GLN:O	2:I:145:GLN:HB2	2.10	0.51
3:J:207:ILE:O	3:J:211:ASN:N	2.43	0.51
3:J:381:ALA:O	3:J:384:ALA:HB3	2.10	0.51
3:K:105:VAL:HA	3:K:108:GLN:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:530:SER:O	3:K:534:ILE:HB	2.11	0.51
3:L:181:GLN:NE2	3:L:768:VAL:O	2.41	0.51
3:L:943:ILE:O	3:L:947:GLU:HB2	2.11	0.51
1:B:17:LEU:O	1:B:21:ALA:HB3	2.11	0.51
1:C:24:ARG:NH1	1:C:95:ASP:OD1	2.40	0.51
1:C:180:GLU:HA	1:C:183:ARG:HB3	1.92	0.51
2:G:42:VAL:HG22	2:G:360:VAL:HG13	1.93	0.51
3:K:81:ASN:HA	3:K:817:GLU:HA	1.93	0.51
3:L:937:LEU:HA	3:L:940:LYS:HE3	1.91	0.51
1:A:81:TRP:O	1:A:85:THR:OG1	2.24	0.51
1:B:8:GLN:OE1	1:B:11:ARG:NH2	2.44	0.51
1:B:15:PRO:O	1:B:19:LYS:HB3	2.11	0.51
1:C:68:SER:HA	1:C:254:THR:O	2.11	0.51
1:C:385:GLU:O	1:C:389:ALA:CB	2.58	0.51
2:H:325:VAL:H	2:H:334:THR:HA	1.74	0.51
2:I:223:PHE:CD2	2:I:227:LYS:HE3	2.45	0.51
3:J:685:ILE:O	3:J:687:GLN:NE2	2.44	0.51
3:J:791:VAL:H	3:J:799:VAL:H	1.58	0.51
3:K:80:SER:HB2	3:K:90:ILE:HG23	1.93	0.51
3:K:216:ALA:N	3:L:51:GLY:O	2.41	0.51
3:L:375:VAL:HG22	3:L:484:VAL:HG21	1.92	0.51
3:L:726:GLN:HE21	3:L:810:GLU:HG3	1.76	0.51
3:L:732:ASP:OD2	3:L:735:LYS:N	2.36	0.51
1:B:325:GLN:O	1:B:329:SER:CB	2.58	0.51
1:C:398:LEU:O	1:C:402:SER:CB	2.58	0.51
2:D:217:THR:CB	2:D:273:CYS:SG	2.96	0.51
2:F:310:GLN:NE2	2:F:344:GLY:O	2.44	0.51
2:H:227:LYS:HA	2:H:230:LEU:HB2	1.93	0.51
3:K:242:SER:H	3:K:245:GLU:CD	2.19	0.51
3:L:41:PRO:HG2	3:L:94:PHE:HB2	1.92	0.51
1:A:321:ARG:NH1	1:C:185:ILE:O	2.44	0.51
1:A:350:SER:O	1:A:354:SER:HB2	2.11	0.51
1:B:106:ILE:HG23	1:B:412:LEU:HD13	1.93	0.51
2:E:215:ASP:HB3	2:E:275:THR:HG23	1.93	0.51
3:L:739:LEU:HB3	3:L:741:VAL:HG12	1.93	0.51
1:C:47:ASP:O	1:C:65:THR:HA	2.11	0.51
2:G:219:SER:OG	2:G:220:SER:N	2.42	0.51
2:I:309:PRO:HA	2:I:346:LYS:HA	1.91	0.51
3:J:477:ALA:O	3:J:481:SER:HB3	2.11	0.51
3:L:196:PHE:HB3	3:L:252:LYS:HD3	1.93	0.51
1:A:107:LEU:HD12	1:A:398:LEU:HD23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:GLN:HA	1:A:307:TYR:HD2	1.76	0.50
1:C:100:THR:HA	1:C:103:GLN:HB3	1.93	0.50
1:C:230:GLN:NE2	1:C:313:SER:OG	2.45	0.50
1:C:314:GLU:HA	1:C:317:GLU:HB3	1.92	0.50
2:F:307:LEU:HD21	2:F:343:ILE:HD12	1.92	0.50
3:J:155:SER:O	3:J:159:ALA:HB2	2.11	0.50
3:J:242:SER:OG	3:J:244:GLU:OE1	2.29	0.50
3:K:184:MET:HE1	3:K:243:THR:HG22	1.92	0.50
3:L:122:VAL:O	3:L:126:GLY:N	2.33	0.50
3:L:637:ARG:HB2	3:L:642:ASN:HB3	1.92	0.50
3:L:791:VAL:H	3:L:799:VAL:H	1.57	0.50
1:A:195:ALA:O	1:A:420:SER:N	2.44	0.50
2:F:93:LEU:HB2	2:F:176:VAL:HG12	1.92	0.50
2:G:43:VAL:HG22	2:G:377:GLU:HG2	1.93	0.50
2:H:307:LEU:HD21	2:H:343:ILE:HD12	1.91	0.50
3:J:114:ALA:HA	3:J:117:LEU:HD13	1.93	0.50
3:J:637:ARG:O	3:J:643:LYS:NZ	2.43	0.50
3:K:105:VAL:O	3:K:109:ASN:ND2	2.44	0.50
3:K:140:VAL:O	3:K:287:SER:O	2.28	0.50
3:K:644:VAL:HA	3:K:647:ILE:HD12	1.92	0.50
3:K:681:ASP:HB3	3:K:860:THR:O	2.10	0.50
3:K:998:GLY:HA2	3:K:1001:ASN:HB2	1.93	0.50
3:L:477:ALA:O	3:L:481:SER:HB3	2.11	0.50
1:A:314:GLU:HA	1:A:317:GLU:HB3	1.94	0.50
1:C:10:ALA:O	1:C:14:ASN:N	2.44	0.50
1:C:333:ASN:O	1:C:337:SER:OG	2.21	0.50
2:D:94:TYR:H	2:D:176:VAL:HB	1.75	0.50
2:G:45:VAL:O	2:G:356:GLY:N	2.43	0.50
3:K:222:THR:OG1	3:L:276:ASP:OD1	2.29	0.50
3:K:700:ASN:HA	3:K:703:LEU:HB2	1.93	0.50
1:A:70:GLN:HA	1:A:252:ALA:O	2.11	0.50
1:B:336:ALA:O	1:B:340:SER:CB	2.59	0.50
3:J:841:MET:O	3:J:845:GLU:HB2	2.11	0.50
3:K:181:GLN:NE2	3:K:768:VAL:O	2.38	0.50
3:K:196:PHE:O	3:K:252:LYS:NZ	2.36	0.50
3:K:300:LEU:HA	3:K:334:LYS:HD2	1.92	0.50
3:L:218:GLN:OE1	3:L:231:ASN:ND2	2.44	0.50
3:L:424:GLY:HA3	3:L:502:LYS:HA	1.94	0.50
3:L:685:ILE:O	3:L:856:GLY:N	2.34	0.50
3:L:703:LEU:HD21	3:L:718:PRO:HG3	1.93	0.50
2:D:254:PHE:CE1	2:D:287:LEU:CD1	2.88	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:268:ASP:HB3	2:D:272:GLY:H	1.76	0.50
2:I:257:ASP:OD1	2:I:257:ASP:N	2.42	0.50
3:J:748:THR:O	3:J:752:ALA:HB2	2.10	0.50
3:K:249:ILE:HB	3:K:262:LEU:HB2	1.94	0.50
1:A:87:GLN:O	1:A:91:ALA:HB2	2.12	0.50
1:A:315:GLN:O	1:A:319:ALA:CB	2.60	0.50
1:A:399:ASN:O	1:A:403:ALA:HB2	2.11	0.50
1:C:240:ALA:O	1:C:243:GLY:N	2.44	0.50
2:D:254:PHE:HE1	2:D:287:LEU:HD21	1.77	0.50
2:F:196:GLN:HB2	2:F:199:GLN:HB3	1.92	0.50
2:G:325:VAL:HG22	2:G:359:VAL:HA	1.93	0.50
2:I:342:ALA:HA	2:I:347:TRP:HA	1.94	0.50
3:J:1028:VAL:O	3:J:1032:ARG:HB3	2.12	0.50
3:K:459:PHE:O	3:K:468:ARG:NH2	2.36	0.50
3:L:82:SER:N	3:L:816:LEU:O	2.43	0.50
1:A:86:LEU:O	1:A:90:ALA:HB3	2.11	0.50
1:B:309:PHE:O	1:B:313:SER:OG	2.25	0.50
1:C:77:ASP:OD2	1:C:80:LYS:N	2.34	0.50
1:C:108:ASN:HA	1:C:111:THR:HB	1.93	0.50
1:C:393:TYR:HA	1:C:396:ASN:HD22	1.77	0.50
2:D:138:ILE:HD11	2:D:142:GLU:HB2	1.93	0.50
2:F:268:ASP:HB3	2:F:272:GLY:H	1.77	0.50
2:F:340:SER:N	2:F:348:LEU:O	2.45	0.50
2:I:304:ASN:OD1	2:I:304:ASN:N	2.44	0.50
3:J:571:VAL:HG12	3:J:630:SER:HB2	1.93	0.50
3:J:844:MET:O	3:J:848:ALA:N	2.45	0.50
3:K:555:LEU:HB3	3:K:913:LEU:HD13	1.94	0.50
3:K:632:LYS:HE3	3:K:636:ASP:HB3	1.93	0.50
3:L:345:VAL:HA	3:L:348:ILE:HD12	1.94	0.50
1:C:4:MSE:HG2	1:C:416:ASN:HD22	1.76	0.50
1:C:46:ALA:HA	1:C:66:SER:O	2.11	0.50
2:E:83:GLU:HG2	2:E:187:SER:H	1.77	0.50
3:J:204:ILE:HA	3:J:207:ILE:HD12	1.94	0.50
3:J:464:GLY:HA2	3:J:467:TYR:HD2	1.77	0.50
3:K:377:LEU:HA	3:K:380:PHE:HD2	1.77	0.50
3:L:100:ALA:O	3:L:104:GLN:CB	2.60	0.50
3:L:445:ILE:O	3:L:449:LEU:HB2	2.12	0.50
1:A:223:LEU:HB2	1:A:316:LEU:HG	1.94	0.50
1:C:86:LEU:HG	1:C:232:LEU:HG	1.94	0.50
3:J:218:GLN:HA	3:J:233:SER:HA	1.93	0.50
3:J:335:ILE:O	3:J:339:GLU:CB	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:381:ALA:O	3:K:384:ALA:HB3	2.12	0.50
3:L:30:LEU:HD12	3:L:31:PRO:HD2	1.94	0.50
3:L:65:ILE:HG23	3:L:69:MET:HE3	1.94	0.50
1:C:30:LYS:HA	1:C:33:GLU:HG2	1.94	0.49
2:E:115:ALA:O	2:E:119:ALA:CB	2.60	0.49
2:E:304:ASN:N	2:E:304:ASN:OD1	2.45	0.49
2:H:254:PHE:CE1	2:H:287:LEU:HD21	2.47	0.49
3:J:141:GLY:HA3	3:J:324:VAL:HG12	1.94	0.49
3:K:77:TYR:N	3:K:93:THR:OG1	2.44	0.49
3:K:431:THR:HA	3:K:434:SER:HB3	1.94	0.49
3:K:983:ILE:HA	3:K:986:VAL:HG22	1.93	0.49
3:L:184:MET:HB3	3:L:771:VAL:HA	1.92	0.49
3:L:398:MET:HA	3:L:401:ALA:HB3	1.93	0.49
3:L:644:VAL:HA	3:L:647:ILE:HD12	1.93	0.49
1:A:133:ILE:O	1:A:137:LEU:HB3	2.12	0.49
1:A:173:ASN:ND2	1:B:333:ASN:OD1	2.45	0.49
1:B:185:ILE:O	1:C:321:ARG:NH1	2.45	0.49
1:C:194:ALA:HB3	1:C:419:LEU:HD13	1.94	0.49
2:F:57:PRO:HA	2:F:294:ARG:HA	1.93	0.49
3:J:82:SER:N	3:J:816:LEU:O	2.36	0.49
3:J:100:ALA:O	3:J:104:GLN:CB	2.59	0.49
3:J:155:SER:O	3:J:159:ALA:CB	2.61	0.49
3:J:741:VAL:HG13	3:J:746:ILE:HD11	1.93	0.49
3:K:3:ASN:HA	3:K:6:ILE:HB	1.95	0.49
3:K:375:VAL:HG22	3:K:484:VAL:HG21	1.93	0.49
3:K:992:SER:O	3:K:1001:ASN:ND2	2.35	0.49
3:L:70:ASN:O	3:L:110:LYS:NZ	2.40	0.49
1:A:16:GLU:O	1:A:20:SER:CB	2.53	0.49
1:B:29:GLU:HB3	1:C:304:GLN:HE21	1.77	0.49
1:C:103:GLN:O	1:C:107:LEU:HB2	2.12	0.49
1:C:317:GLU:OE2	1:C:321:ARG:NE	2.44	0.49
2:D:314:THR:OG1	2:D:322:THR:O	2.26	0.49
2:F:271:THR:HB	3:J:258:CYS:SG	2.53	0.49
2:G:43:VAL:O	2:G:359:VAL:O	2.30	0.49
3:J:43:VAL:HB	3:J:92:LEU:HB2	1.94	0.49
3:J:564:LEU:HD21	3:J:925:VAL:HB	1.93	0.49
1:A:66:SER:HA	1:A:256:ILE:O	2.12	0.49
1:C:105:LEU:O	1:C:109:THR:CB	2.61	0.49
2:D:131:LYS:HG3	2:D:132:LEU:HG	1.94	0.49
2:G:94:TYR:OH	2:G:187:SER:OG	2.22	0.49
3:J:180:SER:OG	3:J:181:GLN:N	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:118:LEU:HD23	3:K:122:VAL:HG13	1.93	0.49
2:D:98:PRO:O	2:D:102:GLN:N	2.46	0.49
2:H:94:TYR:H	2:H:176:VAL:HB	1.76	0.49
3:L:876:LEU:O	3:L:880:SER:CB	2.59	0.49
2:D:124:LEU:HD13	2:E:144:ASP:HB3	1.94	0.49
2:E:42:VAL:HA	2:E:360:VAL:HA	1.95	0.49
2:H:40:VAL:HG13	2:H:363:GLY:H	1.78	0.49
2:I:43:VAL:H	2:I:360:VAL:C	2.20	0.49
2:I:220:SER:OG	2:I:272:GLY:O	2.29	0.49
3:J:730:ASP:OD2	3:J:808:ARG:NH1	2.44	0.49
3:K:49:TYR:N	3:K:86:GLY:O	2.45	0.49
2:E:101:TYR:O	2:E:105:TYR:HB2	2.12	0.49
2:G:167:ALA:O	2:G:171:LEU:CB	2.60	0.49
2:I:39:ALA:HA	2:I:374:LYS:HB2	1.94	0.49
2:I:90:GLY:N	2:I:178:SER:O	2.44	0.49
2:I:233:GLY:HA2	2:I:236:LYS:HE3	1.94	0.49
3:J:911:GLY:HA3	3:J:1009:GLY:HA3	1.94	0.49
3:K:280:GLU:HA	3:K:285:PRO:HA	1.94	0.49
3:L:356:TYR:HE1	3:L:362:PHE:HA	1.77	0.49
1:A:133:ILE:O	1:A:137:LEU:CB	2.60	0.49
1:A:134:TYR:O	1:A:138:ASP:HB2	2.13	0.49
2:F:162:ALA:O	2:F:166:THR:OG1	2.27	0.49
2:H:212:ILE:N	2:H:280:PHE:O	2.38	0.49
3:J:700:ASN:HA	3:J:703:LEU:HB2	1.94	0.49
3:K:395:MET:HA	3:K:398:MET:HG2	1.94	0.49
3:K:477:ALA:O	3:K:481:SER:HB3	2.13	0.49
3:K:552:MET:O	3:K:556:PHE:HB3	2.12	0.49
1:A:307:TYR:HB3	1:C:22:ALA:HB1	1.93	0.49
1:C:167:ASN:O	1:C:171:ALA:CB	2.60	0.49
2:D:254:PHE:CZ	2:D:287:LEU:HD11	2.46	0.49
2:F:66:ALA:O	2:F:205:THR:HA	2.13	0.49
2:G:141:GLN:O	2:G:145:GLN:CB	2.61	0.49
2:H:124:LEU:HD22	2:H:128:ARG:HH12	1.77	0.49
2:I:223:PHE:CE2	2:I:227:LYS:CE	2.89	0.49
3:J:210:GLN:HE22	3:J:250:LEU:HB3	1.78	0.49
3:K:61:VAL:HG11	3:K:88:VAL:HG21	1.94	0.49
3:K:616:GLY:H	3:K:620:ARG:HA	1.77	0.49
3:K:860:THR:OG1	3:K:861:GLY:N	2.45	0.49
3:K:988:PRO:HA	3:K:991:ILE:HG13	1.95	0.49
3:K:989:LEU:HB3	3:K:1004:GLY:HA3	1.93	0.49
1:B:108:ASN:HA	1:B:111:THR:HB	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:SER:OG	1:C:101:ASP:OD2	2.27	0.49
2:D:289:PRO:O	2:E:269:GLN:NE2	2.38	0.49
2:F:87:ILE:O	2:F:182:GLY:N	2.40	0.49
2:G:76:ILE:N	2:G:193:ALA:O	2.46	0.49
2:G:326:VAL:HA	2:G:332:VAL:HA	1.95	0.49
3:J:395:MET:HA	3:J:398:MET:HG2	1.94	0.49
3:J:685:ILE:HD13	3:J:822:LEU:HB2	1.95	0.49
3:L:139:VAL:HG23	3:L:327:TYR:HD2	1.77	0.49
3:L:198:LEU:HD21	3:L:252:LYS:HD2	1.94	0.49
3:L:280:GLU:HA	3:L:285:PRO:HA	1.95	0.49
1:A:87:GLN:O	1:A:91:ALA:CB	2.61	0.48
1:A:409:GLU:HA	1:A:412:LEU:HB3	1.94	0.48
1:C:336:ALA:O	1:C:340:SER:CB	2.61	0.48
2:I:224:LEU:O	2:I:227:LYS:HB2	2.12	0.48
1:B:184:GLN:OE1	1:C:325:GLN:NE2	2.43	0.48
2:D:306:ILE:O	2:D:349:VAL:N	2.45	0.48
2:F:112:LEU:HD22	2:F:164:VAL:HG21	1.93	0.48
2:F:220:SER:CA	2:F:223:PHE:CD1	2.69	0.48
2:H:112:LEU:HD22	2:H:164:VAL:HG21	1.93	0.48
2:I:115:ALA:O	2:I:119:ALA:CB	2.61	0.48
3:L:190:PRO:O	3:L:194:ASN:CB	2.61	0.48
3:L:934:THR:O	3:L:938:SER:OG	2.27	0.48
1:C:236:GLN:HA	1:C:239:GLN:HB3	1.95	0.48
2:D:112:LEU:HD22	2:D:164:VAL:HG21	1.95	0.48
2:F:229:GLU:HB3	2:F:235:LEU:HD23	1.96	0.48
2:F:288:LEU:CD2	2:G:267:VAL:HG21	2.40	0.48
2:I:101:TYR:O	2:I:105:TYR:CB	2.61	0.48
2:I:244:VAL:HG21	2:I:260:LEU:HD22	1.95	0.48
3:K:584:GLN:O	3:K:588:GLN:CB	2.57	0.48
3:L:78:MET:HG3	3:L:92:LEU:HG	1.96	0.48
3:L:213:GLN:HB2	3:L:239:ARG:HG3	1.95	0.48
3:L:910:ILE:O	3:L:913:LEU:HB2	2.13	0.48
1:B:235:GLU:O	1:B:239:GLN:CB	2.46	0.48
1:B:240:ALA:O	1:B:243:GLY:N	2.47	0.48
2:D:42:VAL:HG22	2:D:360:VAL:HA	1.95	0.48
2:E:77:LEU:HB3	2:E:95:GLN:HB3	1.95	0.48
2:E:141:GLN:O	2:E:145:GLN:CB	2.62	0.48
2:F:56:LEU:HD22	2:F:218:GLN:HE21	1.78	0.48
2:H:254:PHE:HE1	2:H:287:LEU:HD21	1.77	0.48
3:J:438:ILE:HA	3:J:441:ALA:H	1.78	0.48
3:J:977:MET:O	3:J:981:ALA:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:207:ILE:O	3:K:211:ASN:CB	2.60	0.48
3:K:736:ALA:O	3:K:740:GLY:N	2.46	0.48
1:A:385:GLU:O	1:A:389:ALA:CB	2.57	0.48
1:C:17:LEU:O	1:C:21:ALA:CB	2.61	0.48
2:D:214:VAL:HB	2:D:278:ALA:HB3	1.95	0.48
2:D:220:SER:CA	2:D:223:PHE:CD1	2.69	0.48
3:J:163:LYS:HE3	3:J:177:LEU:HB2	1.96	0.48
3:J:410:ILE:HA	3:J:413:VAL:HG22	1.95	0.48
3:K:65:ILE:HG23	3:K:69:MET:HE3	1.95	0.48
3:K:429:GLU:HA	3:K:432:ARG:HD2	1.96	0.48
3:L:253:VAL:HG12	3:L:259:ARG:HA	1.95	0.48
3:L:559:LEU:HD12	3:L:560:PRO:HD2	1.94	0.48
1:A:325:GLN:O	1:A:329:SER:CB	2.61	0.48
1:A:336:ALA:HB1	1:C:169:VAL:HG12	1.95	0.48
1:C:54:TYR:HA	1:C:58:ASN:HB2	1.95	0.48
1:C:249:ASP:HB2	1:C:287:SER:HB3	1.95	0.48
2:F:94:TYR:HH	2:F:187:SER:HG	1.55	0.48
2:I:98:PRO:O	2:I:102:GLN:N	2.46	0.48
2:I:317:PRO:O	3:L:811:TYR:OH	2.24	0.48
3:J:34:GLN:O	3:J:392:THR:N	2.43	0.48
3:K:204:ILE:HA	3:K:207:ILE:HD12	1.95	0.48
3:K:213:GLN:HB2	3:K:239:ARG:HG3	1.96	0.48
3:K:380:PHE:HZ	3:K:395:MET:HE1	1.78	0.48
3:K:721:LEU:HB3	3:K:814:PRO:HG2	1.95	0.48
3:L:527:TYR:OH	3:L:1019:ILE:O	2.32	0.48
3:L:919:ARG:HH11	3:L:1002:ALA:HB2	1.77	0.48
1:A:409:GLU:O	1:A:413:LEU:HB2	2.14	0.48
1:C:409:GLU:HA	1:C:412:LEU:HB3	1.96	0.48
2:E:62:ALA:H	2:E:289:PRO:HB3	1.78	0.48
2:H:188:ASN:ND2	2:H:202:ALA:O	2.39	0.48
3:J:96:SER:OG	3:J:97:GLY:N	2.46	0.48
3:J:391:ASN:O	3:J:395:MET:N	2.33	0.48
3:J:630:SER:OG	3:J:631:LEU:N	2.47	0.48
3:K:84:SER:N	3:K:814:PRO:O	2.44	0.48
3:K:157:TYR:OH	3:K:316:PHE:O	2.31	0.48
3:K:185:ARG:NH2	3:K:774:MET:O	2.46	0.48
3:L:34:GLN:O	3:L:392:THR:N	2.46	0.48
1:A:281:GLN:NE2	1:A:282:ASN:O	2.47	0.48
2:I:223:PHE:HE2	2:I:227:LYS:CE	2.23	0.48
3:J:193:LEU:O	3:J:197:GLN:N	2.47	0.48
3:J:703:LEU:HD21	3:J:718:PRO:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:750:LEU:O	3:J:754:TRP:N	2.47	0.48
3:K:727:PHE:HA	3:K:808:ARG:O	2.13	0.48
1:A:180:GLU:O	1:A:184:GLN:HB2	2.14	0.48
1:B:385:GLU:O	1:B:389:ALA:HB2	2.13	0.48
2:D:299:GLU:HA	2:D:301:LEU:HD13	1.95	0.48
2:E:75:ILE:HG13	2:E:194:LEU:HD13	1.96	0.48
2:G:55:GLU:HA	2:G:296:ARG:HB3	1.95	0.48
2:H:126:VAL:O	2:H:130:GLN:CB	2.58	0.48
2:H:306:ILE:HB	2:H:349:VAL:HB	1.95	0.48
3:J:281:PHE:HE1	3:J:608:SER:HB2	1.78	0.48
3:K:256:ASP:CG	3:K:258:CYS:SG	2.97	0.48
1:B:315:GLN:O	1:B:319:ALA:CB	2.62	0.48
1:C:180:GLU:O	1:C:184:GLN:CB	2.61	0.48
2:D:325:VAL:HG21	2:D:335:ARG:HE	1.78	0.48
2:E:327:GLY:H	2:E:332:VAL:HA	1.79	0.48
2:G:43:VAL:H	2:G:360:VAL:C	2.21	0.48
2:H:42:VAL:HG22	2:H:360:VAL:HA	1.95	0.48
3:J:280:GLU:O	3:J:610:PHE:HA	2.14	0.48
3:J:988:PRO:HA	3:J:991:ILE:HG13	1.96	0.48
3:K:70:ASN:O	3:K:110:LYS:NZ	2.36	0.48
3:K:187:TRP:HB2	3:K:267:LYS:HB3	1.96	0.48
3:K:446:ALA:HB2	3:K:482:VAL:HG11	1.96	0.48
1:A:238:ARG:HA	1:A:241:GLN:HB2	1.96	0.47
1:A:325:GLN:NE2	1:C:184:GLN:OE1	2.43	0.47
1:B:327:VAL:O	1:B:331:PHE:CB	2.60	0.47
1:B:337:SER:OG	1:B:396:ASN:ND2	2.47	0.47
2:E:338:VAL:H	2:E:351:GLU:HB3	1.79	0.47
2:F:63:TYR:HB2	2:F:212:ILE:HA	1.95	0.47
3:J:76:MET:N	3:J:93:THR:O	2.42	0.47
3:J:151:GLN:HE22	3:J:279:ALA:HB3	1.79	0.47
3:K:345:VAL:HA	3:K:348:ILE:HD12	1.96	0.47
3:K:610:PHE:O	3:K:627:ALA:HA	2.14	0.47
3:K:876:LEU:O	3:K:880:SER:OG	2.20	0.47
3:L:81:ASN:HA	3:L:817:GLU:HA	1.96	0.47
3:L:777:ALA:HA	3:L:780:ARG:HG2	1.95	0.47
3:L:832:ALA:HB3	3:L:835:LYS:HB2	1.97	0.47
1:B:238:ARG:HA	1:B:241:GLN:HB2	1.94	0.47
2:G:304:ASN:N	2:G:304:ASN:OD1	2.47	0.47
2:G:360:VAL:HG11	2:G:364:LEU:HD21	1.95	0.47
2:I:42:VAL:HA	2:I:360:VAL:HA	1.96	0.47
2:I:103:ALA:O	2:I:107:SER:CB	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:243:LYS:NZ	2:I:259:THR:OG1	2.36	0.47
3:J:726:GLN:O	3:J:809:TRP:HA	2.13	0.47
3:K:980:LEU:HA	3:K:983:ILE:HG22	1.95	0.47
3:L:395:MET:HA	3:L:398:MET:HG2	1.96	0.47
1:A:143:ARG:HB3	1:A:148:LEU:HD12	1.95	0.47
1:B:75:ILE:C	1:B:248:LEU:O	2.57	0.47
1:B:90:ALA:O	1:B:94:GLN:HB2	2.14	0.47
1:C:234:ARG:HA	1:C:237:ILE:HD12	1.96	0.47
2:D:123:GLN:HE21	2:D:127:ASN:HD21	1.62	0.47
2:E:76:ILE:N	2:E:193:ALA:O	2.46	0.47
3:K:435:MET:O	3:K:439:GLN:HB3	2.14	0.47
3:K:611:ALA:HA	3:K:627:ALA:HA	1.95	0.47
3:K:726:GLN:HE21	3:K:810:GLU:HG3	1.79	0.47
3:K:748:THR:O	3:K:752:ALA:HB2	2.14	0.47
3:K:761:ASP:HA	3:K:769:LYS:O	2.15	0.47
3:L:968:VAL:HA	3:L:971:ARG:HB3	1.95	0.47
3:L:1018:ALA:HA	3:L:1021:PHE:HD2	1.78	0.47
1:B:101:ASP:O	1:B:105:LEU:CB	2.63	0.47
1:B:121:ASP:OD2	1:B:391:TYR:OH	2.25	0.47
2:D:92:SER:HA	2:D:177:THR:HA	1.96	0.47
2:F:254:PHE:CZ	2:F:287:LEU:HD11	2.49	0.47
3:J:69:MET:HB3	3:J:72:ILE:HD13	1.96	0.47
3:J:190:PRO:O	3:J:194:ASN:CB	2.62	0.47
3:J:445:ILE:O	3:J:449:LEU:CB	2.62	0.47
3:J:644:VAL:HA	3:J:647:ILE:HD12	1.96	0.47
3:J:748:THR:O	3:J:752:ALA:CB	2.63	0.47
3:L:213:GLN:HE22	3:L:238:THR:HA	1.79	0.47
3:L:584:GLN:O	3:L:588:GLN:CB	2.56	0.47
1:A:107:LEU:O	1:A:111:THR:CB	2.63	0.47
1:B:30:LYS:O	1:B:34:ALA:HB2	2.15	0.47
1:C:119:ALA:O	1:C:123:LEU:CB	2.63	0.47
1:C:379:LEU:HG	1:C:383:LYS:HE3	1.96	0.47
2:D:282:ASN:HD21	2:D:287:LEU:H	1.62	0.47
2:D:307:LEU:HD21	2:D:343:ILE:HD12	1.95	0.47
3:J:45:ILE:O	3:J:89:GLN:HA	2.14	0.47
3:J:398:MET:HA	3:J:401:ALA:HB3	1.96	0.47
3:J:449:LEU:HD23	3:J:478:MET:HG3	1.96	0.47
3:L:114:ALA:HA	3:L:117:LEU:HD13	1.96	0.47
3:L:911:GLY:HA2	3:L:914:LEU:HG	1.97	0.47
1:A:182:LEU:O	1:A:187:GLY:N	2.46	0.47
1:C:94:GLN:O	1:C:98:TYR:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:116:VAL:HA	1:C:178:ALA:HB1	1.97	0.47
1:C:116:VAL:HG22	1:C:178:ALA:HB1	1.97	0.47
2:I:222:ASP:O	2:I:226:LEU:N	2.43	0.47
3:K:685:ILE:N	3:K:856:GLY:O	2.47	0.47
1:A:18:ARG:NH1	1:B:314:GLU:OE2	2.48	0.47
1:A:107:LEU:HA	1:A:398:LEU:HD23	1.97	0.47
1:A:179:VAL:O	1:A:183:ARG:CB	2.63	0.47
1:A:213:LEU:HD11	1:A:328:ARG:HH21	1.79	0.47
1:A:321:ARG:O	1:A:325:GLN:CB	2.61	0.47
1:C:31:ILE:HG12	1:C:87:GLN:HG3	1.96	0.47
1:C:100:THR:O	1:C:104:THR:HB	2.15	0.47
1:C:261:TYR:HB3	1:C:266:THR:HG21	1.97	0.47
1:C:380:TYR:HA	1:C:383:LYS:HD2	1.95	0.47
2:E:167:ALA:O	2:E:171:LEU:CB	2.59	0.47
2:E:233:GLY:HA2	2:E:236:LYS:HE3	1.96	0.47
2:F:94:TYR:H	2:F:176:VAL:HB	1.80	0.47
2:H:105:TYR:CE1	2:H:171:LEU:HG	2.50	0.47
2:H:220:SER:CB	2:H:223:PHE:CE1	2.72	0.47
2:I:82:LYS:HB2	2:I:85:SER:HB3	1.95	0.47
3:K:158:VAL:HG12	3:K:163:LYS:HB2	1.97	0.47
3:K:697:GLN:O	3:K:701:GLN:CB	2.62	0.47
3:L:138:MET:O	3:L:289:LEU:O	2.32	0.47
3:L:555:LEU:HA	3:L:558:ARG:HG2	1.96	0.47
3:L:909:VAL:O	3:L:913:LEU:N	2.37	0.47
3:L:977:MET:O	3:L:981:ALA:HB2	2.15	0.47
1:A:167:ASN:O	1:A:171:ALA:CB	2.63	0.47
1:B:4:MSE:HG2	1:B:416:ASN:HD22	1.79	0.47
1:B:134:TYR:O	1:B:138:ASP:HB2	2.15	0.47
1:C:15:PRO:O	1:C:19:LYS:HB3	2.15	0.47
1:C:195:ALA:O	1:C:420:SER:N	2.45	0.47
2:E:212:ILE:O	2:E:280:PHE:N	2.38	0.47
3:J:105:VAL:O	3:J:109:ASN:ND2	2.47	0.47
3:J:304:ALA:O	3:J:308:ALA:CB	2.63	0.47
3:J:368:PRO:HB3	3:J:413:VAL:HG11	1.96	0.47
3:K:438:ILE:O	3:K:442:LEU:HB2	2.13	0.47
3:K:445:ILE:O	3:K:449:LEU:CB	2.63	0.47
3:K:464:GLY:HA2	3:K:467:TYR:HD2	1.79	0.47
3:L:68:ASN:HD21	3:L:117:LEU:HD22	1.79	0.47
3:L:438:ILE:HA	3:L:441:ALA:H	1.80	0.47
3:L:568:ASP:OD1	3:L:569:GLN:N	2.48	0.47
1:C:325:GLN:O	1:C:329:SER:CB	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:63:TYR:CG	2:D:211:PRO:HG2	2.49	0.47
2:F:188:ASN:ND2	2:F:202:ALA:O	2.37	0.47
3:J:632:LYS:HE3	3:J:636:ASP:HB3	1.97	0.47
3:J:934:THR:O	3:J:938:SER:OG	2.33	0.47
3:K:721:LEU:HD13	3:K:815:ARG:HH11	1.80	0.47
3:K:952:LEU:HD12	3:K:967:ALA:HB2	1.97	0.47
3:L:419:VAL:HG11	3:L:434:SER:HB2	1.97	0.47
3:L:464:GLY:HA2	3:L:467:TYR:HD2	1.80	0.47
3:L:571:VAL:HA	3:L:629:VAL:O	2.14	0.47
1:B:347:ALA:O	1:B:351:ALA:CB	2.63	0.47
2:E:225:ARG:O	2:E:228:GLN:HB3	2.15	0.47
2:G:57:PRO:HA	2:G:294:ARG:HA	1.95	0.47
2:H:325:VAL:HG21	2:H:335:ARG:HE	1.80	0.47
3:K:68:ASN:HD21	3:K:117:LEU:HD22	1.79	0.47
3:K:185:ARG:HB3	3:K:269:GLU:HG3	1.96	0.47
3:K:243:THR:HA	3:K:246:PHE:HB2	1.97	0.47
1:B:119:ALA:O	1:B:123:LEU:CB	2.62	0.46
2:G:254:PHE:CE1	2:G:287:LEU:HD11	2.50	0.46
3:J:679:GLY:CA	3:J:829:GLY:O	2.53	0.46
3:J:960:LEU:O	3:J:964:THR:OG1	2.27	0.46
3:K:207:ILE:O	3:K:211:ASN:HB3	2.15	0.46
3:K:314:GLU:OE1	3:K:314:GLU:N	2.48	0.46
3:K:438:ILE:HA	3:K:441:ALA:H	1.80	0.46
3:L:511:GLY:O	3:L:515:TRP:HB2	2.15	0.46
1:A:392:ASN:O	1:A:396:ASN:ND2	2.48	0.46
1:A:398:LEU:O	1:A:402:SER:CB	2.60	0.46
1:B:22:ALA:HB1	1:C:307:TYR:HB3	1.97	0.46
1:B:63:ASN:OD1	1:B:260:SER:OG	2.25	0.46
1:C:105:LEU:O	1:C:109:THR:OG1	2.30	0.46
1:C:350:SER:O	1:C:354:SER:HB2	2.15	0.46
2:D:249:SER:OG	2:E:224:LEU:HD12	2.14	0.46
2:H:338:VAL:HB	2:H:351:GLU:HB3	1.98	0.46
2:I:87:ILE:HG21	2:I:93:LEU:HD11	1.97	0.46
3:J:41:PRO:O	3:J:94:PHE:N	2.41	0.46
3:J:184:MET:HG3	3:J:186:ILE:HD11	1.97	0.46
3:J:559:LEU:HD12	3:J:560:PRO:HD2	1.98	0.46
3:K:32:VAL:HG11	3:K:300:LEU:HB2	1.97	0.46
3:K:846:GLN:O	3:K:849:SER:OG	2.31	0.46
3:L:263:ARG:HG2	3:L:264:ASP:H	1.80	0.46
3:L:377:LEU:HA	3:L:380:PHE:HD2	1.79	0.46
3:L:381:ALA:O	3:L:384:ALA:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:ALA:O	1:A:230:GLN:CB	2.59	0.46
1:B:217:GLU:OE2	1:B:320:HIS:ND1	2.47	0.46
1:C:107:LEU:O	1:C:111:THR:OG1	2.27	0.46
1:C:410:GLN:HE22	1:C:413:LEU:HD13	1.80	0.46
2:E:76:ILE:HG23	2:E:94:TYR:HB3	1.97	0.46
2:F:212:ILE:N	2:F:280:PHE:O	2.46	0.46
3:J:686:ASP:OD2	3:J:689:GLY:N	2.48	0.46
3:K:790:TYR:HB3	3:K:798:MET:HB3	1.97	0.46
3:L:65:ILE:O	3:L:69:MET:N	2.48	0.46
3:L:537:SER:HA	3:L:540:ARG:HG2	1.96	0.46
1:B:3:LEU:HB2	1:B:419:LEU:HD11	1.97	0.46
2:G:215:ASP:HB3	2:G:275:THR:HG23	1.97	0.46
3:J:54:ALA:HA	3:J:57:VAL:HB	1.98	0.46
3:K:25:LEU:O	3:K:29:LYS:CB	2.63	0.46
3:K:331:PRO:O	3:K:335:ILE:HB	2.15	0.46
3:K:584:GLN:HA	3:K:587:THR:HB	1.97	0.46
3:K:687:GLN:HE21	3:K:856:GLY:H	1.64	0.46
1:C:7:TYR:OH	1:C:409:GLU:OE2	2.24	0.46
2:F:291:MET:HB3	2:F:293:VAL:HG13	1.96	0.46
3:J:80:SER:HB2	3:J:90:ILE:HG23	1.97	0.46
3:J:697:GLN:O	3:J:701:GLN:HB2	2.16	0.46
3:K:723:ASP:HA	3:K:813:SER:HA	1.96	0.46
3:L:697:GLN:O	3:L:701:GLN:CB	2.63	0.46
3:L:792:ARG:HB3	3:L:796:GLY:HA2	1.97	0.46
1:A:29:GLU:HB3	1:B:304:GLN:HE21	1.80	0.46
1:B:424:SER:OG	1:B:425:THR:N	2.48	0.46
1:C:12:LEU:HD12	1:C:13:SER:HB3	1.96	0.46
2:E:342:ALA:HA	2:E:347:TRP:HA	1.98	0.46
2:F:219:SER:C	2:F:223:PHE:HD1	2.10	0.46
2:H:266:THR:HB	2:H:275:THR:H	1.80	0.46
2:I:43:VAL:O	2:I:359:VAL:O	2.33	0.46
3:J:545:TYR:OH	3:J:903:LEU:O	2.34	0.46
3:K:150:THR:N	3:K:153:ASP:OD2	2.40	0.46
3:K:767:ARG:HB3	3:K:769:LYS:HE3	1.96	0.46
3:L:47:ALA:O	3:L:88:VAL:N	2.48	0.46
3:L:571:VAL:HG12	3:L:630:SER:HA	1.97	0.46
3:L:818:ARG:NE	3:L:821:GLY:O	2.49	0.46
1:A:25:ASP:O	1:A:29:GLU:HB2	2.15	0.46
1:C:179:VAL:O	1:C:183:ARG:HB2	2.16	0.46
2:F:116:GLN:O	2:F:120:ASN:HB2	2.16	0.46
2:G:130:GLN:HA	2:G:133:LEU:HD23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:63:GLN:O	3:K:67:GLN:HB2	2.14	0.46
3:K:118:LEU:HD22	3:K:123:GLN:HB3	1.98	0.46
3:L:281:PHE:HD1	3:L:610:PHE:HB2	1.80	0.46
3:L:317:PHE:HE2	3:L:323:ILE:HD11	1.80	0.46
1:A:357:ALA:HB3	1:C:152:THR:HB	1.97	0.46
2:D:167:ALA:O	2:D:171:LEU:CB	2.57	0.46
2:G:75:ILE:HG13	2:G:194:LEU:HD13	1.97	0.46
2:G:254:PHE:CD1	2:G:287:LEU:HD11	2.50	0.46
3:J:299:ALA:O	3:J:303:ALA:N	2.44	0.46
3:K:256:ASP:OD1	3:K:258:CYS:SG	2.74	0.46
3:K:281:PHE:HD1	3:K:610:PHE:HB2	1.80	0.46
3:K:392:THR:O	3:K:396:PHE:HB2	2.16	0.46
3:K:645:GLU:O	3:K:648:THR:OG1	2.26	0.46
3:K:977:MET:O	3:K:981:ALA:CB	2.64	0.46
3:L:429:GLU:HA	3:L:432:ARG:HD2	1.98	0.46
3:L:449:LEU:HD23	3:L:478:MET:HG3	1.98	0.46
3:L:926:TYR:HB3	3:L:1003:VAL:HG21	1.97	0.46
1:C:213:LEU:HD11	1:C:328:ARG:HH21	1.80	0.46
1:C:326:THR:O	1:C:330:SER:CB	2.64	0.46
2:G:115:ALA:O	2:G:119:ALA:CB	2.64	0.46
2:H:93:LEU:HB2	2:H:176:VAL:HG12	1.97	0.46
2:I:261:GLU:OE2	2:I:264:ASP:N	2.48	0.46
3:J:78:MET:N	3:J:820:ASN:OD1	2.46	0.46
3:K:968:VAL:HA	3:K:971:ARG:HB3	1.98	0.46
3:L:189:ASN:N	3:L:265:VAL:O	2.49	0.46
1:A:15:PRO:O	1:A:19:LYS:HB3	2.16	0.46
1:B:116:VAL:HA	1:B:178:ALA:HB1	1.98	0.46
1:B:133:ILE:O	1:B:137:LEU:CB	2.64	0.46
1:B:167:ASN:O	1:B:171:ALA:HB3	2.15	0.46
1:C:5:GLN:O	1:C:8:GLN:HB2	2.16	0.46
1:C:47:ASP:OD1	1:C:66:SER:OG	2.26	0.46
2:G:365:GLN:HE21	3:K:579:PRO:HG3	1.80	0.46
3:J:588:GLN:OE1	3:J:613:ASN:ND2	2.47	0.46
3:K:138:MET:O	3:K:289:LEU:O	2.34	0.46
3:L:189:ASN:OD1	3:L:191:ASN:ND2	2.49	0.46
3:L:218:GLN:HG2	3:L:233:SER:HA	1.98	0.46
3:L:449:LEU:HG	3:L:453:PHE:HE1	1.80	0.46
1:A:82:ARG:HH12	1:A:89:LYS:HD2	1.81	0.45
1:C:83:ALA:O	1:C:87:GLN:CB	2.63	0.45
2:E:313:VAL:HG21	2:E:347:TRP:CD1	2.51	0.45
2:G:43:VAL:HB	2:G:361:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:241:LYS:HE3	2:G:259:THR:HG22	1.97	0.45
2:G:318:ARG:HH12	3:K:811:TYR:HB2	1.80	0.45
3:J:967:ALA:O	3:J:971:ARG:CB	2.63	0.45
3:L:25:LEU:O	3:L:29:LYS:CB	2.63	0.45
3:L:52:ALA:HB1	3:L:56:THR:HB	1.98	0.45
3:L:105:VAL:O	3:L:109:ASN:HB2	2.16	0.45
3:L:477:ALA:O	3:L:481:SER:CB	2.64	0.45
3:L:874:PRO:HA	3:L:877:TYR:HD2	1.82	0.45
1:B:321:ARG:O	1:B:325:GLN:HB2	2.16	0.45
1:C:314:GLU:O	1:C:318:SER:OG	2.30	0.45
2:F:223:PHE:CZ	2:F:274:ILE:CG1	2.99	0.45
3:J:156:ASP:HA	3:J:159:ALA:HB3	1.99	0.45
3:J:197:GLN:HB3	3:J:798:MET:HE3	1.97	0.45
1:A:36:SER:HA	1:A:39:LEU:HD13	1.96	0.45
1:A:244:HIS:NE2	1:A:298:VAL:HG13	2.31	0.45
1:B:79:SER:O	1:B:83:ALA:N	2.40	0.45
1:B:401:LYS:HD2	1:B:404:LEU:HD12	1.98	0.45
2:E:57:PRO:HA	2:E:294:ARG:HA	1.99	0.45
2:E:59:ARG:HA	2:E:292:PHE:HD1	1.82	0.45
3:K:43:VAL:HG13	3:K:131:LYS:HA	1.98	0.45
1:C:350:SER:O	1:C:354:SER:CB	2.65	0.45
2:D:93:LEU:HB2	2:D:176:VAL:HG12	1.96	0.45
2:F:124:LEU:HD13	2:G:144:ASP:HB3	1.99	0.45
2:H:289:PRO:O	2:I:269:GLN:NE2	2.46	0.45
2:I:51:GLN:HA	2:I:300:GLY:HA3	1.98	0.45
3:J:65:ILE:HG22	3:J:69:MET:HG2	1.98	0.45
3:J:942:ALA:HA	3:J:945:ILE:HD12	1.99	0.45
3:L:75:LEU:HA	3:L:94:PHE:HD1	1.82	0.45
1:B:30:LYS:O	1:B:34:ALA:CB	2.64	0.45
1:B:116:VAL:HG22	1:B:178:ALA:HB1	1.98	0.45
2:D:248:THR:HA	2:D:293:VAL:HB	1.99	0.45
2:F:309:PRO:HA	2:F:346:LYS:HA	1.99	0.45
3:J:158:VAL:O	3:J:162:MET:N	2.47	0.45
3:J:415:ASN:OD1	3:J:418:ARG:NH2	2.40	0.45
3:K:335:ILE:HA	3:K:338:HIS:HB3	1.99	0.45
3:K:449:LEU:HD23	3:K:478:MET:HG3	1.99	0.45
3:K:943:ILE:O	3:K:947:GLU:CB	2.64	0.45
3:L:530:SER:HB3	3:L:534:ILE:HD12	1.99	0.45
3:L:655:PHE:HD1	3:L:658:ILE:HD12	1.82	0.45
1:C:96:VAL:HG13	1:C:221:LEU:HB3	1.98	0.45
3:J:860:THR:OG1	3:J:861:GLY:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:912:ALA:O	3:J:916:ALA:HB2	2.17	0.45
3:K:138:MET:HB3	3:K:328:ASP:CG	2.41	0.45
3:K:303:ALA:HA	3:K:306:ILE:HD12	1.98	0.45
3:L:564:LEU:HD23	3:L:924:ASP:HB2	1.99	0.45
1:A:169:VAL:CG1	1:B:336:ALA:CB	2.93	0.45
1:B:109:THR:O	1:B:113:TYR:HB2	2.17	0.45
1:B:155:GLN:HB2	1:C:354:SER:HB2	1.98	0.45
1:B:399:ASN:O	1:B:403:ALA:CB	2.65	0.45
2:F:168:ARG:O	2:F:172:ALA:CB	2.64	0.45
2:H:310:GLN:NE2	2:H:344:GLY:O	2.50	0.45
1:A:118:ASN:O	1:A:122:VAL:HB	2.17	0.45
2:D:80:ASN:N	2:D:93:LEU:O	2.40	0.45
2:D:101:TYR:CE1	2:D:170:ASN:HB3	2.52	0.45
2:H:87:ILE:O	2:H:182:GLY:N	2.40	0.45
2:H:254:PHE:HZ	2:H:283:PRO:HD2	1.80	0.45
3:J:463:THR:HA	3:J:466:ILE:HD12	1.98	0.45
3:J:477:ALA:O	3:J:481:SER:CB	2.65	0.45
3:J:843:LEU:O	3:J:846:GLN:HG2	2.16	0.45
3:K:100:ALA:O	3:K:104:GLN:CB	2.59	0.45
3:K:568:ASP:OD2	3:K:634:TRP:NE1	2.49	0.45
3:K:756:GLY:N	3:K:774:MET:SD	2.89	0.45
3:L:435:MET:O	3:L:439:GLN:HB3	2.17	0.45
1:B:96:VAL:HG11	1:B:225:GLN:HB2	1.99	0.45
1:B:402:SER:HB2	1:B:407:LEU:HD13	1.99	0.45
1:C:15:PRO:O	1:C:19:LYS:HB2	2.16	0.45
1:C:67:ALA:O	1:C:255:GLY:CA	2.65	0.45
2:G:212:ILE:O	2:G:280:PHE:N	2.45	0.45
2:H:105:TYR:HE1	2:H:168:ARG:HA	1.82	0.45
2:I:343:ILE:N	2:I:346:LYS:O	2.45	0.45
3:J:213:GLN:HB2	3:J:239:ARG:HG3	1.98	0.45
3:J:245:GLU:HA	3:J:248:LYS:HE2	1.99	0.45
3:J:417:GLU:O	3:J:421:ALA:CB	2.65	0.45
3:J:449:LEU:HG	3:J:453:PHE:HE1	1.81	0.45
3:J:971:ARG:NH1	3:J:974:PRO:HB2	2.32	0.45
3:K:122:VAL:O	3:K:126:GLY:N	2.36	0.45
3:K:211:ASN:HA	3:K:240:LEU:HD13	1.98	0.45
3:K:757:SER:HB3	3:K:773:VAL:HG13	1.99	0.45
3:L:105:VAL:O	3:L:109:ASN:ND2	2.50	0.45
3:L:757:SER:HB3	3:L:773:VAL:HG13	1.99	0.45
1:B:220:ASN:HD21	1:B:222:SER:HB2	1.81	0.45
1:B:336:ALA:O	1:B:340:SER:OG	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:125:TYR:O	1:C:129:GLN:HB2	2.17	0.45
2:D:310:GLN:HG2	2:D:347:TRP:CD1	2.52	0.45
2:F:103:ALA:O	2:F:107:SER:OG	2.31	0.45
2:I:309:PRO:HG3	2:I:346:LYS:HE3	1.98	0.45
3:J:278:ILE:O	3:J:613:ASN:CB	2.65	0.45
3:J:522:LYS:O	3:J:526:HIS:CB	2.65	0.45
3:K:843:LEU:HD12	3:K:846:GLN:HE21	1.82	0.45
3:K:1018:ALA:HA	3:K:1021:PHE:HD2	1.82	0.45
3:L:375:VAL:HA	3:L:480:LEU:HD11	1.99	0.45
1:A:47:ASP:O	1:A:65:THR:HA	2.17	0.44
1:A:105:LEU:O	1:A:109:THR:HB	2.17	0.44
1:B:167:ASN:O	1:B:171:ALA:CB	2.65	0.44
1:C:373:LEU:O	1:C:377:THR:OG1	2.29	0.44
2:D:60:THR:HG23	2:D:289:PRO:HA	1.98	0.44
3:J:217:GLY:O	3:J:234:ILE:HB	2.17	0.44
3:L:721:LEU:HB3	3:L:814:PRO:HG2	1.99	0.44
1:A:78:MSE:HA	1:A:81:TRP:HD1	1.81	0.44
1:B:242:ASP:HA	1:B:245:LEU:HD12	1.99	0.44
1:B:336:ALA:O	1:B:340:SER:HB2	2.18	0.44
1:C:234:ARG:HH21	1:C:238:ARG:HH22	1.65	0.44
2:F:306:ILE:N	2:F:349:VAL:O	2.45	0.44
2:H:80:ASN:N	2:H:93:LEU:O	2.42	0.44
2:I:361:ILE:HG22	2:I:362:SER:HB3	1.98	0.44
3:L:490:PRO:O	3:L:494:ALA:CB	2.65	0.44
1:A:105:LEU:O	1:A:109:THR:CB	2.65	0.44
1:A:217:GLU:OE2	1:A:320:HIS:ND1	2.49	0.44
1:A:341:ILE:HG22	1:A:345:LYS:HE2	1.98	0.44
1:C:143:ARG:HB3	1:C:148:LEU:HD12	1.99	0.44
1:C:220:ASN:HD21	1:C:222:SER:HB2	1.82	0.44
2:E:257:ASP:N	2:E:257:ASP:OD1	2.50	0.44
2:I:216:VAL:N	2:I:276:LEU:O	2.46	0.44
3:K:75:LEU:HA	3:K:94:PHE:HD1	1.83	0.44
3:K:281:PHE:HB2	3:K:610:PHE:HD1	1.83	0.44
3:K:900:SER:HB3	3:K:1029:VAL:HG21	1.99	0.44
3:L:251:LEU:N	3:L:260:VAL:O	2.42	0.44
3:L:584:GLN:HA	3:L:587:THR:HB	1.98	0.44
1:A:5:GLN:O	1:A:8:GLN:HB2	2.18	0.44
1:C:330:SER:HA	1:C:333:ASN:HD22	1.82	0.44
2:D:268:ASP:HB3	2:D:272:GLY:N	2.32	0.44
2:E:244:VAL:HG21	2:E:260:LEU:HD22	2.00	0.44
3:J:728:LYS:HA	3:L:235:ILE:HB	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:218:GLN:HG2	3:K:233:SER:HA	1.99	0.44
3:K:1009:GLY:O	3:K:1013:THR:OG1	2.24	0.44
3:L:77:TYR:HB2	3:L:820:ASN:HD21	1.82	0.44
1:C:119:ALA:O	1:C:123:LEU:HB2	2.18	0.44
2:G:116:GLN:O	2:G:120:ASN:HB2	2.18	0.44
2:H:125:THR:O	2:H:129:TYR:HB2	2.18	0.44
3:J:419:VAL:HG11	3:J:434:SER:HB2	1.98	0.44
3:J:874:PRO:HA	3:J:877:TYR:HD2	1.81	0.44
3:K:1010:GLY:O	3:K:1014:ALA:HB2	2.17	0.44
3:L:149:MET:HB3	3:L:153:ASP:HB2	1.98	0.44
3:L:204:ILE:HA	3:L:207:ILE:HD12	1.98	0.44
3:L:330:THR:HA	3:L:333:VAL:HG22	2.00	0.44
3:L:511:GLY:O	3:L:515:TRP:HB3	2.17	0.44
3:L:645:GLU:O	3:L:648:THR:OG1	2.26	0.44
3:L:952:LEU:HB3	3:L:963:ALA:HB1	1.99	0.44
1:A:316:LEU:O	1:A:320:HIS:CB	2.60	0.44
1:A:330:SER:HA	1:A:333:ASN:HD22	1.83	0.44
1:C:157:ALA:O	1:C:161:TYR:CB	2.61	0.44
2:D:53:THR:HG23	2:D:301:LEU:HD21	1.98	0.44
2:H:268:ASP:OD2	2:H:270:THR:OG1	2.36	0.44
2:I:322:THR:HA	2:I:336:PRO:HA	1.99	0.44
3:K:467:TYR:O	3:K:471:SER:HB2	2.18	0.44
1:A:12:LEU:HD12	1:A:13:SER:HB3	1.99	0.44
2:D:124:LEU:HD22	2:D:128:ARG:HH12	1.82	0.44
2:D:230:LEU:HG	2:D:235:LEU:HD21	2.00	0.44
2:E:214:VAL:N	2:E:278:ALA:O	2.51	0.44
2:E:241:LYS:HE3	2:E:259:THR:HG22	1.99	0.44
2:F:80:ASN:N	2:F:93:LEU:O	2.44	0.44
2:H:55:GLU:HA	2:H:295:ALA:O	2.17	0.44
2:H:133:LEU:HD23	2:H:138:ILE:HG23	2.00	0.44
3:J:58:GLN:HA	3:J:62:THR:HB	1.99	0.44
3:J:912:ALA:O	3:J:916:ALA:CB	2.66	0.44
3:K:187:TRP:NE1	3:K:269:GLU:OE2	2.38	0.44
3:K:775:SER:OG	3:K:776:GLU:N	2.45	0.44
3:L:142:VAL:HG12	3:L:323:ILE:HA	1.99	0.44
1:A:242:ASP:HA	1:A:245:LEU:HD12	2.00	0.44
1:B:314:GLU:HA	1:B:317:GLU:HB3	1.99	0.44
2:D:318:ARG:NH2	3:L:243:THR:OG1	2.49	0.44
2:E:299:GLU:HA	2:E:300:GLY:HA2	1.85	0.44
2:F:133:LEU:HD23	2:F:138:ILE:HG23	1.99	0.44
2:G:342:ALA:HA	2:G:347:TRP:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:43:VAL:HA	2:I:377:GLU:HG2	1.99	0.44
3:K:151:GLN:HE22	3:K:279:ALA:HB3	1.82	0.44
3:K:910:ILE:HA	3:K:913:LEU:HD12	2.00	0.44
3:L:685:ILE:HG12	3:L:824:SER:HB3	2.00	0.44
1:A:103:GLN:O	1:A:107:LEU:HB2	2.18	0.44
1:A:107:LEU:O	1:A:111:THR:OG1	2.28	0.44
1:A:312:ALA:HA	1:A:315:GLN:HB2	2.00	0.44
2:D:222:ASP:OD2	2:D:225:ARG:NH2	2.51	0.44
2:E:222:ASP:O	2:E:226:LEU:N	2.44	0.44
2:F:167:ALA:HA	2:F:170:ASN:HD22	1.82	0.44
2:F:216:VAL:HB	2:F:276:LEU:HB2	2.00	0.44
2:I:103:ALA:O	2:I:107:SER:HB3	2.18	0.44
2:I:218:GLN:N	2:I:274:ILE:O	2.48	0.44
3:J:303:ALA:HB2	3:J:330:THR:HG21	1.99	0.44
3:J:674:LEU:HB3	3:J:862:MET:HG2	1.99	0.44
3:J:945:ILE:HG12	3:J:971:ARG:HG2	2.00	0.44
3:K:188:MET:H	3:K:775:SER:HA	1.82	0.44
3:K:477:ALA:O	3:K:481:SER:CB	2.66	0.44
3:K:578:LEU:HB2	3:K:623:ASN:HB2	1.99	0.44
3:L:140:VAL:O	3:L:287:SER:O	2.36	0.44
1:A:336:ALA:CB	1:C:169:VAL:HG12	2.47	0.43
1:B:330:SER:HA	1:B:333:ASN:HD22	1.84	0.43
1:C:179:VAL:O	1:C:183:ARG:CB	2.66	0.43
2:D:66:ALA:O	2:D:205:THR:HA	2.18	0.43
2:E:39:ALA:HA	2:E:374:LYS:HB2	2.00	0.43
2:E:90:GLY:HA2	2:E:177:THR:HB	1.99	0.43
3:J:25:LEU:O	3:J:29:LYS:CB	2.65	0.43
3:J:568:ASP:OD1	3:J:569:GLN:N	2.51	0.43
3:J:685:ILE:HD11	3:J:819:TYR:HB3	2.00	0.43
3:J:752:ALA:HA	3:J:757:SER:HB2	2.00	0.43
3:J:965:LEU:HA	3:J:968:VAL:HG12	2.00	0.43
3:K:107:VAL:HA	3:K:110:LYS:HG2	2.00	0.43
3:K:213:GLN:NE2	3:K:237:GLN:O	2.50	0.43
3:K:328:ASP:OD1	3:K:329:THR:N	2.51	0.43
3:K:544:LEU:HD22	3:K:547:ILE:HD11	1.98	0.43
3:K:945:ILE:HG12	3:K:971:ARG:HG2	2.00	0.43
3:L:699:ARG:O	3:L:702:LEU:N	2.51	0.43
1:A:94:GLN:HA	1:A:97:THR:HG22	2.00	0.43
1:A:96:VAL:HG11	1:A:225:GLN:HB2	1.99	0.43
1:A:125:TYR:HB2	1:A:384:GLN:HE21	1.82	0.43
1:B:75:ILE:O	1:B:248:LEU:HB3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:LEU:O	1:C:111:THR:CB	2.66	0.43
2:G:235:LEU:HB3	2:G:301:LEU:HB3	2.00	0.43
2:G:282:ASN:HD21	2:G:287:LEU:H	1.65	0.43
2:H:229:GLU:HG2	2:H:235:LEU:HD23	2.01	0.43
3:K:192:GLU:HB3	3:K:265:VAL:HG12	2.00	0.43
3:L:158:VAL:O	3:L:162:MET:N	2.51	0.43
3:L:187:TRP:O	3:L:266:ALA:CA	2.64	0.43
3:L:609:VAL:HG22	3:L:629:VAL:HG13	2.00	0.43
1:A:214:LYS:O	1:A:218:LYS:CB	2.65	0.43
1:C:136:GLN:O	1:C:140:THR:OG1	2.28	0.43
2:D:103:ALA:O	2:D:107:SER:OG	2.28	0.43
2:D:307:LEU:HD23	2:D:307:LEU:HA	1.90	0.43
2:F:282:ASN:HD21	2:F:287:LEU:H	1.66	0.43
2:H:105:TYR:CE1	2:H:168:ARG:HA	2.54	0.43
3:J:138:MET:HG2	3:J:291:ILE:HB	1.99	0.43
3:J:168:ARG:NE	3:K:820:ASN:O	2.46	0.43
3:J:974:PRO:O	3:J:978:THR:OG1	2.31	0.43
3:K:559:LEU:HD12	3:K:560:PRO:HD2	2.00	0.43
1:C:392:ASN:O	1:C:396:ASN:ND2	2.50	0.43
2:E:224:LEU:O	2:E:227:LYS:HB2	2.17	0.43
2:G:340:SER:N	2:G:348:LEU:O	2.44	0.43
3:K:278:ILE:O	3:K:613:ASN:N	2.49	0.43
3:L:611:ALA:HA	3:L:627:ALA:HA	2.01	0.43
1:A:108:ASN:HA	1:A:111:THR:HB	1.99	0.43
1:A:219:ARG:HH11	1:A:406:THR:HG22	1.82	0.43
1:A:347:ALA:O	1:A:351:ALA:CB	2.66	0.43
2:D:85:SER:H	2:D:184:ILE:HG22	1.83	0.43
2:E:307:LEU:HD21	2:E:343:ILE:HD12	2.00	0.43
2:H:85:SER:H	2:H:184:ILE:HG22	1.82	0.43
2:I:43:VAL:HB	2:I:361:ILE:HG13	2.00	0.43
2:I:79:ARG:H	2:I:191:GLU:HG2	1.83	0.43
2:I:335:ARG:HE	2:I:353:LEU:HD21	1.83	0.43
3:J:725:PRO:HA	3:J:810:GLU:O	2.18	0.43
3:K:83:ASP:OD2	3:K:87:THR:OG1	2.32	0.43
3:K:685:ILE:HG12	3:K:824:SER:HB3	1.99	0.43
3:L:158:VAL:HG12	3:L:163:LYS:HB2	2.01	0.43
3:L:446:ALA:HB2	3:L:482:VAL:HG21	2.00	0.43
1:A:237:ILE:HA	1:A:302:VAL:HA	2.01	0.43
1:B:249:ASP:HB2	1:B:287:SER:HB3	1.98	0.43
1:B:382:ALA:O	1:B:386:LEU:HB2	2.18	0.43
2:H:183:ARG:N	2:H:207:GLN:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:59:ARG:HA	2:I:292:PHE:HD1	1.82	0.43
3:J:165:ALA:O	3:J:169:THR:OG1	2.33	0.43
3:K:114:ALA:HA	3:K:117:LEU:HD13	1.99	0.43
3:K:748:THR:O	3:K:752:ALA:CB	2.67	0.43
3:L:843:LEU:O	3:L:846:GLN:HG2	2.18	0.43
3:L:929:VAL:HA	3:L:932:LEU:HD22	1.99	0.43
1:A:249:ASP:HB2	1:A:287:SER:HB3	2.01	0.43
1:A:304:GLN:HA	1:A:307:TYR:CD2	2.53	0.43
1:A:348:VAL:O	1:A:352:GLN:CB	2.67	0.43
1:B:100:THR:O	1:B:104:THR:HB	2.18	0.43
1:B:133:ILE:O	1:B:137:LEU:HB3	2.18	0.43
1:C:52:ASN:HA	1:C:61:ASN:HD22	1.84	0.43
2:G:105:TYR:HE1	2:G:168:ARG:HB2	1.83	0.43
2:H:39:ALA:H	2:H:366:LYS:HZ1	1.67	0.43
2:H:66:ALA:O	2:H:205:THR:HA	2.19	0.43
3:J:58:GLN:O	3:J:63:GLN:N	2.40	0.43
3:J:441:ALA:HB2	3:J:947:GLU:HG3	2.01	0.43
3:J:530:SER:O	3:J:534:ILE:HB	2.18	0.43
3:J:800:PRO:HG2	3:J:803:ALA:HB2	2.01	0.43
3:K:142:VAL:HG12	3:K:323:ILE:HA	2.00	0.43
3:K:183:ALA:H	3:K:271:GLY:H	1.67	0.43
3:K:218:GLN:HA	3:K:233:SER:HA	2.01	0.43
3:K:222:THR:HA	3:K:224:PRO:HD3	1.99	0.43
3:K:552:MET:HB2	3:K:910:ILE:HD11	2.01	0.43
3:K:942:ALA:HA	3:K:945:ILE:HD12	2.01	0.43
3:L:228:GLN:HE21	3:L:230:LEU:H	1.65	0.43
3:L:574:THR:O	3:L:626:ILE:HA	2.19	0.43
3:L:756:GLY:N	3:L:774:MET:SD	2.92	0.43
1:A:108:ASN:O	1:A:112:ALA:CB	2.67	0.43
1:A:315:GLN:O	1:A:319:ALA:HB2	2.19	0.43
1:A:336:ALA:O	1:A:340:SER:CB	2.67	0.43
2:E:256:GLN:HE21	2:E:281:PRO:HB2	1.84	0.43
2:H:79:ARG:HH22	2:I:64:ARG:HH12	1.65	0.43
2:H:92:SER:HA	2:H:177:THR:HA	2.01	0.43
2:H:167:ALA:O	2:H:171:LEU:CB	2.64	0.43
2:H:309:PRO:HA	2:H:346:LYS:HA	2.01	0.43
2:I:212:ILE:O	2:I:280:PHE:N	2.36	0.43
3:J:888:LEU:HD23	3:J:888:LEU:HA	1.86	0.43
3:L:314:GLU:OE1	3:L:314:GLU:N	2.48	0.43
1:A:169:VAL:CG1	1:B:336:ALA:HA	2.48	0.43
2:G:115:ALA:O	2:G:119:ALA:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:331:LYS:HB3	2:G:370:GLY:HA2	2.01	0.43
3:K:328:ASP:OD2	3:K:330:THR:OG1	2.27	0.43
3:K:330:THR:HB	3:K:334:LYS:HG2	2.01	0.43
3:K:591:LEU:HD11	3:K:625:GLY:HA3	1.99	0.43
3:L:83:ASP:OD2	3:L:87:THR:OG1	2.28	0.43
3:L:417:GLU:O	3:L:421:ALA:CB	2.66	0.43
3:L:649:MET:O	3:L:652:THR:OG1	2.29	0.43
3:L:727:PHE:HA	3:L:808:ARG:O	2.19	0.43
3:L:948:PHE:HD2	3:L:971:ARG:HB2	1.83	0.43
1:C:175:LEU:HD12	1:C:178:ALA:HB3	2.01	0.42
2:D:249:SER:OG	2:E:224:LEU:HD11	2.17	0.42
2:F:123:GLN:HE21	2:F:127:ASN:HD21	1.66	0.42
2:I:324:LEU:HD12	2:I:334:THR:HB	1.99	0.42
3:J:336:SER:HA	3:J:339:GLU:HB3	2.01	0.42
3:J:447:MET:O	3:J:450:SER:OG	2.36	0.42
3:K:574:THR:CB	3:K:627:ALA:O	2.67	0.42
3:K:912:ALA:O	3:K:915:ALA:HB3	2.19	0.42
3:L:45:ILE:HG23	3:L:129:VAL:HA	2.01	0.42
3:L:81:ASN:HB3	3:L:817:GLU:HG2	2.01	0.42
3:L:363:ARG:NH2	3:L:496:MET:O	2.52	0.42
3:L:463:THR:HA	3:L:466:ILE:HD12	2.00	0.42
3:L:497:LEU:HD23	3:L:497:LEU:HA	1.83	0.42
1:B:385:GLU:O	1:B:389:ALA:HB3	2.18	0.42
1:B:398:LEU:O	1:B:402:SER:CB	2.62	0.42
2:D:268:ASP:OD2	2:D:270:THR:OG1	2.36	0.42
2:G:59:ARG:HA	2:G:292:PHE:HD1	1.84	0.42
2:G:60:THR:HA	2:G:214:VAL:HA	2.00	0.42
2:I:226:LEU:O	2:I:230:LEU:N	2.51	0.42
3:J:251:LEU:HB2	3:J:260:VAL:HB	2.01	0.42
3:J:695:LEU:O	3:J:699:ARG:HB2	2.20	0.42
3:K:683:GLU:O	3:K:857:TYR:CA	2.60	0.42
3:K:911:GLY:HA2	3:K:914:LEU:HG	2.01	0.42
3:L:818:ARG:HG2	3:L:823:PRO:HG3	2.01	0.42
3:L:965:LEU:HA	3:L:968:VAL:HG12	2.02	0.42
1:C:336:ALA:O	1:C:340:SER:HB2	2.19	0.42
2:D:309:PRO:HA	2:D:346:LYS:HA	2.01	0.42
2:G:290:GLY:HA2	2:G:292:PHE:CE1	2.54	0.42
3:J:27:ILE:HG13	3:J:28:LEU:HD12	2.02	0.42
3:J:314:GLU:OE1	3:J:314:GLU:N	2.48	0.42
3:J:721:LEU:O	3:J:813:SER:OG	2.32	0.42
3:K:54:ALA:HA	3:K:57:VAL:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:143:ILE:HB	3:K:286:ALA:HA	2.00	0.42
3:K:713:LEU:HD23	3:K:831:ALA:HA	2.02	0.42
3:K:919:ARG:NH1	3:K:1001:ASN:HB3	2.34	0.42
3:L:218:GLN:HA	3:L:233:SER:HA	2.01	0.42
3:L:574:THR:HB	3:L:627:ALA:H	1.84	0.42
3:L:801:PHE:HA	3:L:804:PHE:CZ	2.53	0.42
1:C:30:LYS:HG2	1:C:87:GLN:HE22	1.83	0.42
1:C:385:GLU:O	1:C:389:ALA:HB3	2.19	0.42
2:D:128:ARG:HH21	2:E:140:LYS:HE2	1.84	0.42
2:H:105:TYR:CZ	2:H:171:LEU:CD2	3.03	0.42
2:I:50:LEU:HD23	2:I:52:ILE:H	1.84	0.42
2:I:310:GLN:HG2	2:I:347:TRP:HE1	1.85	0.42
3:J:61:VAL:O	3:J:65:ILE:HG12	2.19	0.42
3:J:975:ILE:O	3:J:979:SER:OG	2.26	0.42
3:K:193:LEU:O	3:K:197:GLN:N	2.52	0.42
3:L:555:LEU:HD22	3:L:913:LEU:HB3	2.01	0.42
1:A:165:LEU:O	1:A:169:VAL:CG2	2.49	0.42
1:A:180:GLU:HB3	1:B:325:GLN:HG3	2.01	0.42
1:A:384:GLN:O	1:A:388:ASN:HB3	2.19	0.42
1:C:75:ILE:C	1:C:248:LEU:O	2.62	0.42
1:C:96:VAL:HG11	1:C:225:GLN:HB2	2.01	0.42
2:D:133:LEU:HD23	2:D:138:ILE:HG23	2.02	0.42
2:F:126:VAL:O	2:F:130:GLN:HB2	2.19	0.42
2:I:130:GLN:HA	2:I:133:LEU:HD23	2.02	0.42
3:J:429:GLU:HA	3:J:432:ARG:HD2	2.01	0.42
3:J:687:GLN:HE21	3:J:856:GLY:N	2.17	0.42
3:J:912:ALA:HA	3:J:1006:GLY:HA2	2.02	0.42
3:J:1018:ALA:HA	3:J:1021:PHE:HD2	1.83	0.42
3:L:183:ALA:H	3:L:271:GLY:H	1.68	0.42
3:L:445:ILE:O	3:L:449:LEU:CB	2.67	0.42
2:D:282:ASN:OD1	2:D:287:LEU:HG	2.19	0.42
2:G:318:ARG:NH1	3:K:811:TYR:HB2	2.35	0.42
2:H:310:GLN:HG2	2:H:347:TRP:CD1	2.55	0.42
3:K:27:ILE:HG13	3:K:28:LEU:HD12	2.02	0.42
3:K:410:ILE:O	3:K:414:GLU:CB	2.68	0.42
3:K:522:LYS:O	3:K:526:HIS:CB	2.68	0.42
2:F:92:SER:HA	2:F:177:THR:HA	2.01	0.42
2:G:299:GLU:HA	2:G:300:GLY:HA2	1.91	0.42
2:H:73:SER:HG	2:H:197:ASN:H	1.64	0.42
3:J:937:LEU:HA	3:J:940:LYS:HE3	2.00	0.42
3:K:801:PHE:O	3:K:805:SER:N	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:158:VAL:HG11	3:L:289:LEU:HD11	2.02	0.42
3:L:687:GLN:N	3:L:854:GLY:O	2.52	0.42
1:C:107:LEU:HA	1:C:398:LEU:HD23	2.02	0.42
2:D:240:GLY:O	2:D:262:PHE:N	2.51	0.42
2:F:124:LEU:HD22	2:F:128:ARG:HH12	1.85	0.42
2:F:254:PHE:HE1	2:F:287:LEU:HD21	1.84	0.42
2:G:315:ARG:HD3	2:G:321:ALA:HB2	2.02	0.42
3:J:375:VAL:HG22	3:J:484:VAL:HG21	2.01	0.42
3:J:544:LEU:HD22	3:J:547:ILE:HD11	2.02	0.42
3:K:888:LEU:HD23	3:K:888:LEU:HA	1.91	0.42
3:L:63:GLN:O	3:L:67:GLN:HB2	2.20	0.42
2:E:241:LYS:HA	2:E:260:LEU:O	2.19	0.42
2:I:81:PHE:HD1	2:I:93:LEU:HD22	1.85	0.42
3:J:697:GLN:O	3:J:701:GLN:CB	2.68	0.42
3:K:251:LEU:N	3:K:260:VAL:O	2.44	0.42
3:K:391:ASN:O	3:K:395:MET:N	2.30	0.42
3:L:563:PHE:HE2	3:L:862:MET:HB3	1.85	0.42
3:L:721:LEU:HD13	3:L:815:ARG:HH11	1.85	0.42
3:L:911:GLY:O	3:L:915:ALA:N	2.46	0.42
1:A:8:GLN:HE22	1:A:11:ARG:NH2	2.18	0.42
1:A:191:PRO:O	1:A:425:THR:N	2.47	0.42
1:A:212:LEU:O	1:A:216:ALA:CB	2.68	0.42
1:C:105:LEU:O	1:C:109:THR:HB	2.19	0.42
2:D:278:ALA:HB1	2:D:280:PHE:CZ	2.54	0.42
2:F:79:ARG:HA	2:F:94:TYR:HD1	1.85	0.42
2:F:322:THR:HG22	2:F:336:PRO:HA	2.00	0.42
2:G:314:THR:OG1	2:G:322:THR:O	2.26	0.42
3:J:38:ILE:HG21	3:J:466:ILE:HD11	2.02	0.42
3:J:846:GLN:O	3:J:849:SER:OG	2.31	0.42
3:J:876:LEU:HA	3:J:879:ILE:HG12	2.02	0.42
3:K:968:VAL:O	3:K:972:LEU:CB	2.53	0.42
3:L:196:PHE:O	3:L:252:LYS:NZ	2.41	0.42
3:L:324:VAL:HG13	3:L:326:PRO:HD3	2.02	0.42
1:A:307:TYR:HA	1:A:310:VAL:HG12	2.01	0.41
1:B:325:GLN:O	1:B:329:SER:HB3	2.20	0.41
1:C:24:ARG:HG3	1:C:94:GLN:HG3	2.02	0.41
1:C:78:MSE:O	1:C:82:ARG:N	2.43	0.41
2:D:219:SER:CA	2:D:223:PHE:CE1	3.03	0.41
2:G:171:LEU:O	2:G:174:THR:OG1	2.29	0.41
2:H:230:LEU:HD23	2:H:235:LEU:HD11	2.02	0.41
2:I:315:ARG:HD3	2:I:321:ALA:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:63:GLN:O	3:J:67:GLN:HB2	2.20	0.41
3:K:399:VAL:HA	3:K:402:ILE:HG13	2.01	0.41
3:K:423:GLU:N	3:K:423:GLU:OE1	2.53	0.41
3:K:750:LEU:O	3:K:754:TRP:CB	2.57	0.41
3:K:997:SER:HB2	3:K:1001:ASN:HD22	1.84	0.41
3:L:143:ILE:HB	3:L:286:ALA:HA	2.02	0.41
3:L:200:PRO:HD2	3:L:749:THR:HG23	2.02	0.41
1:C:336:ALA:O	1:C:340:SER:OG	2.31	0.41
2:D:241:LYS:HG2	2:D:261:GLU:HA	2.01	0.41
2:F:73:SER:HG	2:F:197:ASN:H	1.67	0.41
2:F:310:GLN:HG2	2:F:347:TRP:CD1	2.55	0.41
2:G:288:LEU:HB3	2:H:269:GLN:NE2	2.32	0.41
2:H:282:ASN:OD1	2:H:287:LEU:HG	2.20	0.41
2:I:38:PRO:HB2	2:I:366:LYS:NZ	2.35	0.41
2:I:63:TYR:CD2	2:I:64:ARG:HG2	2.56	0.41
3:J:192:GLU:HB3	3:J:265:VAL:HG12	2.02	0.41
3:J:775:SER:OG	3:J:776:GLU:N	2.54	0.41
3:J:1027:VAL:HB	3:J:1031:ARG:HD3	2.01	0.41
3:K:935:ILE:O	3:K:939:ALA:HB3	2.20	0.41
3:L:185:ARG:HH12	3:L:774:MET:HB3	1.85	0.41
3:L:364:ALA:HA	3:L:497:LEU:HD21	2.02	0.41
2:F:60:THR:HG23	2:F:289:PRO:HA	2.01	0.41
2:G:42:VAL:HA	2:G:360:VAL:HA	2.01	0.41
3:J:235:ILE:HB	3:K:728:LYS:HA	2.02	0.41
3:K:411:VAL:HG12	3:K:978:THR:HG21	2.02	0.41
3:L:942:ALA:HA	3:L:945:ILE:HD12	2.02	0.41
1:B:44:LEU:HA	1:B:68:SER:O	2.20	0.41
1:C:8:GLN:HE22	1:C:11:ARG:NH2	2.19	0.41
3:J:373:PRO:O	3:J:376:LEU:HG	2.21	0.41
3:J:555:LEU:HA	3:J:558:ARG:HG2	2.03	0.41
3:J:801:PHE:HA	3:J:804:PHE:CZ	2.55	0.41
3:K:139:VAL:HG23	3:K:327:TYR:HD2	1.86	0.41
3:K:196:PHE:HB3	3:K:252:LYS:HE2	2.02	0.41
3:K:198:LEU:HA	3:K:792:ARG:NH1	2.35	0.41
3:K:213:GLN:HE22	3:K:238:THR:HA	1.86	0.41
3:K:375:VAL:HA	3:K:480:LEU:HD11	2.01	0.41
3:K:445:ILE:O	3:K:449:LEU:HB3	2.19	0.41
3:K:844:MET:HA	3:K:847:LEU:HB2	2.02	0.41
3:K:874:PRO:HA	3:K:877:TYR:HD2	1.85	0.41
3:L:243:THR:HB	3:L:268:ILE:HG21	2.02	0.41
3:L:399:VAL:HA	3:L:402:ILE:HG13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:696:THR:HG23	3:L:699:ARG:HH21	1.85	0.41
3:L:841:MET:O	3:L:845:GLU:HB2	2.20	0.41
3:L:940:LYS:NZ	3:L:941:ASN:OD1	2.53	0.41
3:L:977:MET:O	3:L:981:ALA:CB	2.68	0.41
1:A:52:ASN:HA	1:A:61:ASN:HD22	1.85	0.41
1:C:40:PRO:HA	1:C:72:THR:O	2.20	0.41
2:D:40:VAL:HG13	2:D:363:GLY:H	1.86	0.41
2:F:314:THR:OG1	2:F:322:THR:O	2.30	0.41
2:G:76:ILE:HG23	2:G:94:TYR:HB3	2.02	0.41
2:H:162:ALA:O	2:H:166:THR:OG1	2.27	0.41
3:J:21:LEU:HD13	3:J:21:LEU:HA	1.90	0.41
3:J:574:THR:O	3:J:626:ILE:HA	2.21	0.41
3:K:41:PRO:O	3:K:94:PHE:N	2.45	0.41
3:K:523:SER:O	3:K:527:TYR:HB2	2.21	0.41
3:L:157:TYR:OH	3:L:316:PHE:O	2.38	0.41
3:L:317:PHE:CG	3:L:321:LEU:HD23	2.56	0.41
3:L:576:VAL:HA	3:L:663:VAL:HG22	2.01	0.41
1:C:165:LEU:O	1:C:169:VAL:CG2	2.65	0.41
2:D:82:LYS:O	2:D:85:SER:OG	2.37	0.41
2:F:316:THR:HA	2:F:317:PRO:HA	1.95	0.41
2:G:227:LYS:O	2:G:231:ALA:N	2.50	0.41
2:H:70:PRO:HD3	2:H:203:LEU:HG	2.03	0.41
2:I:76:ILE:N	2:I:193:ALA:O	2.44	0.41
3:J:446:ALA:HB2	3:J:482:VAL:HG21	2.03	0.41
3:J:980:LEU:HA	3:J:983:ILE:HG22	2.03	0.41
3:L:610:PHE:O	3:L:627:ALA:HA	2.19	0.41
3:L:998:GLY:O	3:L:1002:ALA:CB	2.68	0.41
1:B:299:ASN:HA	1:B:302:VAL:HB	2.03	0.41
1:C:217:GLU:OE2	1:C:320:HIS:ND1	2.41	0.41
2:G:261:GLU:OE1	2:G:264:ASP:N	2.54	0.41
2:H:168:ARG:O	2:H:172:ALA:HB2	2.20	0.41
3:J:115:MET:HA	3:J:118:LEU:HD13	2.02	0.41
3:K:819:TYR:N	3:K:822:LEU:O	2.43	0.41
3:L:92:LEU:HB3	3:L:94:PHE:CZ	2.56	0.41
3:L:165:ALA:HA	3:L:168:ARG:HB2	2.03	0.41
3:L:222:THR:HA	3:L:224:PRO:HD3	2.01	0.41
1:B:134:TYR:HB2	1:B:161:TYR:HE1	1.86	0.41
1:B:214:LYS:O	1:B:218:LYS:CB	2.69	0.41
1:C:210:ASN:HA	1:C:213:LEU:HG	2.01	0.41
2:E:210:ASP:HA	2:E:282:ASN:O	2.21	0.41
2:F:131:LYS:HG3	2:F:132:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:50:LEU:HD22	2:H:301:LEU:HB3	2.03	0.41
2:H:105:TYR:CE1	2:H:171:LEU:CD2	3.04	0.41
3:J:187:TRP:NE1	3:J:269:GLU:OE2	2.34	0.41
3:J:977:MET:O	3:J:981:ALA:HB2	2.19	0.41
3:K:58:GLN:HA	3:K:62:THR:HB	2.02	0.41
3:K:243:THR:HA	3:K:246:PHE:HD2	1.86	0.41
3:K:317:PHE:CG	3:K:321:LEU:HD23	2.55	0.41
3:K:463:THR:HA	3:K:466:ILE:HD12	2.03	0.41
3:K:695:LEU:O	3:K:699:ARG:CB	2.67	0.41
3:L:26:ALA:O	3:L:30:LEU:N	2.49	0.41
3:L:841:MET:HE3	3:L:859:TRP:CD1	2.56	0.41
1:A:4:MSE:HA	1:A:7:TYR:HB3	2.03	0.41
1:A:248:LEU:HD12	1:A:249:ASP:H	1.86	0.41
1:B:70:GLN:HA	1:B:252:ALA:O	2.21	0.41
1:C:213:LEU:HD21	1:C:328:ARG:HE	1.85	0.41
2:D:87:ILE:O	2:D:182:GLY:N	2.40	0.41
2:D:196:GLN:HB2	2:D:199:GLN:HB3	2.03	0.41
2:D:254:PHE:HZ	2:D:283:PRO:HD2	1.85	0.41
2:F:318:ARG:NH2	3:J:243:THR:OG1	2.47	0.41
2:I:40:VAL:HG13	2:I:363:GLY:HA3	2.02	0.41
2:I:94:TYR:HD1	2:I:94:TYR:HA	1.67	0.41
2:I:313:VAL:HG21	2:I:347:TRP:CD1	2.55	0.41
3:J:108:GLN:O	3:J:112:GLN:HG2	2.21	0.41
3:J:184:MET:HE1	3:J:243:THR:HG22	2.03	0.41
3:J:332:PHE:O	3:J:336:SER:CB	2.54	0.41
3:J:363:ARG:HE	3:J:497:LEU:HA	1.86	0.41
3:J:454:VAL:HG23	3:J:455:PRO:HD3	2.02	0.41
3:J:556:PHE:HA	3:J:913:LEU:HD21	2.02	0.41
3:J:818:ARG:NH1	3:J:823:PRO:HG3	2.36	0.41
3:K:364:ALA:HA	3:K:367:ILE:HD13	2.03	0.41
3:K:574:THR:OG1	3:K:627:ALA:O	2.32	0.41
3:K:616:GLY:N	3:K:620:ARG:HA	2.35	0.41
3:K:801:PHE:HA	3:K:804:PHE:CZ	2.56	0.41
3:L:334:LYS:HE3	3:L:334:LYS:HB3	1.91	0.41
3:L:376:LEU:O	3:L:379:THR:CB	2.65	0.41
3:L:426:PRO:HA	3:L:427:PRO:HD3	1.86	0.41
3:L:877:TYR:OH	3:L:928:GLN:OE1	2.34	0.41
3:L:899:PHE:O	3:L:902:MET:HB2	2.21	0.41
1:A:86:LEU:O	1:A:90:ALA:CB	2.69	0.41
1:A:108:ASN:O	1:A:112:ALA:HB2	2.21	0.41
1:B:12:LEU:HD12	1:B:13:SER:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:GLN:HG3	2:G:137:TYR:HE1	1.86	0.41
1:C:63:ASN:OD1	1:C:260:SER:OG	2.35	0.41
1:C:291:PRO:HB3	1:C:294:GLN:HE21	1.86	0.41
2:D:237:GLN:NE2	2:D:300:GLY:HA3	2.36	0.41
2:E:46:LYS:HE2	2:E:46:LYS:HB2	1.92	0.41
2:E:103:ALA:O	2:E:107:SER:HB3	2.21	0.41
3:K:52:ALA:HB1	3:K:56:THR:HB	2.02	0.41
3:K:289:LEU:HA	3:K:289:LEU:HD23	1.84	0.41
3:K:392:THR:O	3:K:396:PHE:CB	2.69	0.41
3:K:633:ASP:OD1	3:K:634:TRP:N	2.54	0.41
3:L:373:PRO:O	3:L:376:LEU:HG	2.21	0.41
1:B:67:ALA:O	1:B:255:GLY:CA	2.57	0.40
2:F:337:ILE:HA	2:F:352:GLY:HA3	2.02	0.40
2:G:103:ALA:O	2:G:107:SER:HB3	2.21	0.40
2:H:314:THR:OG1	2:H:322:THR:O	2.28	0.40
3:J:105:VAL:O	3:J:109:ASN:HB2	2.21	0.40
3:J:223:PRO:HD3	3:K:275:TYR:CG	2.56	0.40
3:J:699:ARG:O	3:J:702:LEU:N	2.53	0.40
3:K:607:GLU:N	3:K:630:SER:O	2.54	0.40
3:L:108:GLN:O	3:L:112:GLN:HG2	2.21	0.40
3:L:742:SER:OG	3:L:745:ASP:OD2	2.36	0.40
1:A:172:ARG:HH12	1:A:427:PRO:HD2	1.87	0.40
1:A:421:LYS:HA	1:A:422:PRO:HD3	1.93	0.40
2:F:237:GLN:NE2	2:F:299:GLU:O	2.55	0.40
2:F:254:PHE:HZ	2:F:283:PRO:HD2	1.85	0.40
2:G:142:GLU:HA	2:G:145:GLN:HB3	2.03	0.40
2:G:353:LEU:HD23	2:G:353:LEU:HA	1.92	0.40
2:I:222:ASP:N	2:I:222:ASP:OD1	2.52	0.40
3:J:467:TYR:O	3:J:471:SER:HB2	2.22	0.40
3:K:78:MET:N	3:K:820:ASN:OD1	2.50	0.40
3:K:552:MET:O	3:K:556:PHE:CB	2.68	0.40
3:K:841:MET:HA	3:K:859:TRP:CH2	2.57	0.40
3:L:58:GLN:O	3:L:63:GLN:N	2.49	0.40
3:L:187:TRP:NE1	3:L:269:GLU:OE2	2.43	0.40
3:L:822:LEU:HD23	3:L:822:LEU:HA	1.93	0.40
1:B:157:ALA:O	1:B:161:TYR:CB	2.59	0.40
1:B:210:ASN:HD22	1:B:213:LEU:HD12	1.87	0.40
1:C:240:ALA:HB1	1:C:298:VAL:HG13	2.02	0.40
2:E:235:LEU:HD23	2:E:301:LEU:HB3	2.02	0.40
3:J:83:ASP:OD2	3:J:87:THR:N	2.54	0.40
3:J:682:PHE:O	3:J:827:ILE:CB	2.58	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:591:LEU:O	3:K:595:THR:OG1	2.25	0.40
3:L:980:LEU:HA	3:L:983:ILE:HG22	2.02	0.40
3:L:1025:PHE:HA	3:L:1028:VAL:HG12	2.03	0.40
1:A:14:ASN:HB3	1:A:17:LEU:HB2	2.03	0.40
1:B:63:ASN:O	1:B:259:THR:CA	2.66	0.40
2:F:101:TYR:HB3	2:F:171:LEU:HB3	2.03	0.40
2:F:227:LYS:HA	2:F:230:LEU:HB2	2.03	0.40
2:G:39:ALA:HA	2:G:374:LYS:HB2	2.04	0.40
2:G:40:VAL:HB	2:G:373:VAL:HG13	2.02	0.40
3:J:369:THR:O	3:J:372:VAL:HB	2.21	0.40
3:L:633:ASP:OD1	3:L:634:TRP:N	2.54	0.40
3:L:713:LEU:HD23	3:L:831:ALA:HA	2.02	0.40
3:L:739:LEU:HD21	3:L:804:PHE:CE1	2.55	0.40
1:A:47:ASP:OD1	1:A:66:SER:OG	2.26	0.40
1:A:354:SER:HB2	1:C:155:GLN:HB2	2.02	0.40
1:A:382:ALA:O	1:A:386:LEU:CB	2.70	0.40
1:A:399:ASN:O	1:A:403:ALA:HB3	2.21	0.40
2:D:288:LEU:HD23	2:E:267:VAL:HG21	1.74	0.40
2:E:103:ALA:O	2:E:107:SER:CB	2.69	0.40
2:E:105:TYR:HE1	2:E:168:ARG:HB2	1.86	0.40
2:F:41:GLY:HA2	2:F:377:GLU:HG2	2.03	0.40
3:J:185:ARG:HB3	3:J:269:GLU:HG3	2.02	0.40
3:J:490:PRO:O	3:J:494:ALA:HB2	2.21	0.40
3:J:686:ASP:OD2	3:J:690:LEU:N	2.48	0.40
3:J:688:ALA:HB3	3:J:690:LEU:HG	2.03	0.40
3:J:1010:GLY:O	3:J:1014:ALA:HB2	2.22	0.40
3:K:45:ILE:HG23	3:K:129:VAL:HA	2.04	0.40
3:K:65:ILE:HG21	3:K:90:ILE:HD13	2.03	0.40
3:K:225:VAL:HG12	3:K:228:GLN:HB2	2.03	0.40
3:K:376:LEU:O	3:K:379:THR:CB	2.62	0.40
3:L:982:PHE:HB3	3:L:1011:MET:HE2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	426/442 (96%)	407 (96%)	19 (4%)	0	100	100
1	B	426/442 (96%)	406 (95%)	20 (5%)	0	100	100
1	C	426/442 (96%)	407 (96%)	19 (4%)	0	100	100
2	D	338/397 (85%)	300 (89%)	36 (11%)	2 (1%)	21	59
2	E	338/397 (85%)	301 (89%)	37 (11%)	0	100	100
2	F	338/397 (85%)	306 (90%)	30 (9%)	2 (1%)	21	59
2	G	338/397 (85%)	299 (88%)	39 (12%)	0	100	100
2	H	338/397 (85%)	306 (90%)	30 (9%)	2 (1%)	21	59
2	I	338/397 (85%)	306 (90%)	32 (10%)	0	100	100
3	J	1035/1049 (99%)	949 (92%)	86 (8%)	0	100	100
3	K	1035/1049 (99%)	948 (92%)	85 (8%)	2 (0%)	43	78
3	L	1035/1049 (99%)	952 (92%)	82 (8%)	1 (0%)	48	83
All	All	6411/6855 (94%)	5887 (92%)	515 (8%)	9 (0%)	49	83

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	52	ILE
2	F	52	ILE
2	H	52	ILE
3	K	264	ASP
3	K	263	ARG
3	L	264	ASP
2	D	51	GLN
2	F	51	GLN
2	H	51	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	358/364 (98%)	356 (99%)	2 (1%)	78	83
1	B	358/364 (98%)	358 (100%)	0	100	100
1	C	358/364 (98%)	357 (100%)	1 (0%)	86	86
2	D	274/318 (86%)	272 (99%)	2 (1%)	76	81
2	E	274/318 (86%)	273 (100%)	1 (0%)	84	84
2	F	274/318 (86%)	273 (100%)	1 (0%)	84	84
2	G	274/318 (86%)	273 (100%)	1 (0%)	84	84
2	H	274/318 (86%)	274 (100%)	0	100	100
2	I	274/318 (86%)	274 (100%)	0	100	100
3	J	826/855 (97%)	822 (100%)	4 (0%)	81	83
3	K	826/855 (97%)	820 (99%)	6 (1%)	76	81
3	L	826/855 (97%)	822 (100%)	4 (0%)	81	83
All	All	5196/5565 (93%)	5174 (100%)	22 (0%)	81	84

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	LEU
1	A	412	LEU
1	C	412	LEU
2	D	72	VAL
2	D	301	LEU
2	E	360	VAL
2	F	171	LEU
2	G	56	LEU
3	J	6	ILE
3	J	367	ILE
3	J	454	VAL
3	J	480	LEU
3	K	6	ILE
3	K	263	ARG
3	K	367	ILE
3	K	405	LEU
3	K	480	LEU
3	K	904	VAL
3	L	6	ILE
3	L	367	ILE
3	L	405	LEU
3	L	480	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (149) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	41	GLN
1	A	61	ASN
1	A	73	GLN
1	A	87	GLN
1	A	103	GLN
1	A	118	ASN
1	A	127	GLN
1	A	177	ASN
1	A	197	ASN
1	A	225	GLN
1	A	230	GLN
1	A	281	GLN
1	A	333	ASN
1	A	335	ASN
1	A	346	GLN
1	A	384	GLN
1	A	392	ASN
1	A	396	ASN
1	A	410	GLN
1	B	41	GLN
1	B	73	GLN
1	B	87	GLN
1	B	94	GLN
1	B	108	ASN
1	B	142	GLN
1	B	145	ASN
1	B	167	ASN
1	B	173	ASN
1	B	177	ASN
1	B	230	GLN
1	B	282	ASN
1	B	299	ASN
1	B	304	GLN
1	B	335	ASN
1	B	384	GLN
1	B	396	ASN
1	C	8	GLN
1	C	41	GLN
1	C	61	ASN
1	C	73	GLN

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Mol	Chain	Res	Type
1	C	87	GLN
1	C	103	GLN
1	C	145	ASN
1	C	173	ASN
1	C	230	GLN
1	C	244	HIS
1	C	281	GLN
1	C	294	GLN
1	C	304	GLN
1	C	333	ASN
1	C	335	ASN
1	C	384	GLN
1	C	396	ASN
1	C	410	GLN
2	D	127	ASN
2	D	136	GLN
2	D	154	ASN
2	D	196	GLN
2	D	239	ASN
2	E	127	ASN
2	E	136	GLN
2	E	199	GLN
2	E	207	GLN
2	E	282	ASN
2	F	127	ASN
2	F	154	ASN
2	F	170	ASN
2	F	218	GLN
2	G	127	ASN
2	G	199	GLN
2	G	218	GLN
2	G	232	ASN
2	G	239	ASN
2	G	269	GLN
2	G	282	ASN
2	G	302	ASN
2	G	311	GLN
2	G	365	GLN
2	H	154	ASN
2	H	269	GLN
2	H	285	HIS
2	I	95	GLN

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Mol	Chain	Res	Type
2	I	102	GLN
2	I	127	ASN
2	I	136	GLN
2	I	218	GLN
2	I	239	ASN
2	I	269	GLN
2	I	282	ASN
2	I	311	GLN
3	J	58	GLN
3	J	68	ASN
3	J	123	GLN
3	J	125	GLN
3	J	151	GLN
3	J	191	ASN
3	J	361	ASN
3	J	469	GLN
3	J	517	ASN
3	J	605	ASN
3	J	687	GLN
3	J	709	HIS
3	J	726	GLN
3	J	733	GLN
3	J	744	ASN
3	J	747	ASN
3	J	1001	ASN
3	K	3	ASN
3	K	68	ASN
3	K	74	ASN
3	K	109	ASN
3	K	112	GLN
3	K	123	GLN
3	K	144	ASN
3	K	151	GLN
3	K	191	ASN
3	K	228	GLN
3	K	284	GLN
3	K	298	ASN
3	K	361	ASN
3	K	469	GLN
3	K	517	ASN
3	K	592	ASN
3	K	605	ASN

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Mol	Chain	Res	Type
3	K	687	GLN
3	K	709	HIS
3	K	719	ASN
3	K	733	GLN
3	K	747	ASN
3	K	846	GLN
3	L	3	ASN
3	L	58	GLN
3	L	68	ASN
3	L	109	ASN
3	L	123	GLN
3	L	125	GLN
3	L	144	ASN
3	L	151	GLN
3	L	191	ASN
3	L	228	GLN
3	L	229	GLN
3	L	284	GLN
3	L	298	ASN
3	L	517	ASN
3	L	592	ASN
3	L	726	GLN
3	L	733	GLN
3	L	747	ASN

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 [i](#)

There are no chain breaks in this entry.

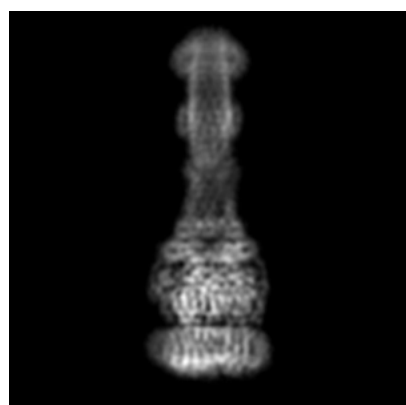
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8636. These allow visual inspection of the internal detail of the map and identification of artifacts.

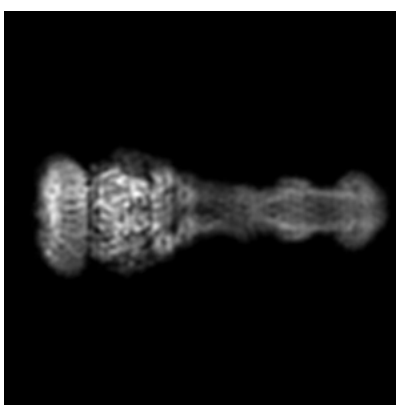
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

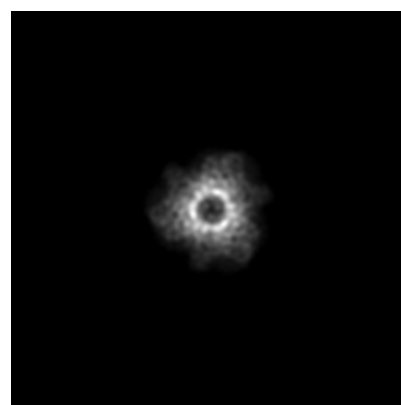
6.1.1 Primary map



X



Y



Z

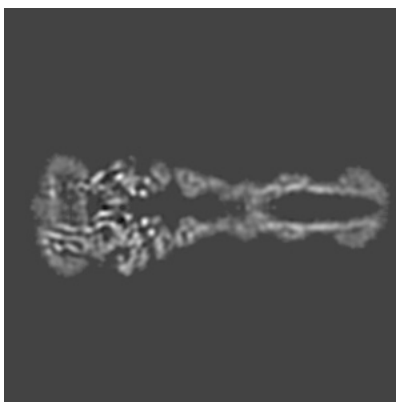
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

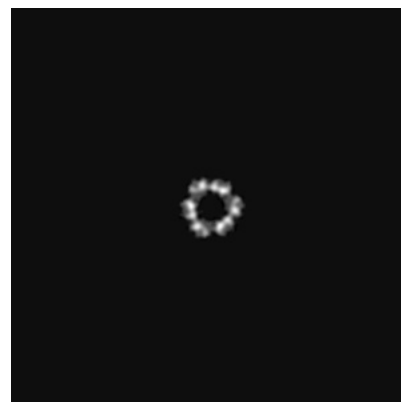
6.2.1 Primary map



X Index: 190



Y Index: 190



Z Index: 190

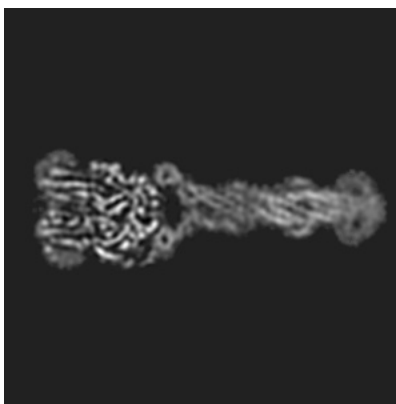
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

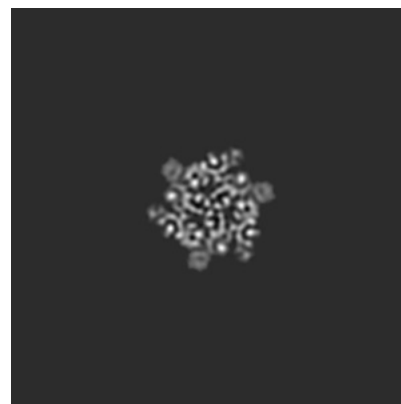
6.3.1 Primary map



X Index: 204



Y Index: 175

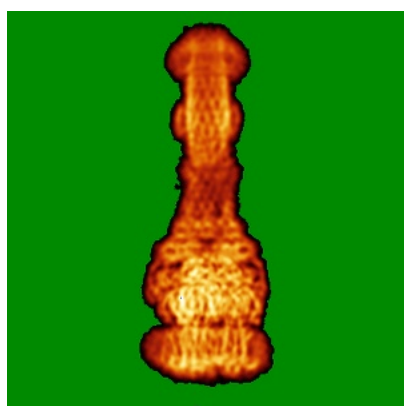


Z Index: 107

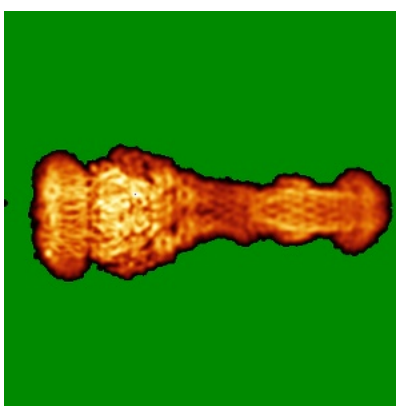
The images above show the largest variance slices of the map in three orthogonal directions.

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

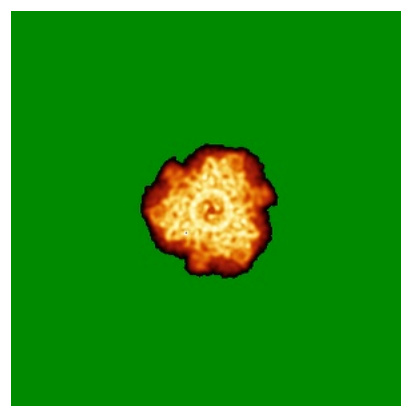
6.4.1 Primary map



X



Y

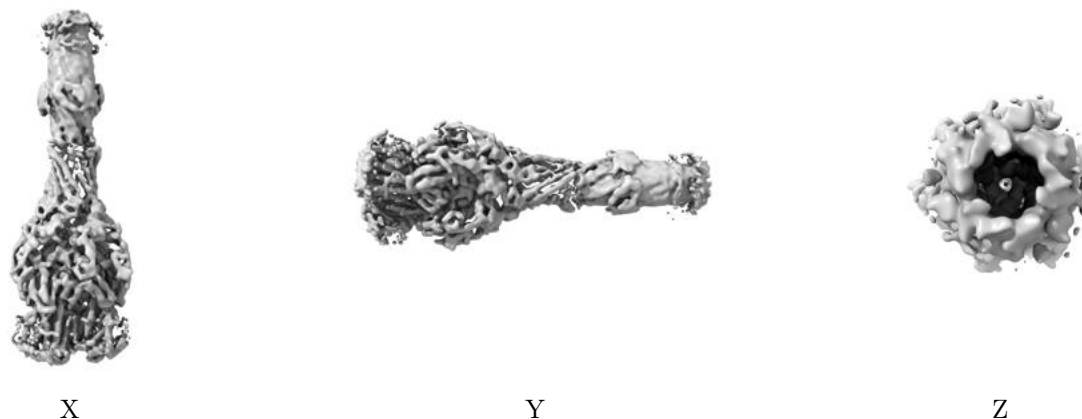


Z

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 0.0266. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

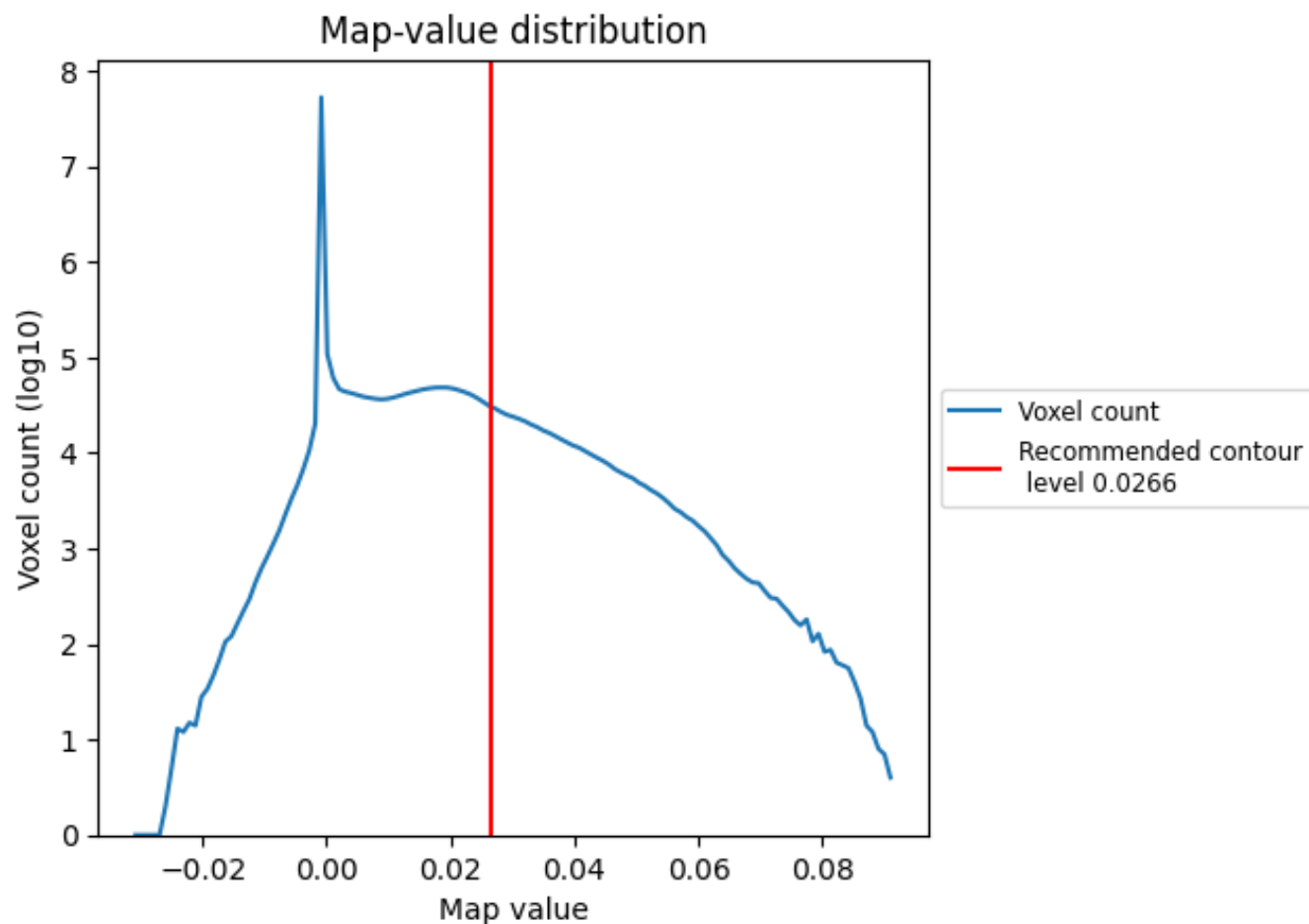
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

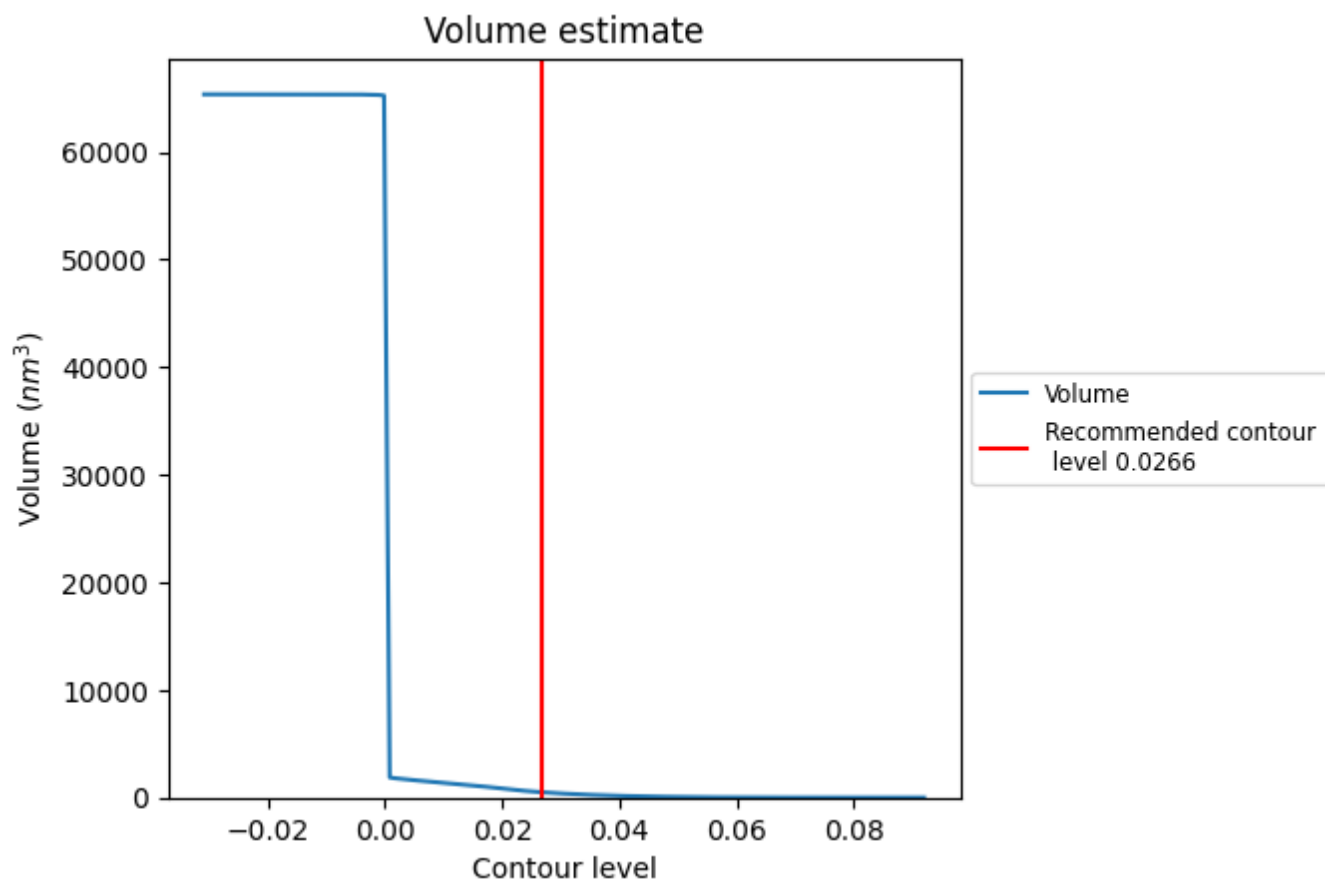
This section contains the results of statistical analysis of the map.

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.

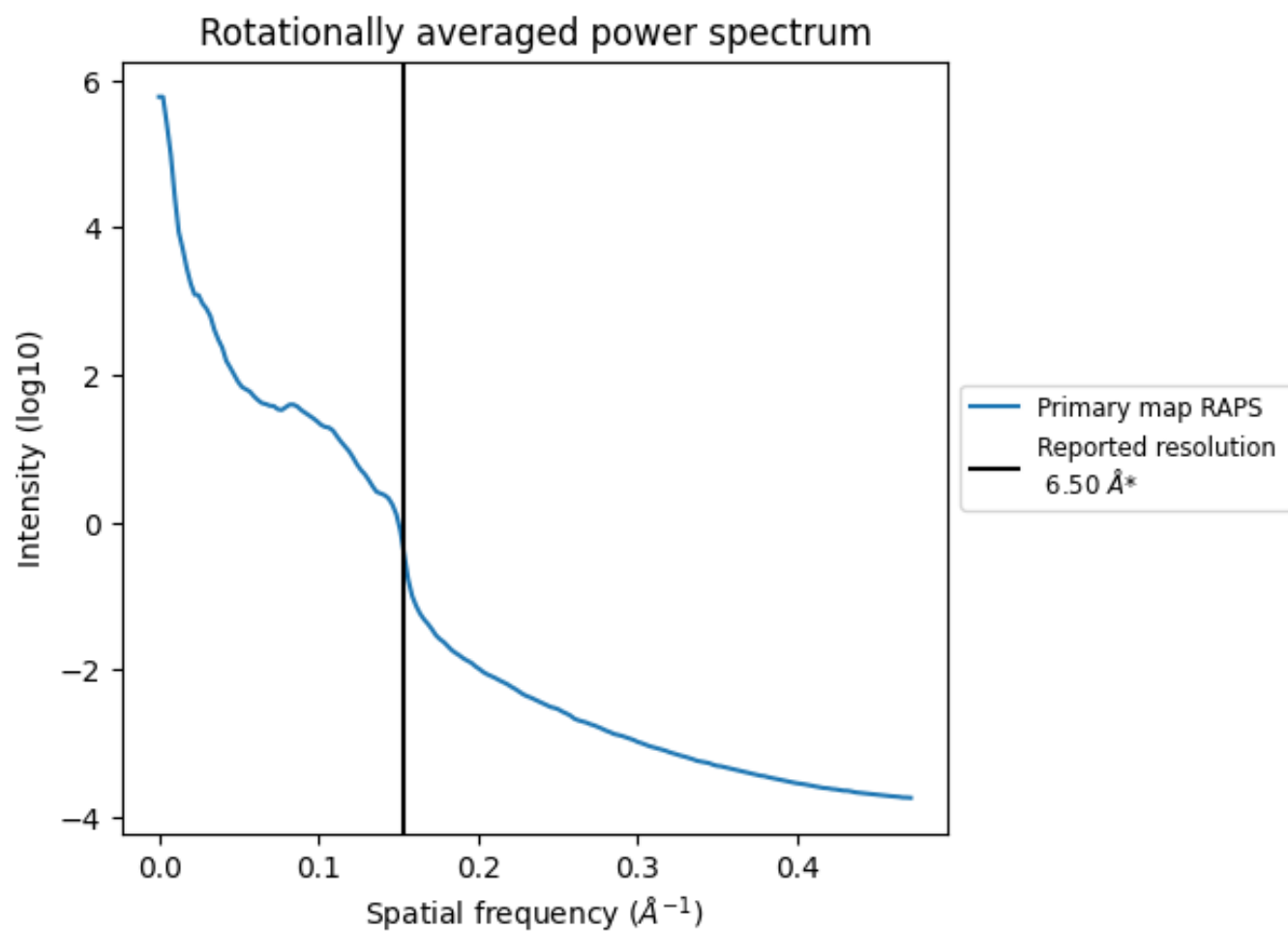
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 501 nm³; this corresponds to an approximate mass of 452 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 ⓘ

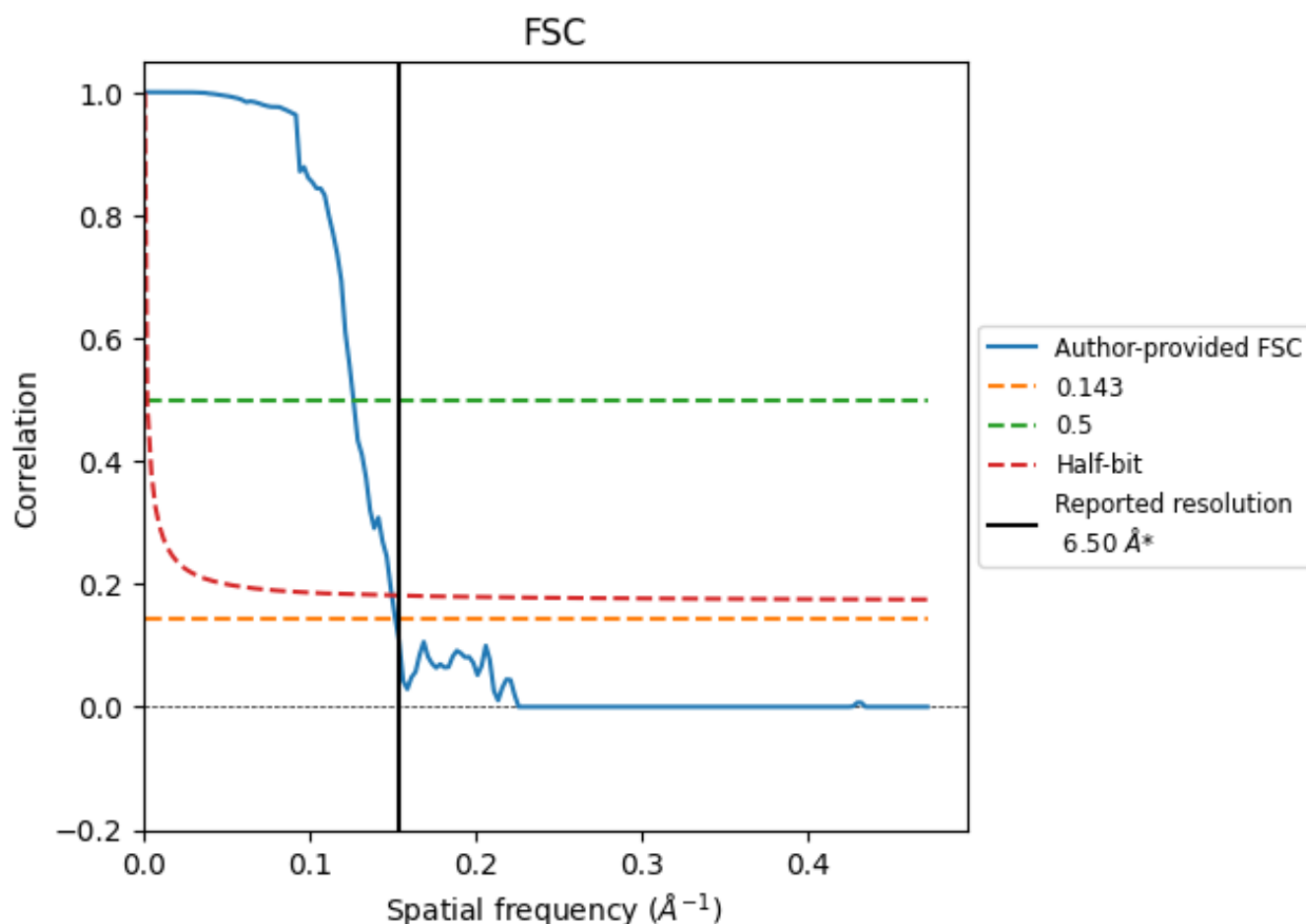


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

8.2 Resolution estimates [i](#)

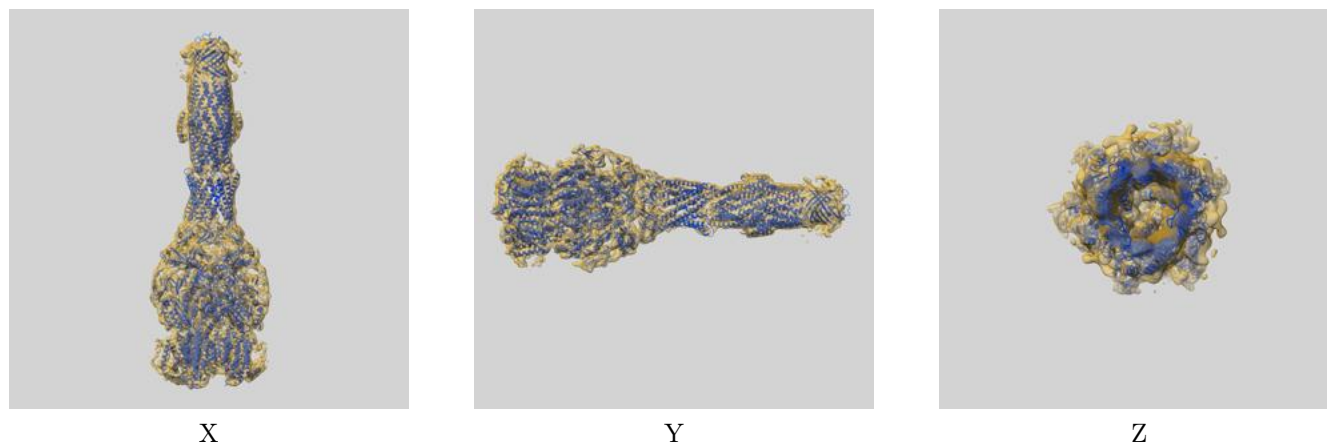
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	6.59	7.91	6.68
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

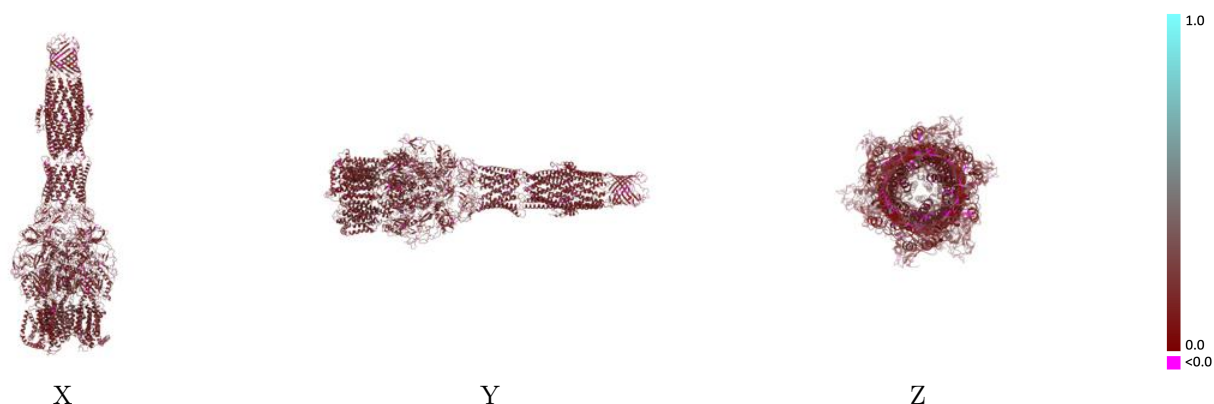
This section contains information regarding the fit between EMDB map EMD-8636 and PDB model 5V5S. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



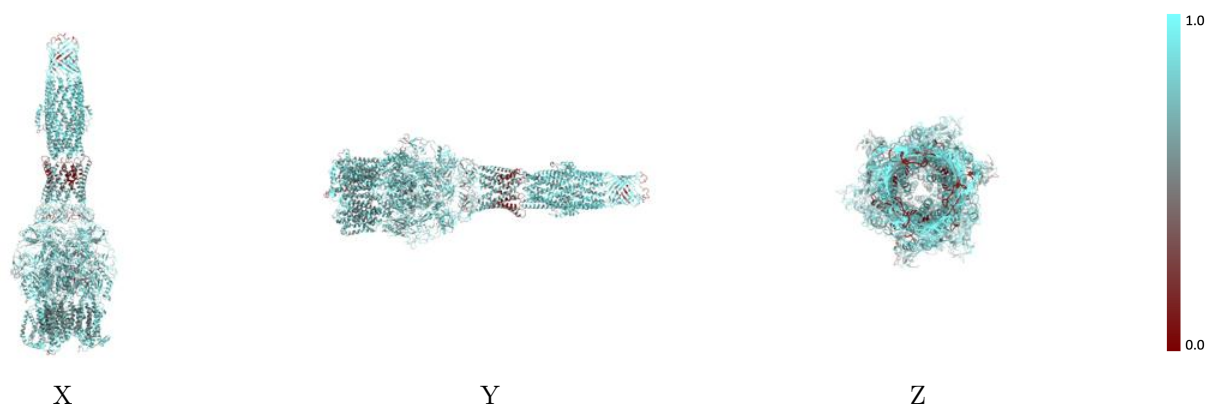
The images above show the 3D surface view of the map at the recommended contour level 0.0266 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



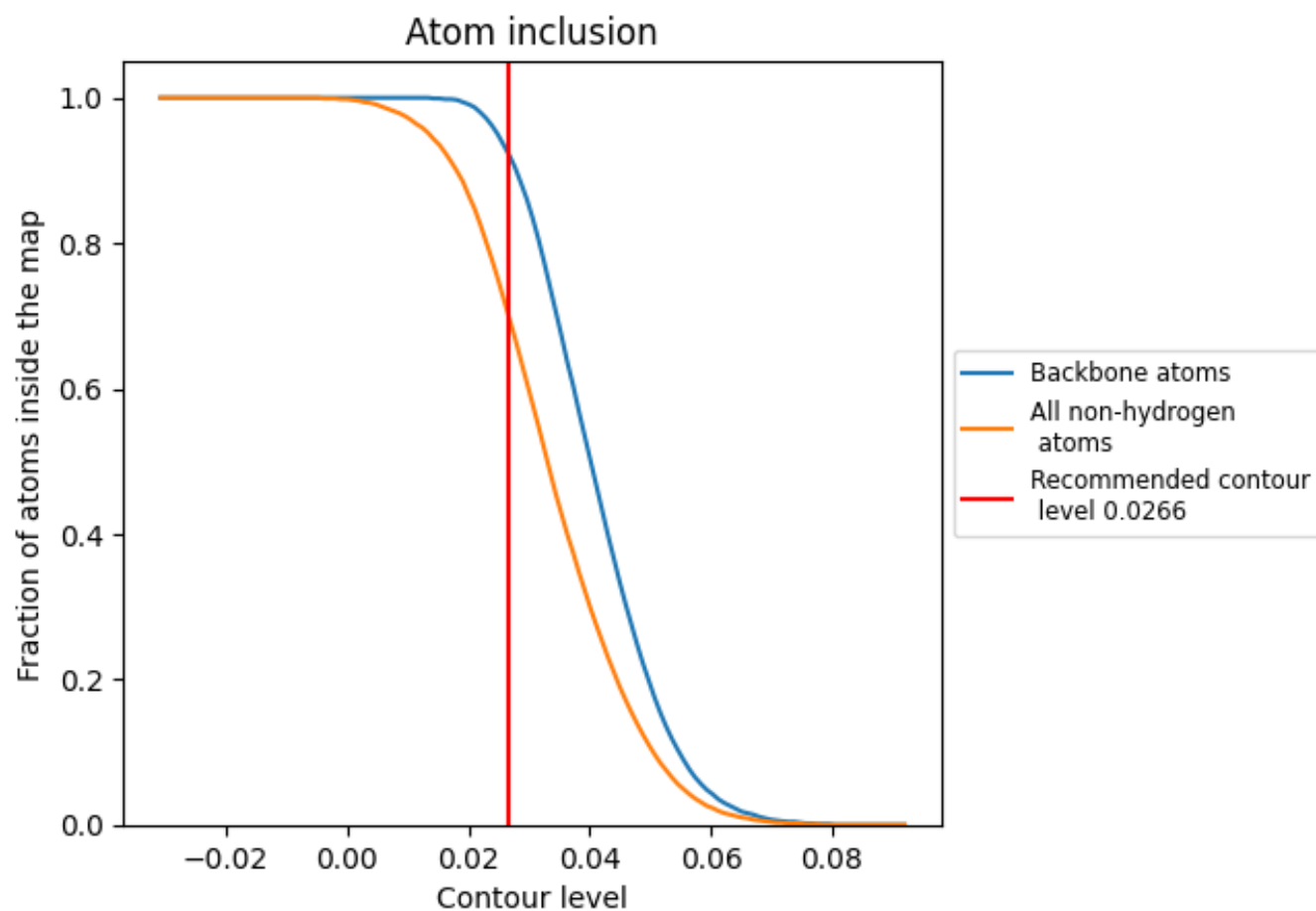
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0266).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 70% 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 (0.0266) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7010	0.1930
A	0.7600	0.1660
B	0.7520	0.1710
C	0.7480	0.1720
D	0.6180	0.1910
E	0.6480	0.2000
F	0.6070	0.1940
G	0.6480	0.1990
H	0.6150	0.1970
I	0.6480	0.2010
J	0.7190	0.2000
K	0.7280	0.1990
L	0.7270	0.2000

1.0

0.0

<0.0