



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:11 PM UTC

PDB ID : 3S2C / pdb_00003s2c
Title : Structure of the thermostable GH51 alpha-L-arabinofuranosidase from
Thermotoga petrophila RKU-1
Authors : Souza, T.A.C.B.; Santos, C.R.; Souza, A.R.; Oldiges, D.P.; Ruller, R.; Prade,
R.A.; Squina, F.M.; Murakami, M.T.
Deposited on : 2011-05-16
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

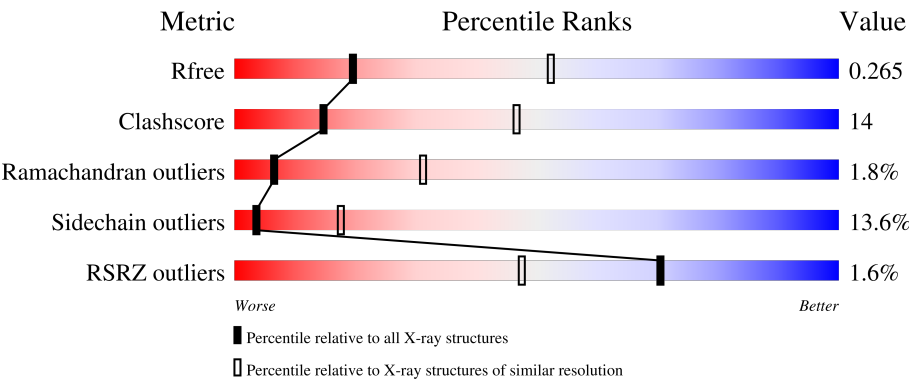
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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

Mol	Chain	Length	Quality of chain
1	A	484	% 64%29%7%.
1	B	484	67%25%6%.
1	C	484	% 67%27%6%
1	D	484	% 63%31%5%.
1	E	484	% 64%28%8%

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Mol	Chain	Length	Quality of chain
1	F	484	% 64% 31% 5%
1	G	484	% 65% 26% 8%
1	H	484	% 60% 32% 7%
1	I	484	4% 63% 29% 7%
1	J	484	3% 65% 27% 7%
1	K	484	2% 67% 26% 7%
1	L	484	2% 60% 34% 6%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 47152 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Alpha-N-arabinofuranosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	B	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	C	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	D	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	E	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	F	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	G	483	Total	C	N	O	S	0	1	0
			3904	2505	653	731	15			
1	H	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	I	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	J	481	Total	C	N	O	S	0	0	0
			3876	2488	647	726	15			
1	K	483	Total	C	N	O	S	0	0	0
			3893	2499	649	730	15			
1	L	483	Total	C	N	O	S	0	1	0
			3902	2504	650	733	15			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	42	Total	O	0	0
			42	42		
2	B	43	Total	O	0	0
			43	43		

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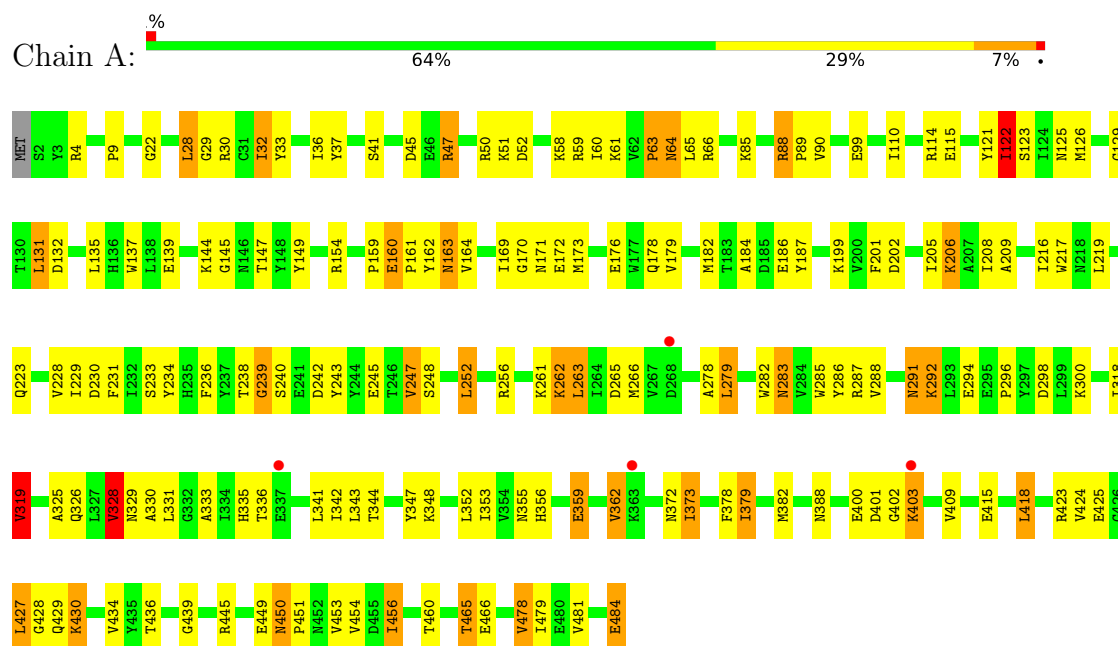
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	50	Total 50	O 50	0	0
2	D	54	Total 54	O 54	0	0
2	E	45	Total 45	O 45	0	0
2	F	39	Total 39	O 39	0	0
2	G	30	Total 30	O 30	0	0
2	H	28	Total 28	O 28	0	0
2	I	27	Total 27	O 27	0	0
2	J	23	Total 23	O 23	0	0
2	K	32	Total 32	O 32	0	0
2	L	20	Total 20	O 20	0	0

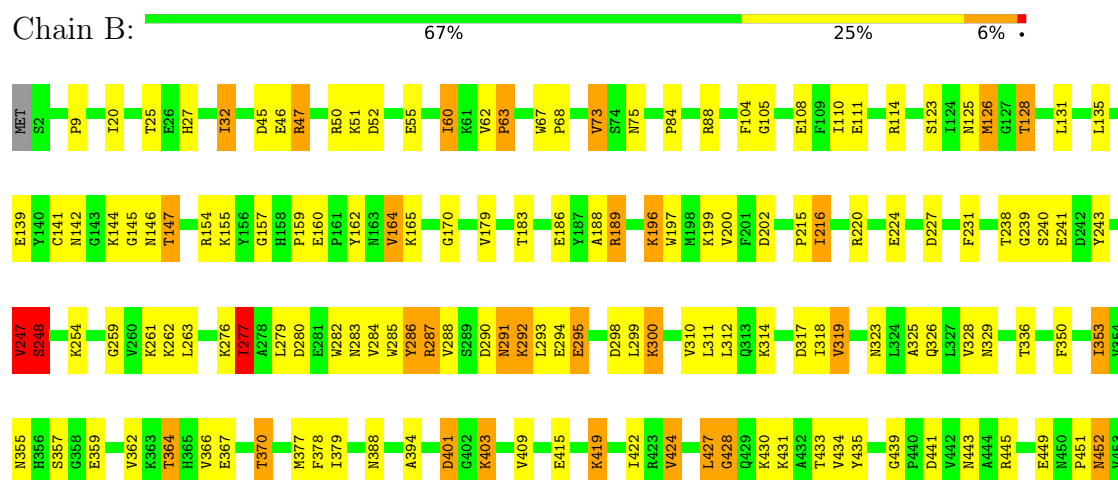
3 Residue-property plots

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

• Molecule 1: Alpha-N-arabinofuranosidase

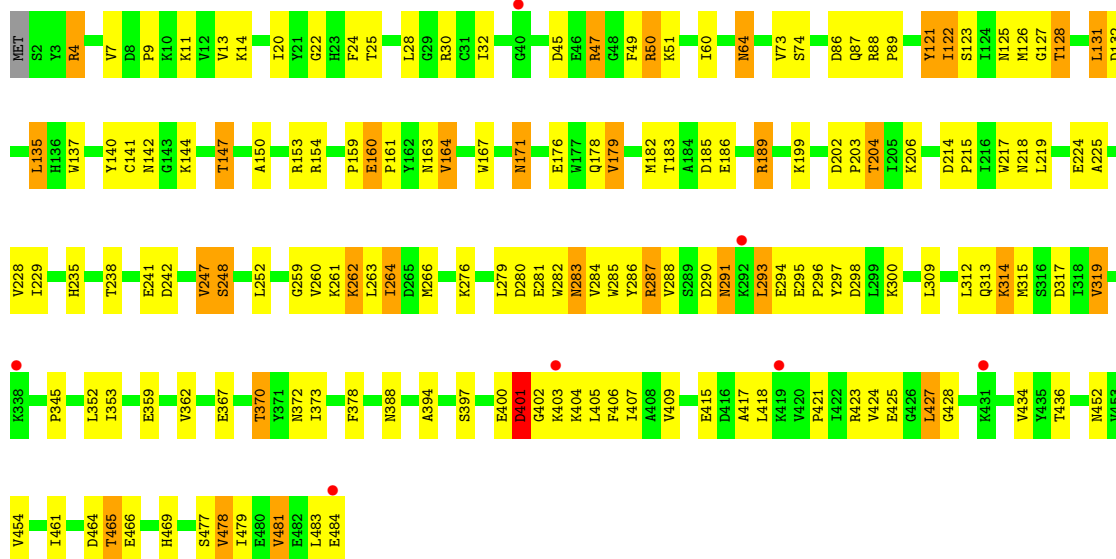


• Molecule 1: Alpha-N-arabinofuranosidase

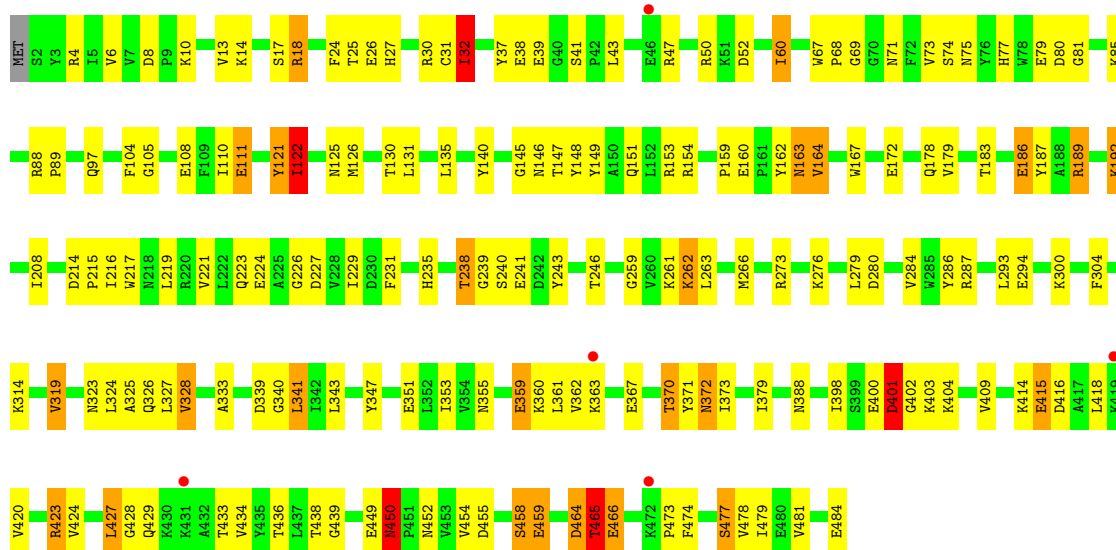




• Molecule 1: Alpha-N-arabinofuranosidase

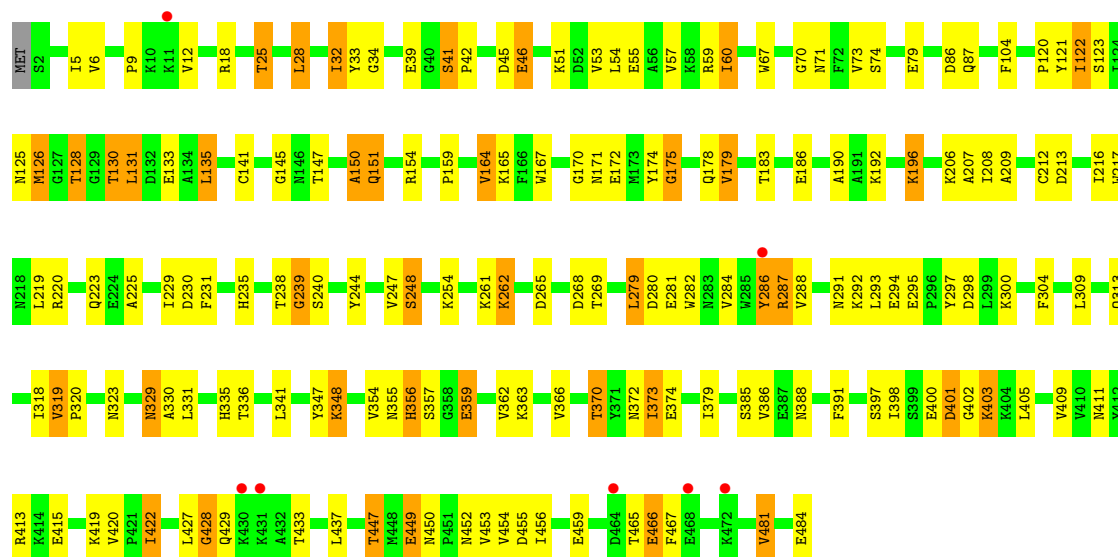


• Molecule 1: Alpha-N-arabinofuranosidase

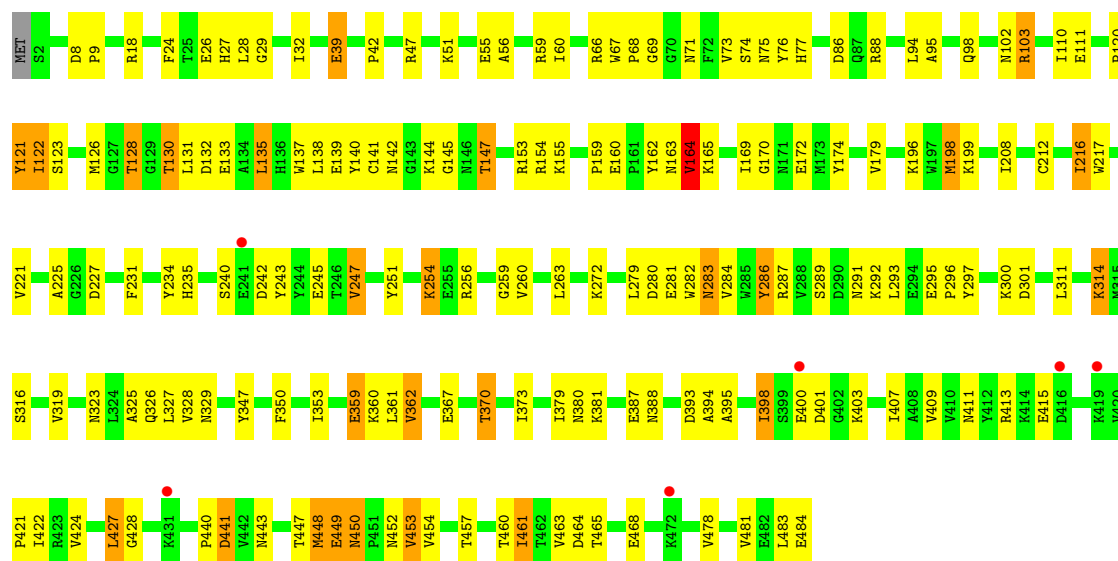


• Molecule 1: Alpha-N-arabinofuranosidase

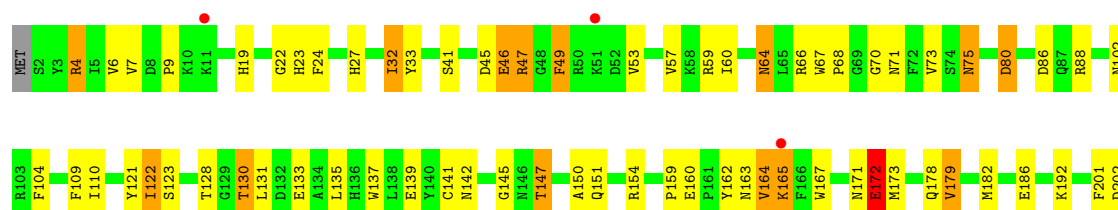


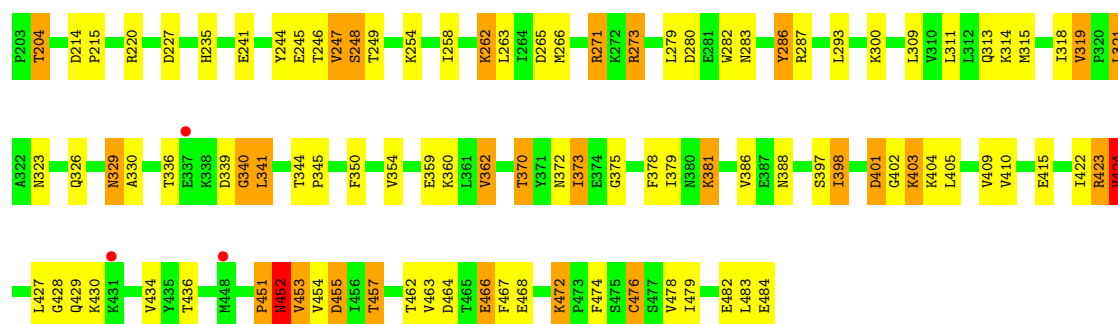


• Molecule 1: Alpha-N-arabinofuranosidase

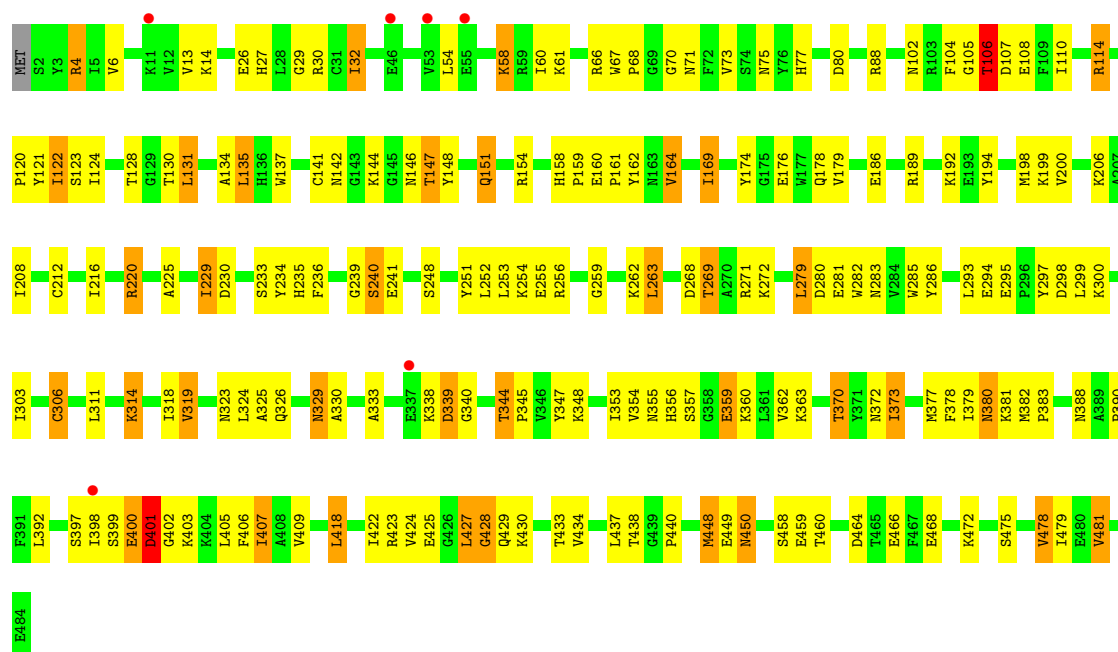


• Molecule 1: Alpha-N-arabinofuranosidase

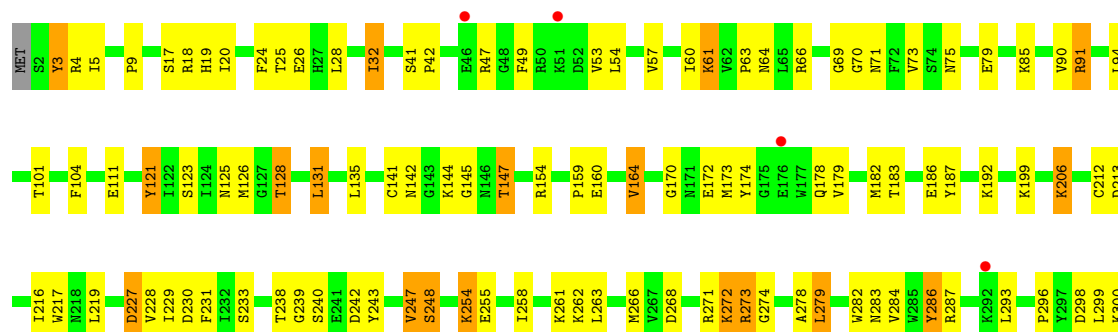


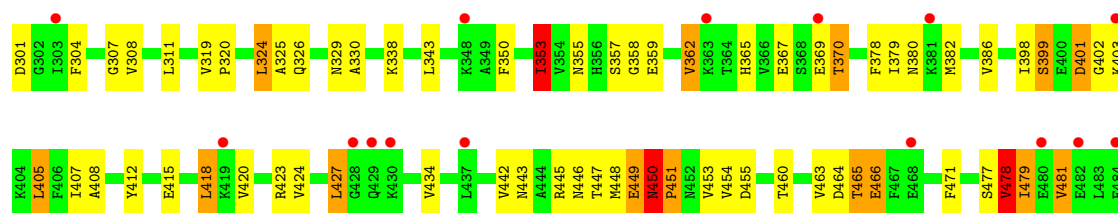


● Molecule 1: Alpha-N-arabinofuranosidase

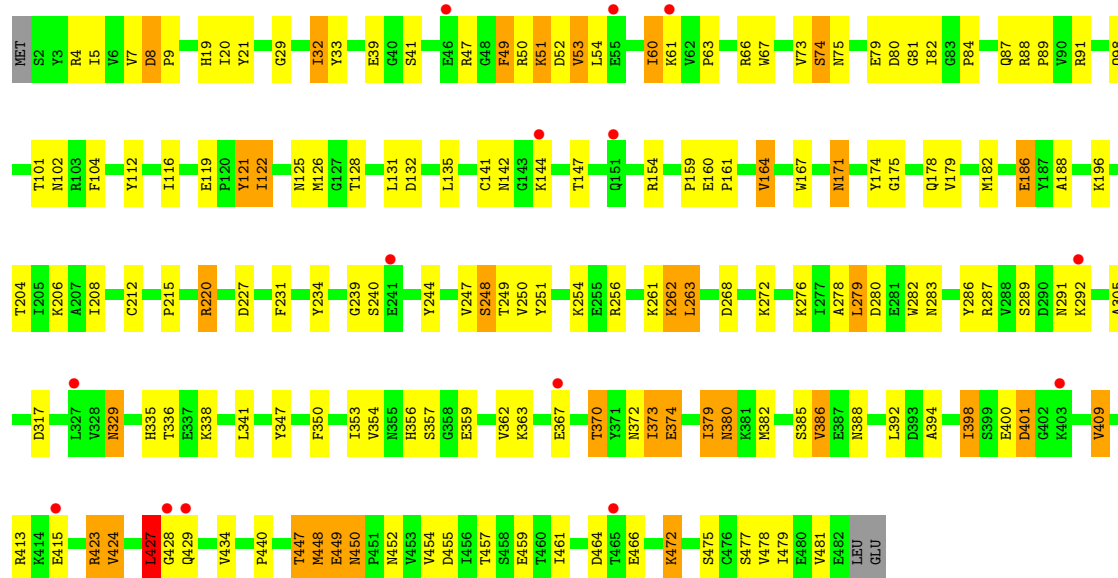


● Molecule 1: Alpha-N-arabinofuranosidase

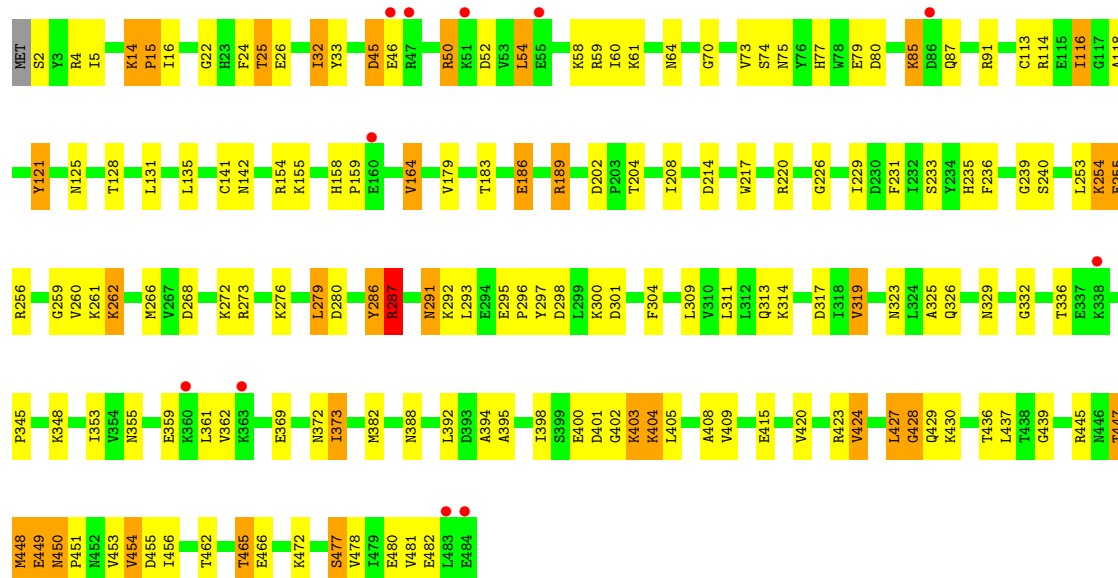




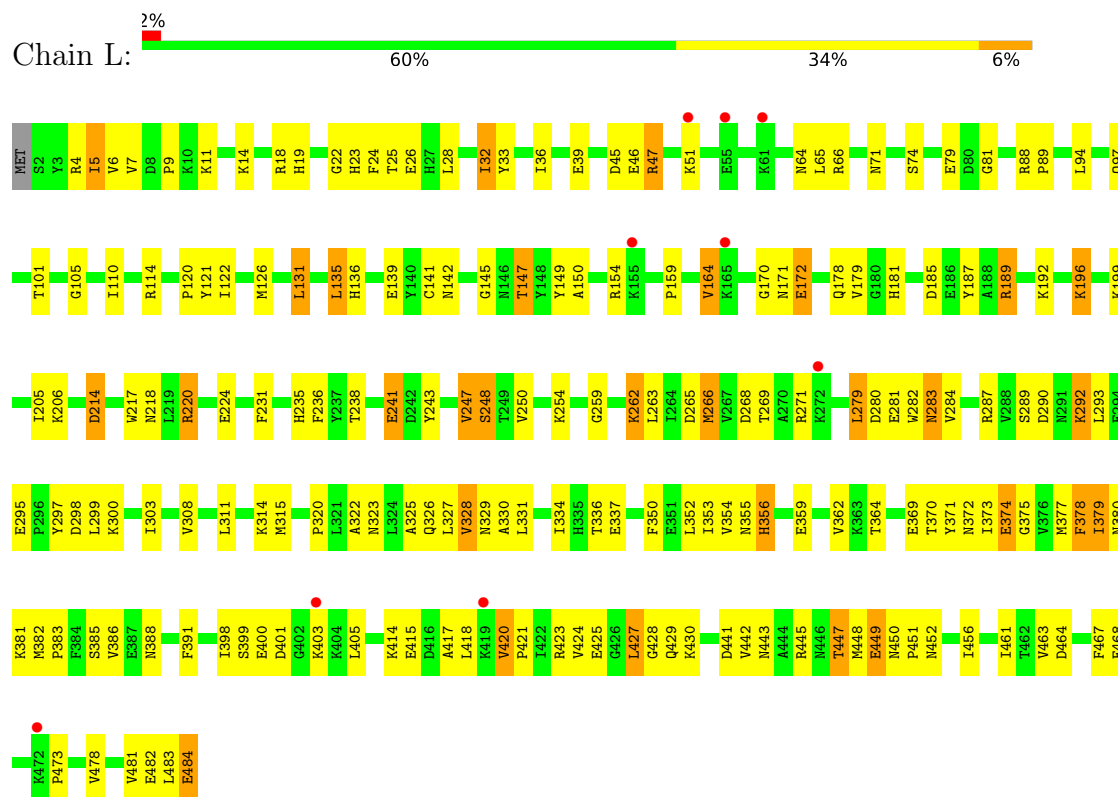
• Molecule 1: Alpha-N-arabinofuranosidase



• Molecule 1: Alpha-N-arabinofuranosidase



● Molecule 1: Alpha-N-arabinofuranosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.95Å 187.29Å 180.64Å 90.00° 90.87° 90.00°	Depositor
Resolution (Å)	49.24 – 3.00 49.24 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.2 (49.24-3.00) 97.6 (49.24-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.195 , 0.268 0.195 , 0.265	Depositor DCC
R_{free} test set	6914 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	54.9	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k 0.000 for -h,l,k 0.013 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	47152	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.66	0/3990	0.99	14/5413 (0.3%)
1	B	0.67	0/3990	0.99	11/5413 (0.2%)
1	C	0.67	0/3990	0.99	11/5413 (0.2%)
1	D	0.66	0/3990	1.00	11/5413 (0.2%)
1	E	0.70	0/3990	0.99	11/5413 (0.2%)
1	F	0.67	1/3990 (0.0%)	0.96	4/5413 (0.1%)
1	G	0.64	0/4001	0.98	7/5427 (0.1%)
1	H	0.65	0/3990	0.97	3/5413 (0.1%)
1	I	0.63	0/3990	0.94	3/5413 (0.1%)
1	J	0.61	0/3973	0.97	12/5390 (0.2%)
1	K	0.63	0/3990	0.97	10/5413 (0.2%)
1	L	0.62	0/3999	0.98	10/5426 (0.2%)
All	All	0.65	1/47883 (0.0%)	0.98	107/64960 (0.2%)

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	1
1	B	0	1
1	D	0	2
1	J	0	1
1	K	0	2
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	164	VAL	CA-CB	5.61	1.60	1.53

All (107) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	401	ASP	N-CA-C	10.29	122.08	111.07
1	G	401	ASP	N-CA-C	8.96	120.66	111.07
1	J	427	LEU	N-CA-C	8.89	116.07	108.78
1	D	401	ASP	N-CA-C	8.38	122.00	111.69
1	C	401	ASP	N-CA-C	8.31	120.11	111.14
1	J	41	SER	N-CA-C	7.92	118.70	109.60
1	A	319	VAL	CA-C-N	7.75	127.38	119.56
1	A	319	VAL	C-N-CA	7.75	127.38	119.56
1	J	8	ASP	CA-C-N	7.44	127.15	119.56
1	J	8	ASP	C-N-CA	7.44	127.15	119.56
1	C	160	GLU	CA-C-N	7.00	126.99	119.78
1	C	160	GLU	C-N-CA	7.00	126.99	119.78
1	L	328	VAL	N-CA-C	6.98	117.88	108.11
1	I	268	ASP	N-CA-C	6.97	119.72	111.71
1	K	292	LYS	N-CA-C	-6.95	105.35	114.31
1	L	461	ILE	N-CA-C	6.91	116.96	108.53
1	E	319	VAL	CA-C-N	6.90	126.53	119.56
1	E	319	VAL	C-N-CA	6.90	126.53	119.56
1	A	41	SER	N-CA-C	6.86	118.36	109.64
1	K	15	PRO	CA-C-N	6.77	133.89	121.70
1	K	15	PRO	C-N-CA	6.77	133.89	121.70
1	D	450	ASN	CA-C-N	-6.76	111.39	119.84
1	D	450	ASN	C-N-CA	-6.76	111.39	119.84
1	K	439	GLY	CA-C-N	6.64	128.14	119.84
1	K	439	GLY	C-N-CA	6.64	128.14	119.84
1	G	319	VAL	CA-C-N	6.46	126.04	119.19
1	G	319	VAL	C-N-CA	6.46	126.04	119.19
1	J	119	GLU	CA-C-N	6.42	127.87	119.84
1	J	119	GLU	C-N-CA	6.42	127.87	119.84
1	C	214	ASP	CA-C-N	6.39	125.62	118.97
1	C	214	ASP	C-N-CA	6.39	125.62	118.97
1	A	228	VAL	N-CA-C	6.32	116.99	111.56
1	H	269	THR	N-CA-C	-6.31	97.35	110.80
1	B	202	ASP	CA-C-N	6.29	125.92	119.56
1	B	202	ASP	C-N-CA	6.29	125.92	119.56
1	E	41	SER	CA-C-N	6.29	126.76	119.47
1	E	41	SER	C-N-CA	6.29	126.76	119.47
1	G	340	GLY	N-CA-C	6.14	121.38	112.60
1	J	450	ASN	CA-C-N	6.03	125.73	119.64
1	J	450	ASN	C-N-CA	6.03	125.73	119.64
1	A	88	ARG	CA-C-N	5.98	125.92	119.76
1	A	88	ARG	C-N-CA	5.98	125.92	119.76
1	J	249	THR	N-CA-C	-5.98	105.25	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	418	LEU	N-CA-C	5.94	119.16	109.24
1	L	456	ILE	N-CA-C	5.91	116.95	107.73
1	B	355	ASN	N-CA-C	-5.91	102.17	110.50
1	F	39	GLU	N-CA-C	5.84	117.52	111.03
1	B	328	VAL	N-CA-C	5.84	116.53	108.12
1	A	252	LEU	N-CA-C	-5.79	104.57	111.69
1	J	82	ILE	N-CA-C	5.69	116.94	108.46
1	J	449	GLU	N-CA-C	-5.69	101.48	109.96
1	A	239	GLY	N-CA-C	-5.66	102.93	110.97
1	D	8	ASP	CA-C-N	5.66	125.36	119.82
1	D	8	ASP	C-N-CA	5.66	125.36	119.82
1	L	290	ASP	N-CA-C	5.64	114.16	108.75
1	G	452	ASN	N-CA-C	5.62	122.77	110.80
1	I	353	ILE	N-CA-C	5.60	116.62	111.81
1	E	34	GLY	N-CA-C	-5.59	107.60	115.32
1	E	175	GLY	N-CA-C	5.58	118.84	111.03
1	K	319	VAL	CA-C-N	5.56	125.08	119.19
1	K	319	VAL	C-N-CA	5.56	125.08	119.19
1	D	327	LEU	N-CA-C	5.55	117.01	111.07
1	F	289	SER	N-CA-C	5.53	117.52	110.61
1	D	122	ILE	N-CA-C	5.53	116.44	108.48
1	B	364	THR	CB-CA-C	-5.51	104.21	111.82
1	D	239	GLY	N-CA-C	-5.42	97.58	113.30
1	A	122	ILE	N-CA-C	5.40	115.67	108.11
1	C	417	ALA	N-CA-C	-5.40	103.27	110.55
1	E	356	HIS	N-CA-C	5.39	118.55	111.28
1	H	158	HIS	CA-C-N	5.38	125.03	119.05
1	H	158	HIS	C-N-CA	5.38	125.03	119.05
1	L	181	HIS	N-CA-C	5.38	117.83	110.24
1	G	227	ASP	N-CA-C	-5.37	106.60	114.39
1	L	315	MET	N-CA-C	5.34	117.28	110.61
1	L	420	VAL	N-CA-C	5.33	113.31	107.60
1	L	418	LEU	N-CA-C	5.33	117.48	109.23
1	A	439	GLY	CA-C-N	5.32	126.50	119.84
1	A	439	GLY	C-N-CA	5.32	126.50	119.84
1	C	228	VAL	N-CA-C	5.32	116.59	112.12
1	F	292	LYS	N-CA-C	-5.29	107.84	114.56
1	A	65	LEU	N-CA-C	5.28	117.02	108.41
1	B	277	ILE	CB-CA-C	-5.27	103.86	111.34
1	B	88	ARG	CA-C-N	5.25	125.01	119.76
1	B	88	ARG	C-N-CA	5.25	125.01	119.76
1	C	319	VAL	CA-C-N	5.24	125.32	119.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	319	VAL	C-N-CA	5.24	125.32	119.87
1	L	39	GLU	N-CA-C	5.22	116.97	111.28
1	D	333	ALA	N-CA-C	-5.22	105.48	111.07
1	A	328	VAL	N-CA-C	5.22	116.23	108.46
1	L	447	THR	N-CA-C	5.20	118.68	111.71
1	E	39	GLU	N-CA-C	5.17	116.61	110.97
1	E	292	LYS	N-CA-C	-5.17	108.24	114.75
1	K	287	ARG	CB-CA-C	5.16	117.69	109.02
1	C	315	MET	N-CA-C	5.15	118.61	111.71
1	G	41	SER	N-CA-C	5.13	116.13	109.72
1	J	175	GLY	N-CA-C	5.12	118.20	111.03
1	E	150	ALA	N-CA-C	-5.12	105.34	111.03
1	K	85	LYS	N-CA-C	5.10	118.97	112.34
1	B	439	GLY	CA-C-N	5.09	126.21	119.84
1	B	439	GLY	C-N-CA	5.09	126.21	119.84
1	D	355	ASN	N-CA-C	-5.08	102.75	110.28
1	B	247	VAL	N-CA-C	-5.07	102.49	110.09
1	I	478	VAL	N-CA-C	5.06	115.14	107.75
1	K	420	VAL	N-CA-C	5.04	113.48	107.73
1	D	32	ILE	CB-CA-C	5.03	115.84	110.91
1	C	252	LEU	N-CA-C	-5.02	105.28	111.40
1	E	239	GLY	N-CA-C	-5.01	103.88	110.74

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	63	PRO	Peptide
1	B	63	PRO	Peptide
1	D	238	THR	Peptide
1	D	240	SER	Peptide
1	J	448	MET	Peptide
1	K	14	LYS	Peptide
1	K	15	PRO	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	3893	0	3818	124	0
1	B	3893	0	3818	98	0
1	C	3893	0	3818	104	0
1	D	3893	0	3818	120	0
1	E	3893	0	3818	115	0
1	F	3893	0	3818	98	0
1	G	3904	0	3830	109	0
1	H	3893	0	3818	124	0
1	I	3893	0	3818	115	0
1	J	3876	0	3801	91	0
1	K	3893	0	3818	103	0
1	L	3902	0	3824	128	0
2	A	42	0	0	1	0
2	B	43	0	0	3	0
2	C	50	0	0	0	0
2	D	54	0	0	1	0
2	E	45	0	0	3	0
2	F	39	0	0	4	0
2	G	30	0	0	3	0
2	H	28	0	0	3	0
2	I	27	0	0	2	0
2	J	23	0	0	2	0
2	K	32	0	0	1	0
2	L	20	0	0	1	0
All	All	47152	0	45817	1290	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 14.

All (1290) 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)
1:B:291:ASN:HB3	2:B:495:HOH:O	1.43	1.19
1:E:125:ASN:HD21	1:E:128:THR:HG22	1.05	1.11
1:L:154:ARG:HG2	1:L:159:PRO:HA	1.36	1.05
1:G:4:ARG:HG3	1:G:4:ARG:HH11	1.21	1.02
1:F:154:ARG:HG2	1:F:159:PRO:HA	1.37	1.01
1:L:329:ASN:HD21	1:L:336:THR:H	1.07	1.00
1:L:428:GLY:HA3	1:L:464:ASP:HA	1.42	1.00
1:L:26:GLU:HG2	1:L:326:GLN:HE22	1.26	0.99
1:J:60:ILE:HD11	1:J:350:PHE:CB	1.93	0.99
1:I:60:ILE:HD11	1:I:350:PHE:CB	1.92	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:154:ARG:HG2	1:G:159:PRO:HA	1.43	0.98
1:J:60:ILE:HD11	1:J:350:PHE:HB3	0.99	0.97
1:I:60:ILE:HD11	1:I:350:PHE:HB2	1.46	0.97
1:B:247:VAL:O	1:B:248:SER:HB3	1.64	0.95
1:J:60:ILE:CD1	1:J:350:PHE:HB3	1.95	0.95
1:L:126:MET:HE1	1:L:187:TYR:HE1	1.31	0.95
1:D:126:MET:HE1	1:D:187:TYR:HE1	1.32	0.95
1:L:429:GLN:HG3	1:L:464:ASP:HB2	1.49	0.94
1:D:126:MET:HE1	1:D:187:TYR:CE1	2.02	0.94
1:E:125:ASN:ND2	1:E:128:THR:HG22	1.82	0.94
1:H:372:ASN:ND2	1:H:388:ASN:H	1.64	0.93
1:L:370:THR:HG23	1:L:388:ASN:HA	1.50	0.92
1:I:450:ASN:H	1:I:451:PRO:HD3	1.33	0.92
1:L:220:ARG:HG3	1:L:220:ARG:HH11	1.34	0.92
1:D:464:ASP:O	1:D:466:GLU:N	2.04	0.90
1:A:223:GLN:HE22	1:B:216:ILE:HD11	1.35	0.89
1:J:32:ILE:HG23	1:J:33:TYR:H	1.37	0.89
1:F:59:ARG:HD3	2:F:523:HOH:O	1.73	0.88
1:B:239:GLY:HA3	1:B:240:SER:OG	1.74	0.88
1:J:373:ILE:HD12	1:J:386:VAL:HG13	1.52	0.88
1:K:287:ARG:HD3	1:K:296:PRO:HD2	1.54	0.88
1:J:329:ASN:HD21	1:J:336:THR:H	1.22	0.87
1:K:348:LYS:HB3	1:K:437:LEU:HD21	1.56	0.87
1:L:189:ARG:HG3	1:L:189:ARG:HH11	1.38	0.87
1:A:126:MET:HE1	1:A:187:TYR:HE1	1.39	0.87
1:C:287:ARG:HD3	1:C:296:PRO:HD2	1.56	0.87
1:H:372:ASN:HD21	1:H:388:ASN:H	1.21	0.87
1:H:4:ARG:HH11	1:H:4:ARG:HG3	1.41	0.86
1:J:142:ASN:HD21	1:J:164:VAL:H	1.20	0.85
1:L:126:MET:HE2	1:L:170:GLY:HA3	1.57	0.85
1:A:449:GLU:O	1:A:450:ASN:HB2	1.75	0.85
1:B:292:LYS:HG3	1:B:294:GLU:HG3	1.58	0.85
1:A:32:ILE:HG23	1:A:33:TYR:H	1.42	0.85
1:B:189:ARG:HG3	1:B:189:ARG:HH11	1.42	0.85
1:C:125:ASN:HD21	1:C:128:THR:H	1.20	0.85
1:J:154:ARG:HG2	1:J:159:PRO:HA	1.57	0.84
1:K:262:LYS:HG2	1:L:259:GLY:HA2	1.59	0.83
1:A:359:GLU:HG3	1:A:400:GLU:HG2	1.59	0.83
1:D:126:MET:CE	1:D:187:TYR:HE1	1.89	0.83
1:I:449:GLU:O	1:I:450:ASN:HB2	1.76	0.82
1:F:126:MET:CE	1:F:169:ILE:HG22	2.09	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:424:VAL:HG13	1:J:427:LEU:HG	1.61	0.82
1:A:262:LYS:HZ2	1:A:262:LYS:HB2	1.44	0.81
1:B:139:GLU:HG2	1:B:147:THR:HG21	1.63	0.81
1:D:47:ARG:NH1	1:D:111:GLU:OE1	2.13	0.80
1:C:247:VAL:O	1:C:248:SER:HB3	1.80	0.80
1:D:449:GLU:O	1:D:450:ASN:HB2	1.80	0.80
1:L:398:ILE:HG22	1:L:399:SER:O	1.82	0.79
1:C:405:LEU:HB3	1:C:481:VAL:HG12	1.63	0.79
1:G:142:ASN:HD21	1:G:164:VAL:H	1.29	0.79
1:D:26:GLU:HG3	1:D:69:GLY:HA2	1.65	0.79
1:E:53:VAL:O	1:E:57:VAL:HG23	1.83	0.79
1:B:47:ARG:HH11	1:B:47:ARG:HB2	1.46	0.78
1:F:359:GLU:HG3	1:F:400:GLU:HG2	1.65	0.78
1:L:329:ASN:ND2	1:L:336:THR:H	1.80	0.78
1:D:415:GLU:HG2	1:D:416:ASP:OD1	1.84	0.78
1:I:147:THR:HB	2:I:485:HOH:O	1.84	0.78
1:C:291:ASN:H	1:C:291:ASN:HD22	1.30	0.77
1:I:247:VAL:O	1:I:248:SER:HB3	1.85	0.77
1:E:147:THR:HG22	2:E:486:HOH:O	1.84	0.77
1:H:268:ASP:HB3	1:H:271:ARG:NH1	2.00	0.77
1:L:282:TRP:O	1:L:283:ASN:HB2	1.85	0.77
1:C:142:ASN:HD21	1:C:164:VAL:H	1.30	0.77
1:L:247:VAL:O	1:L:248:SER:HB3	1.83	0.77
1:I:131:LEU:HD22	1:I:135:LEU:HD23	1.66	0.76
1:F:142:ASN:HD21	1:F:164:VAL:H	1.33	0.76
1:B:68:PRO:HG2	1:B:73:VAL:HG23	1.68	0.76
1:C:436:THR:HG23	1:C:477:SER:HB3	1.68	0.76
1:I:60:ILE:HD11	1:I:350:PHE:HB3	1.65	0.76
1:I:464:ASP:O	1:I:466:GLU:N	2.19	0.76
1:J:220:ARG:HD2	2:J:852:HOH:O	1.86	0.76
1:L:26:GLU:HG2	1:L:326:GLN:NE2	2.01	0.76
1:H:269:THR:HG23	2:H:711:HOH:O	1.86	0.75
1:J:50:ARG:HG3	1:J:52:ASP:OD1	1.85	0.75
1:K:291:ASN:N	1:K:291:ASN:HD22	1.83	0.75
1:J:80:ASP:OD2	1:J:91:ARG:NE	2.19	0.75
1:A:372:ASN:HD22	1:A:388:ASN:H	1.32	0.75
1:D:371:TYR:C	1:D:372:ASN:HD22	1.93	0.75
1:H:283:ASN:ND2	1:H:324:LEU:HD11	2.02	0.75
1:G:7:VAL:O	1:G:424:VAL:HA	1.87	0.75
1:F:126:MET:HE2	1:F:169:ILE:HG22	1.67	0.75
1:F:120:PRO:HG2	1:F:164:VAL:HB	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:329:ASN:HD21	1:G:336:THR:H	1.36	0.74
1:E:247:VAL:O	1:E:248:SER:HB3	1.86	0.74
1:A:126:MET:HE1	1:A:187:TYR:CE1	2.22	0.74
1:A:262:LYS:HB2	1:A:262:LYS:NZ	2.03	0.74
1:I:154:ARG:HG2	1:I:159:PRO:HA	1.67	0.74
1:E:370:THR:HG23	1:E:388:ASN:HA	1.70	0.73
1:K:298:ASP:HB3	1:K:445:ARG:HH21	1.53	0.73
1:C:160:GLU:HG3	1:C:161:PRO:HD2	1.71	0.73
1:E:372:ASN:ND2	1:E:388:ASN:H	1.85	0.73
1:H:235:HIS:HD2	1:H:281:GLU:HB2	1.52	0.73
1:D:189:ARG:HG3	1:D:189:ARG:HH11	1.53	0.73
1:H:429:GLN:O	1:H:430:LYS:HD2	1.89	0.73
1:A:262:LYS:HG2	1:B:259:GLY:HA2	1.70	0.72
1:G:370:THR:HG23	1:G:388:ASN:HA	1.71	0.72
1:H:240:SER:HB2	1:H:377:MET:HA	1.70	0.72
1:J:276:LYS:HD2	1:J:317:ASP:O	1.89	0.72
1:B:154:ARG:HG2	1:B:159:PRO:HA	1.69	0.72
1:D:121:TYR:CZ	1:D:208:ILE:HD13	2.24	0.72
1:D:160:GLU:CD	1:D:160:GLU:H	1.97	0.72
1:E:154:ARG:HG2	1:E:159:PRO:HA	1.70	0.72
1:E:248:SER:OG	1:E:373:ILE:HD11	1.88	0.72
1:K:254:LYS:HG2	1:K:311:LEU:HD11	1.72	0.72
1:L:401:ASP:HB2	1:L:403:LYS:H	1.53	0.72
1:A:401:ASP:HB2	1:A:402:GLY:HA2	1.72	0.72
1:J:74:SER:OG	1:J:178:GLN:NE2	2.23	0.71
1:L:417:ALA:HB2	1:L:473:PRO:HD3	1.72	0.71
1:K:25:THR:HG23	1:K:25:THR:O	1.88	0.71
1:A:372:ASN:ND2	1:A:388:ASN:H	1.89	0.71
1:E:447:THR:HG22	1:E:450:ASN:H	1.54	0.71
1:E:126:MET:HG3	1:E:170:GLY:HA3	1.72	0.71
1:H:14:LYS:NZ	1:H:314:LYS:O	2.19	0.71
1:D:372:ASN:HD22	1:D:372:ASN:N	1.86	0.70
1:C:202:ASP:OD1	1:C:204:THR:OG1	2.09	0.70
1:B:141:CYS:C	1:B:142:ASN:HD22	2.00	0.70
1:J:372:ASN:ND2	1:J:388:ASN:H	1.89	0.70
1:B:247:VAL:O	1:B:248:SER:CB	2.39	0.70
1:E:73:VAL:HG21	1:E:123:SER:O	1.91	0.70
1:J:81:GLY:HA2	1:J:88:ARG:HD3	1.74	0.70
1:C:45:ASP:HB3	1:C:51:LYS:HE3	1.73	0.70
1:E:403:LYS:HG2	1:E:403:LYS:O	1.91	0.70
1:F:60:ILE:HD12	1:F:350:PHE:HB3	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:LEU:O	1:A:465:THR:HG22	1.91	0.69
1:F:217:TRP:O	1:F:221:VAL:HG23	1.91	0.69
1:I:141:CYS:C	1:I:142:ASN:HD22	1.99	0.69
1:G:130:THR:HG22	1:G:133:GLU:H	1.57	0.69
1:L:122:ILE:HG22	1:L:164:VAL:HG21	1.73	0.69
1:I:131:LEU:HD22	1:I:135:LEU:CD2	2.22	0.69
1:H:401:ASP:OD1	1:H:402:GLY:HA2	1.92	0.69
1:G:381:LYS:HE2	2:G:490:HOH:O	1.93	0.69
1:H:141:CYS:C	1:H:142:ASN:HD22	1.99	0.69
1:D:464:ASP:C	1:D:466:GLU:H	2.01	0.69
1:L:32:ILE:HA	1:L:36:ILE:HG12	1.73	0.69
1:A:173:MET:CE	1:A:182:MET:HE3	2.22	0.69
1:J:234:TYR:OH	1:J:256:ARG:HD2	1.92	0.69
1:K:54:LEU:HD22	1:K:58:LYS:HE2	1.75	0.69
1:I:450:ASN:N	1:I:451:PRO:HD3	2.08	0.68
1:D:359:GLU:HG3	1:D:400:GLU:HG2	1.76	0.68
1:G:273:ARG:HG3	1:G:273:ARG:HH11	1.59	0.68
1:E:247:VAL:O	1:E:248:SER:CB	2.41	0.68
1:L:81:GLY:O	1:L:105:GLY:HA3	1.93	0.68
1:A:186:GLU:OE1	1:D:189:ARG:NH2	2.26	0.68
1:C:403:LYS:HB2	1:C:484:GLU:HG3	1.76	0.68
1:F:42:PRO:HD3	1:G:429:GLN:HE22	1.57	0.68
1:G:280:ASP:HA	1:G:323:ASN:HD22	1.59	0.68
1:K:329:ASN:HD21	1:K:336:THR:H	1.42	0.68
1:L:231:PHE:HE1	1:L:320:PRO:HG2	1.58	0.68
1:H:348:LYS:HB3	1:H:437:LEU:HD11	1.76	0.68
1:A:248:SER:OG	1:A:373:ILE:HD11	1.94	0.67
1:G:265:ASP:HA	1:G:271:ARG:HG3	1.75	0.67
1:H:428:GLY:CA	1:H:464:ASP:HA	2.24	0.67
1:L:298:ASP:OD1	1:L:300:LYS:HG2	1.92	0.67
1:G:186:GLU:OE1	1:K:189:ARG:NH2	2.27	0.67
1:B:47:ARG:HH11	1:B:47:ARG:CB	2.07	0.67
1:I:126:MET:HE1	1:I:187:TYR:CE1	2.29	0.67
1:K:372:ASN:ND2	1:K:388:ASN:H	1.93	0.67
1:E:374:GLU:HG2	1:E:385:SER:HB3	1.77	0.67
1:K:141:CYS:C	1:K:142:ASN:HD22	2.03	0.67
1:A:126:MET:CE	1:A:187:TYR:HE1	2.09	0.66
1:G:4:ARG:HG3	1:G:4:ARG:NH1	2.00	0.66
1:L:401:ASP:HB3	1:L:403:LYS:HG2	1.77	0.66
1:D:38:GLU:HG2	1:D:41:SER:HB2	1.77	0.66
1:G:67:TRP:CD1	1:G:68:PRO:HA	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:451:PRO:O	1:G:453:VAL:N	2.27	0.66
1:H:122:ILE:HD11	1:H:137:TRP:CE2	2.31	0.66
1:B:189:ARG:HG3	1:B:189:ARG:NH1	2.10	0.66
1:L:19:HIS:HD2	1:L:64:ASN:HB2	1.60	0.66
1:G:372:ASN:ND2	1:G:388:ASN:H	1.93	0.66
1:G:235:HIS:CE1	1:G:280:ASP:OD1	2.49	0.66
1:D:189:ARG:HG3	1:D:189:ARG:NH1	2.11	0.66
1:L:126:MET:HE1	1:L:187:TYR:CE1	2.22	0.66
1:B:366:VAL:HG12	1:B:367:GLU:H	1.61	0.65
1:G:454:VAL:O	1:G:455:ASP:HB3	1.95	0.65
1:K:262:LYS:CG	1:L:259:GLY:HA2	2.26	0.65
1:A:292:LYS:HG3	1:A:294:GLU:HG3	1.77	0.65
1:B:183:THR:OG1	1:B:186:GLU:HG2	1.97	0.65
1:G:315:MET:HB2	1:G:318:ILE:HD12	1.77	0.65
1:L:25:THR:O	1:L:25:THR:HG23	1.96	0.65
1:L:122:ILE:CG2	1:L:164:VAL:HG21	2.27	0.65
1:L:142:ASN:HD21	1:L:164:VAL:H	1.43	0.65
1:K:348:LYS:HB3	1:K:437:LEU:CD2	2.27	0.65
1:A:242:ASP:HB3	1:A:245:GLU:HB2	1.79	0.65
1:H:239:GLY:HA3	1:H:240:SER:OG	1.97	0.65
1:L:189:ARG:HG3	1:L:189:ARG:NH1	2.03	0.65
1:H:151:GLN:HA	1:H:151:GLN:HE21	1.61	0.65
1:D:360:LYS:HB2	1:D:398:ILE:HG22	1.78	0.64
1:K:239:GLY:HA3	1:K:240:SER:OG	1.97	0.64
1:H:169:ILE:HG22	1:H:169:ILE:O	1.97	0.64
1:H:428:GLY:HA3	1:H:464:ASP:HA	1.79	0.64
1:E:447:THR:HG22	1:E:449:GLU:H	1.62	0.64
1:G:273:ARG:HH11	1:G:273:ARG:CG	2.10	0.64
1:D:130:THR:HG23	2:D:576:HOH:O	1.96	0.64
1:D:449:GLU:O	1:D:450:ASN:CB	2.44	0.64
1:H:279:LEU:HD22	1:H:282:TRP:HB3	1.80	0.64
1:G:4:ARG:HH11	1:G:4:ARG:CG	2.06	0.64
1:B:110:ILE:HG21	1:B:162:TYR:CD2	2.33	0.64
1:C:171:ASN:HD22	1:C:178:GLN:HE22	1.46	0.63
1:C:13:VAL:HG12	1:C:14:LYS:HG2	1.79	0.63
1:B:125:ASN:HD21	1:B:128:THR:HG23	1.64	0.63
1:C:4:ARG:HB3	1:C:367:GLU:HB2	1.80	0.63
1:A:223:GLN:NE2	1:B:216:ILE:HD11	2.11	0.63
1:E:126:MET:HG3	1:E:170:GLY:CA	2.28	0.63
1:F:295:GLU:HG2	1:F:297:TYR:CE1	2.34	0.63
1:H:299:LEU:O	1:H:303:ILE:HG12	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:220:ARG:HG3	1:L:220:ARG:NH1	2.05	0.63
1:G:220[A]:ARG:HH11	1:G:220[A]:ARG:HA	1.64	0.63
1:H:110:ILE:O	1:H:114:ARG:HD2	1.99	0.63
1:I:183:THR:OG1	1:I:186:GLU:HG3	1.99	0.63
1:J:244:TYR:O	1:J:247:VAL:O	2.17	0.63
1:L:447:THR:HG23	1:L:450:ASN:H	1.64	0.63
1:C:235:HIS:CE1	1:C:280:ASP:OD1	2.52	0.62
1:K:276:LYS:HD2	1:K:317:ASP:O	1.99	0.62
1:B:428:GLY:HA3	1:B:464:ASP:OD2	1.99	0.62
1:I:126:MET:HE1	1:I:187:TYR:HE1	1.64	0.62
1:C:427:LEU:O	1:C:465:THR:HG22	1.98	0.62
1:D:343:LEU:HD13	1:D:347:TYR:CE2	2.34	0.62
1:K:401:ASP:HB2	1:K:402:GLY:CA	2.29	0.62
1:L:369:GLU:HB3	1:L:391:PHE:HD2	1.64	0.62
1:C:461:ILE:HD13	1:C:469:HIS:HD2	1.64	0.62
1:A:202:ASP:O	1:A:205:ILE:HG12	1.99	0.62
1:E:45:ASP:HB3	1:E:51:LYS:HD3	1.82	0.62
1:C:154:ARG:HG2	1:C:159:PRO:HA	1.81	0.62
1:H:235:HIS:CD2	1:H:281:GLU:HB2	2.33	0.62
1:J:73:VAL:C	1:J:75:ASN:H	2.07	0.62
1:L:248:SER:HB2	1:L:371:TYR:OH	2.00	0.62
1:B:142:ASN:HD21	1:B:164:VAL:H	1.48	0.61
1:H:283:ASN:ND2	1:H:324:LEU:CD1	2.63	0.61
1:G:235:HIS:HE1	1:G:280:ASP:OD1	1.83	0.61
1:K:266:MET:HE1	1:L:263:LEU:HD13	1.82	0.61
1:I:73:VAL:HG21	1:I:123:SER:O	2.00	0.61
1:H:370:THR:HG23	1:H:388:ASN:HA	1.81	0.61
1:K:25:THR:O	1:K:25:THR:CG2	2.48	0.61
1:L:377:MET:O	1:L:378:PHE:HB3	2.00	0.61
1:K:73:VAL:C	1:K:75:ASN:H	2.09	0.61
1:G:53:VAL:O	1:G:57:VAL:HG23	1.99	0.61
1:H:88:ARG:NH1	1:H:102:ASN:O	2.33	0.61
1:H:344:THR:HG22	1:H:345:PRO:HD2	1.82	0.61
1:I:160:GLU:CD	1:I:160:GLU:H	2.09	0.61
1:J:374:GLU:HG3	1:J:385:SER:HB3	1.82	0.61
1:F:111:GLU:HG3	2:F:494:HOH:O	2.01	0.61
1:H:70:GLY:O	1:H:73:VAL:HG12	2.00	0.61
1:B:239:GLY:H	1:B:378:PHE:H	1.49	0.60
1:C:73:VAL:O	1:C:125:ASN:HB2	2.01	0.60
1:C:131:LEU:HD22	1:C:135:LEU:HD23	1.83	0.60
1:H:66:ARG:HA	1:H:121:TYR:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:450:ASN:H	1:I:451:PRO:CD	2.10	0.60
1:F:29:GLY:H	1:F:98:GLN:HE22	1.50	0.60
1:E:401:ASP:OD1	1:E:401:ASP:N	2.29	0.60
1:I:271:ARG:O	1:I:272:LYS:HB2	2.01	0.60
1:G:70:GLY:O	1:G:73:VAL:HG12	2.01	0.60
1:G:122:ILE:HD11	1:G:137:TRP:CE2	2.36	0.60
1:D:163:ASN:HD22	1:D:163:ASN:C	2.10	0.60
1:F:126:MET:HE1	1:F:169:ILE:HG22	1.82	0.60
1:A:173:MET:HE2	1:A:182:MET:HE3	1.83	0.60
1:J:32:ILE:HG23	1:J:33:TYR:N	2.12	0.60
1:L:483:LEU:O	1:L:484:GLU:HB2	2.01	0.60
1:A:450:ASN:HB3	1:A:453:VAL:HG23	1.83	0.59
1:L:337:GLU:OE2	1:L:337:GLU:HA	2.01	0.59
1:J:49:PHE:HD1	1:J:49:PHE:N	2.00	0.59
1:A:99:GLU:OE1	1:D:146:ASN:HB2	2.02	0.59
1:B:370:THR:HG23	1:B:388:ASN:HA	1.83	0.59
1:F:360:LYS:HB2	1:F:398:ILE:HG22	1.83	0.59
1:A:63:PRO:HG2	1:A:64:ASN:HB2	1.84	0.59
1:D:429:GLN:HA	1:D:464:ASP:HB2	1.85	0.59
1:G:71:ASN:ND2	1:G:178:GLN:HE22	1.99	0.59
1:A:449:GLU:O	1:A:450:ASN:CB	2.48	0.59
1:A:450:ASN:H	1:A:451:PRO:HD3	1.67	0.59
1:D:14:LYS:NZ	1:D:314:LYS:O	2.32	0.59
1:F:147:THR:CG2	2:F:486:HOH:O	2.51	0.59
1:J:248:SER:OG	1:J:373:ILE:HD13	2.03	0.59
1:K:430:LYS:HG2	1:K:482:GLU:O	2.03	0.59
1:D:280:ASP:HA	1:D:323:ASN:HD22	1.68	0.59
1:D:439:GLY:HA3	1:D:454:VAL:HG12	1.85	0.59
1:K:229:ILE:O	1:K:273:ARG:NH1	2.35	0.59
1:K:301:ASP:O	1:K:304:PHE:HB3	2.03	0.59
1:A:282:TRP:O	1:A:283:ASN:HB2	2.02	0.58
1:B:285:TRP:NE1	1:B:379:ILE:HD11	2.18	0.58
1:B:287:ARG:HG2	1:B:295:GLU:OE1	2.03	0.58
1:A:359:GLU:CG	1:A:400:GLU:HG2	2.29	0.58
1:A:171:ASN:HD22	1:A:178:GLN:HE22	1.50	0.58
1:A:423:ARG:HG2	1:A:466:GLU:OE1	2.03	0.58
1:E:359:GLU:HG3	1:E:400:GLU:HG2	1.84	0.58
1:E:5:ILE:HG12	1:E:366:VAL:HG22	1.85	0.58
1:L:447:THR:O	1:L:449:GLU:N	2.30	0.58
1:E:125:ASN:HD21	1:E:128:THR:CG2	1.97	0.58
1:G:373:ILE:CD1	1:G:386:VAL:HB	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ASN:HD22	1:A:178:GLN:NE2	2.02	0.58
1:G:266:MET:HE1	1:H:263:LEU:HD13	1.85	0.58
1:I:299:LEU:HB3	1:I:442:VAL:O	2.04	0.58
1:E:403:LYS:HB2	1:E:484:GLU:HA	1.85	0.58
1:G:130:THR:CG2	1:G:133:GLU:H	2.16	0.58
1:I:60:ILE:CD1	1:I:350:PHE:HB3	2.33	0.58
1:J:49:PHE:N	1:J:49:PHE:CD1	2.71	0.58
1:C:9:PRO:HA	1:C:362:VAL:HG21	1.85	0.58
1:H:448:MET:HG2	1:H:449:GLU:N	2.18	0.58
1:J:32:ILE:CG2	1:J:33:TYR:H	2.15	0.58
1:K:259:GLY:HA2	1:L:262:LYS:HD3	1.86	0.58
1:L:24:PHE:HD1	1:L:66:ARG:HB3	1.69	0.58
1:H:54:LEU:O	1:H:58:LYS:HD3	2.04	0.57
1:L:9:PRO:O	1:L:398:ILE:HD11	2.03	0.57
1:I:173:MET:HE3	1:I:182:MET:HG3	1.86	0.57
1:C:247:VAL:O	1:C:247:VAL:CG2	2.51	0.57
1:E:220:ARG:HD3	2:E:899:HOH:O	2.03	0.57
1:I:229:ILE:O	1:I:273:ARG:NH1	2.38	0.57
1:E:25:THR:HG22	1:E:25:THR:O	2.03	0.57
1:G:19:HIS:O	1:G:321:LEU:HA	2.04	0.57
1:G:141:CYS:C	1:G:142:ASN:HD22	2.12	0.57
1:B:145:GLY:O	1:B:154:ARG:NH2	2.36	0.57
1:B:254:LYS:HG3	1:B:311:LEU:HD11	1.84	0.57
1:D:110:ILE:HG21	1:D:162:TYR:CD2	2.40	0.57
1:E:401:ASP:CB	1:E:402:GLY:HA2	2.34	0.57
1:I:401:ASP:H	1:I:402:GLY:HA2	1.70	0.57
1:K:77:HIS:CE1	1:K:128:THR:HG22	2.40	0.57
1:D:438:THR:OG1	1:D:439:GLY:N	2.37	0.57
1:H:144:LYS:HD3	1:H:161:PRO:HG3	1.86	0.57
1:A:296:PRO:HB2	1:A:445:ARG:HE	1.68	0.57
1:D:147:THR:HG22	1:D:149:TYR:H	1.70	0.57
1:D:370:THR:HG23	1:D:388:ASN:HA	1.86	0.57
1:D:452:ASN:HA	1:D:455:ASP:HB2	1.85	0.57
1:E:235:HIS:CD2	1:E:281:GLU:HB2	2.40	0.57
1:F:327:LEU:HG	1:F:328:VAL:HG23	1.86	0.57
1:K:314:LYS:HE2	1:K:395:ALA:HB2	1.87	0.57
1:L:189:ARG:HH11	1:L:189:ARG:CG	2.15	0.57
1:A:22:GLY:CA	1:A:64:ASN:HB3	2.34	0.57
1:B:220:ARG:HD3	2:B:502:HOH:O	2.04	0.57
1:J:472:LYS:O	1:J:475:SER:HB3	2.05	0.57
1:C:147:THR:HG22	1:C:150:ALA:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:208:ILE:HG13	1:J:231:PHE:HB2	1.85	0.57
1:K:401:ASP:CG	1:K:403:LYS:HD3	2.29	0.57
1:L:7:VAL:HG13	1:L:362:VAL:HG11	1.87	0.57
1:B:366:VAL:HG12	1:B:367:GLU:N	2.20	0.57
1:H:71:ASN:HA	1:H:178:GLN:HE22	1.69	0.57
1:A:32:ILE:HG23	1:A:33:TYR:N	2.16	0.56
1:F:110:ILE:HG21	1:F:162:TYR:CD2	2.40	0.56
1:H:319:VAL:HG22	1:H:319:VAL:O	2.05	0.56
1:I:145:GLY:O	1:I:154:ARG:NH2	2.37	0.56
1:J:373:ILE:CD1	1:J:386:VAL:HG13	2.31	0.56
1:G:24:PHE:CD1	1:G:66:ARG:HB3	2.40	0.56
1:H:67:TRP:CD1	1:H:68:PRO:HA	2.40	0.56
1:H:239:GLY:H	1:H:377:MET:HB2	1.69	0.56
1:A:262:LYS:CG	1:B:259:GLY:HA2	2.35	0.56
1:B:277:ILE:HB	1:B:319:VAL:HB	1.88	0.56
1:B:428:GLY:HA2	1:B:464:ASP:HA	1.87	0.56
1:F:126:MET:HE3	1:F:170:GLY:HA3	1.86	0.56
1:H:254:LYS:HB2	1:H:311:LEU:HD11	1.86	0.56
1:K:448:MET:O	1:K:449:GLU:HB2	2.05	0.56
1:F:130:THR:CG2	1:F:132:ASP:HB2	2.35	0.56
1:F:163:ASN:ND2	1:F:165:LYS:HE2	2.21	0.56
1:H:151:GLN:NE2	1:H:154:ARG:HE	2.04	0.56
1:F:208:ILE:HG13	1:F:231:PHE:HB2	1.88	0.56
1:I:227:ASP:HB3	1:I:228:VAL:HG13	1.87	0.56
1:I:442:VAL:HG23	1:I:443:ASN:OD1	2.05	0.56
1:A:125:ASN:O	1:A:129:GLY:HA3	2.06	0.56
1:B:47:ARG:HH11	1:B:47:ARG:CG	2.19	0.56
1:D:418:LEU:HD12	1:D:420:VAL:CG2	2.35	0.56
1:F:254:LYS:HG3	1:F:311:LEU:HD11	1.88	0.56
1:F:282:TRP:O	1:F:283:ASN:HB2	2.06	0.56
1:I:401:ASP:N	1:I:402:GLY:HA2	2.20	0.56
1:G:49:PHE:N	1:G:49:PHE:CD1	2.74	0.56
1:H:142:ASN:HD22	1:H:142:ASN:N	2.04	0.56
1:K:233:SER:HB2	1:K:280:ASP:OD1	2.06	0.56
1:G:67:TRP:CG	1:G:68:PRO:HA	2.41	0.56
1:A:22:GLY:HA2	1:A:64:ASN:HB3	1.87	0.56
1:D:4:ARG:NH2	1:D:423:ARG:HG3	2.20	0.56
1:E:67:TRP:HE3	1:E:122:ILE:HG22	1.71	0.56
1:F:240:SER:HB3	1:F:286:TYR:CD2	2.40	0.56
1:J:428:GLY:HA3	1:J:429:GLN:C	2.30	0.56
1:D:418:LEU:HD12	1:D:420:VAL:HG23	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:74:SER:OG	1:E:178:GLN:NE2	2.27	0.55
1:F:27:HIS:CD2	1:F:32:ILE:HG13	2.41	0.55
1:A:401:ASP:HB2	1:A:402:GLY:CA	2.35	0.55
1:E:294:GLU:OE2	1:E:335:HIS:HE1	1.90	0.55
1:G:32:ILE:HD11	1:G:104:PHE:CB	2.36	0.55
1:G:344:THR:HB	1:G:345:PRO:HD2	1.88	0.55
1:I:71:ASN:HA	1:I:178:GLN:HE22	1.71	0.55
1:K:125:ASN:HD21	1:K:128:THR:HB	1.71	0.55
1:L:145:GLY:O	1:L:154:ARG:NH2	2.39	0.55
1:C:370:THR:OG1	1:C:388:ASN:HA	2.05	0.55
1:I:75:ASN:HD21	1:I:94:LEU:H	1.53	0.55
1:I:142:ASN:HD21	1:I:164:VAL:H	1.55	0.55
1:B:329:ASN:HD21	1:B:336:THR:H	1.54	0.55
1:C:28:LEU:HD11	1:C:293:LEU:HD23	1.88	0.55
1:E:405:LEU:HB3	1:E:481:VAL:HG22	1.88	0.55
1:G:326:GLN:HB2	1:G:330:ALA:O	2.06	0.55
1:B:403:LYS:O	1:B:403:LYS:HG2	2.07	0.55
1:K:291:ASN:HD22	1:K:291:ASN:H	1.51	0.55
1:A:298:ASP:OD1	1:A:300:LYS:HG2	2.07	0.55
1:H:405:LEU:HB3	1:H:481:VAL:HG13	1.86	0.55
1:I:369:GLU:O	1:I:370:THR:HB	2.06	0.55
1:A:122:ILE:HD11	1:A:137:TRP:CE2	2.42	0.55
1:A:401:ASP:HB2	1:A:403:LYS:H	1.72	0.55
1:H:26:GLU:HG2	1:H:27:HIS:H	1.71	0.55
1:K:202:ASP:OD1	1:K:204:THR:OG1	2.23	0.55
1:F:398:ILE:HD11	1:F:483:LEU:HD11	1.89	0.55
1:I:298:ASP:OD1	1:I:300:LYS:HG2	2.06	0.55
1:J:247:VAL:O	1:J:248:SER:CB	2.54	0.55
1:D:77:HIS:O	1:D:80:ASP:HB2	2.07	0.55
1:G:67:TRP:O	1:G:122:ILE:HA	2.07	0.55
1:I:126:MET:CE	1:I:187:TYR:HE1	2.19	0.55
1:D:229:ILE:O	1:D:273:ARG:NH1	2.40	0.55
1:F:172:GLU:OE2	1:F:235:HIS:CD2	2.60	0.55
1:H:77:HIS:O	1:H:80:ASP:HB2	2.07	0.55
1:H:239:GLY:HA3	1:H:378:PHE:H	1.72	0.55
1:L:442:VAL:HG23	1:L:443:ASN:HD22	1.72	0.55
1:C:215:PRO:HG3	1:D:266:MET:HB3	1.88	0.54
1:G:220[A]:ARG:HH11	1:G:220[A]:ARG:CA	2.20	0.54
1:I:300:LYS:HG3	1:I:301:ASP:N	2.21	0.54
1:E:329:ASN:HD21	1:E:336:THR:H	1.54	0.54
1:A:356:HIS:HB3	1:A:478:VAL:HG21	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:TRP:O	1:B:283:ASN:HB2	2.07	0.54
1:C:225:ALA:HB1	1:C:229:ILE:HG23	1.89	0.54
1:F:280:ASP:HA	1:F:323:ASN:HD22	1.71	0.54
1:H:61:LYS:HE2	1:H:355:ASN:OD1	2.06	0.54
1:J:50:ARG:O	1:J:53:VAL:HG12	2.06	0.54
1:L:279:LEU:O	1:L:322:ALA:HA	2.08	0.54
1:D:434:VAL:HG22	1:D:479:ILE:HG12	1.89	0.54
1:L:372:ASN:ND2	1:L:388:ASN:H	2.05	0.54
1:A:403:LYS:O	1:A:403:LYS:HG2	2.08	0.54
1:H:239:GLY:HA3	1:H:240:SER:CB	2.38	0.54
1:H:283:ASN:HD22	1:H:324:LEU:CD1	2.21	0.54
1:C:122:ILE:HG23	1:C:164:VAL:HG21	1.87	0.54
1:H:370:THR:CG2	1:H:388:ASN:HA	2.38	0.54
1:K:217:TRP:CD1	1:K:217:TRP:C	2.86	0.54
1:B:239:GLY:N	1:B:378:PHE:H	2.05	0.54
1:F:130:THR:HG22	1:F:132:ASP:N	2.22	0.54
1:G:436:THR:HB	1:G:457:THR:HG22	1.90	0.54
1:J:171:ASN:ND2	1:J:178:GLN:HE22	2.06	0.54
1:L:26:GLU:CG	1:L:326:GLN:HE22	2.08	0.54
1:D:71:ASN:HA	1:D:178:GLN:HE22	1.73	0.54
1:D:427:LEU:HB3	1:D:465:THR:H	1.72	0.54
1:C:140:TYR:O	1:C:153:ARG:HD3	2.08	0.54
1:E:261:LYS:NZ	1:E:265:ASP:OD2	2.40	0.54
1:I:420:VAL:CG2	1:I:471:PHE:HE2	2.21	0.54
1:A:292:LYS:CG	1:A:294:GLU:HG3	2.38	0.54
1:A:343:LEU:HD13	1:A:347:TYR:CE2	2.42	0.54
1:B:32:ILE:HD11	1:B:104:PHE:CB	2.38	0.54
1:H:120:PRO:HD2	2:H:1007:HOH:O	2.07	0.54
1:F:411:ASN:OD1	1:F:413:ARG:HG3	2.08	0.53
1:G:6:VAL:HG22	1:G:423:ARG:HB2	1.90	0.53
1:I:434:VAL:HG22	1:I:479:ILE:HG13	1.90	0.53
1:K:372:ASN:HD22	1:K:388:ASN:H	1.56	0.53
1:B:419:LYS:HG2	1:B:470:THR:OG1	2.08	0.53
1:E:465:THR:O	1:E:466:GLU:HB2	2.08	0.53
1:H:428:GLY:HA2	1:H:464:ASP:HA	1.89	0.53
1:K:268:ASP:O	1:K:272:LYS:HG3	2.08	0.53
1:B:32:ILE:HD13	1:B:32:ILE:C	2.33	0.53
1:B:239:GLY:H	1:B:378:PHE:N	2.06	0.53
1:H:122:ILE:HD11	1:H:137:TRP:CZ2	2.43	0.53
1:J:434:VAL:HG22	1:J:479:ILE:HG12	1.90	0.53
1:L:329:ASN:HD21	1:L:336:THR:N	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:ASN:HD21	1:B:336:THR:N	2.07	0.53
1:H:434:VAL:HG22	1:H:479:ILE:HG12	1.89	0.53
1:I:272:LYS:H	1:I:274:GLY:H	1.57	0.53
1:I:353:ILE:O	1:I:357:SER:HB3	2.09	0.53
1:K:24:PHE:CE1	1:K:26:GLU:HB3	2.42	0.53
1:B:20:ILE:HB	1:B:312:LEU:HD13	1.90	0.53
1:E:341:LEU:HD12	1:E:341:LEU:C	2.33	0.53
1:I:238:THR:HG21	1:I:304:PHE:CZ	2.44	0.53
1:J:125:ASN:HD21	1:J:128:THR:HB	1.73	0.53
1:K:329:ASN:ND2	1:K:336:THR:H	2.05	0.53
1:A:32:ILE:CG2	1:A:33:TYR:H	2.19	0.53
1:F:461:ILE:HG22	1:F:463:VAL:HG13	1.90	0.53
1:I:398:ILE:HG22	1:I:399:SER:O	2.09	0.53
1:L:280:ASP:HA	1:L:323:ASN:HD22	1.74	0.53
1:E:248:SER:OG	1:E:373:ILE:CD1	2.55	0.53
1:G:428:GLY:CA	1:G:429:GLN:C	2.82	0.53
1:H:392:LEU:HD13	1:H:418:LEU:HD11	1.90	0.53
1:I:57:VAL:O	1:I:60:ILE:HG22	2.09	0.53
1:J:268:ASP:N	2:J:495:HOH:O	2.41	0.53
1:L:378:PHE:CE2	1:L:379:ILE:HG22	2.44	0.53
1:L:447:THR:C	1:L:449:GLU:H	2.14	0.53
1:B:276:LYS:HE3	1:B:317:ASP:O	2.09	0.53
1:B:401:ASP:HB2	1:B:403:LYS:N	2.24	0.53
1:D:37:TYR:CE2	1:D:39:GLU:HG3	2.44	0.53
1:I:296:PRO:HB2	1:I:445:ARG:HH12	1.74	0.53
1:K:447:THR:O	1:K:451:PRO:HA	2.09	0.53
1:L:298:ASP:HB3	1:L:445:ARG:HH21	1.74	0.53
1:E:370:THR:HB	2:E:956:HOH:O	2.08	0.53
1:K:154:ARG:HG2	1:K:159:PRO:HA	1.91	0.53
1:L:131:LEU:HD22	1:L:135:LEU:CD2	2.39	0.53
1:C:141:CYS:C	1:C:142:ASN:HD22	2.18	0.52
1:E:32:ILE:HD11	1:E:104:PHE:CB	2.39	0.52
1:G:130:THR:HG22	1:G:133:GLU:HB2	1.91	0.52
1:H:134:ALA:HB1	1:H:198:MET:HE3	1.91	0.52
1:C:427:LEU:HD22	1:C:428:GLY:H	1.75	0.52
1:E:286:TYR:C	1:E:286:TYR:CD2	2.87	0.52
1:F:122:ILE:HD13	1:F:137:TRP:CH2	2.44	0.52
1:F:73:VAL:HA	1:F:76:TYR:HB3	1.91	0.52
1:H:32:ILE:HD11	1:H:104:PHE:CG	2.45	0.52
1:J:370:THR:HG23	1:J:388:ASN:HA	1.92	0.52
1:G:428:GLY:HA2	1:G:429:GLN:C	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:247:VAL:O	1:I:247:VAL:HG23	2.08	0.52
1:L:24:PHE:CD1	1:L:66:ARG:HB3	2.44	0.52
1:L:362:VAL:CG2	1:L:398:ILE:HG13	2.40	0.52
1:G:262:LYS:HE3	1:G:265:ASP:OD2	2.10	0.52
1:I:279:LEU:HD22	1:I:282:TRP:HB3	1.91	0.52
1:J:84:PRO:HB2	1:J:87:GLN:OE1	2.09	0.52
1:K:427:LEU:O	1:K:428:GLY:O	2.28	0.52
1:L:24:PHE:CD1	1:L:66:ARG:HD3	2.45	0.52
1:L:374:GLU:HG3	1:L:385:SER:HB3	1.92	0.52
1:A:262:LYS:HE3	1:A:265:ASP:OD2	2.09	0.52
1:B:67:TRP:CD1	1:B:68:PRO:HA	2.45	0.52
1:G:309:LEU:O	1:G:313:GLN:HG3	2.09	0.52
1:J:67:TRP:O	1:J:122:ILE:HA	2.10	0.52
1:J:347:TYR:C	1:J:347:TYR:CD2	2.88	0.52
1:K:348:LYS:HD2	1:K:455:ASP:HA	1.91	0.52
1:L:14:LYS:HE3	1:L:314:LYS:O	2.10	0.52
1:G:60:ILE:O	1:G:354:VAL:HG11	2.10	0.52
1:G:145:GLY:O	1:G:154:ARG:NH2	2.42	0.52
1:C:11:LYS:O	1:C:362:VAL:HG23	2.09	0.52
1:C:260:VAL:O	1:C:264:ILE:HD12	2.10	0.52
1:I:91:ARG:HG3	2:I:507:HOH:O	2.09	0.52
1:I:231:PHE:HE1	1:I:320:PRO:HG2	1.73	0.52
1:K:80:ASP:CG	1:K:91:ARG:HH21	2.17	0.52
1:C:125:ASN:ND2	1:C:128:THR:H	2.00	0.52
1:I:219:LEU:HD11	1:J:215:PRO:HB2	1.91	0.52
1:I:464:ASP:C	1:I:466:GLU:H	2.16	0.52
1:K:142:ASN:HD21	1:K:164:VAL:H	1.58	0.52
1:A:122:ILE:HD12	1:A:137:TRP:CZ2	2.45	0.51
1:F:66:ARG:HA	1:F:121:TYR:O	2.10	0.51
1:F:141:CYS:C	1:F:142:ASN:HD22	2.18	0.51
1:H:121:TYR:CE1	1:H:208:ILE:HD12	2.45	0.51
1:A:163:ASN:C	1:A:163:ASN:HD22	2.17	0.51
1:B:286:TYR:HA	1:B:379:ILE:HD13	1.92	0.51
1:E:244:TYR:O	1:E:247:VAL:O	2.28	0.51
1:G:49:PHE:N	1:G:49:PHE:HD1	2.09	0.51
1:L:236:PHE:O	1:L:282:TRP:HA	2.11	0.51
1:L:265:ASP:O	1:L:271:ARG:NH1	2.44	0.51
1:A:110:ILE:HG21	1:A:162:TYR:CD2	2.45	0.51
1:A:252:LEU:O	1:A:256:ARG:HG2	2.11	0.51
1:B:32:ILE:HD11	1:B:104:PHE:CG	2.46	0.51
1:C:182:MET:HB3	1:C:186:GLU:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:ARG:HH11	1:D:189:ARG:CG	2.21	0.51
1:D:341:LEU:C	1:D:341:LEU:HD12	2.35	0.51
1:F:234:TYR:OH	1:F:256:ARG:HD3	2.09	0.51
1:F:242:ASP:HB3	1:F:245:GLU:HB2	1.91	0.51
1:G:286:TYR:OH	1:G:300:LYS:NZ	2.36	0.51
1:H:13:VAL:HG12	1:H:14:LYS:HD3	1.93	0.51
1:I:408:ALA:HA	1:I:478:VAL:HB	1.92	0.51
1:J:248:SER:OG	1:J:373:ILE:CD1	2.59	0.51
1:L:268:ASP:O	1:L:269:THR:C	2.54	0.51
1:C:4:ARG:NH1	1:C:421:PRO:HB2	2.26	0.51
1:E:262:LYS:HD3	1:F:259:GLY:HA2	1.92	0.51
1:F:407:ILE:O	1:F:478:VAL:HA	2.10	0.51
1:J:278:ALA:O	1:J:280:ASP:N	2.44	0.51
1:D:436:THR:OG1	1:D:477:SER:HB3	2.11	0.51
1:D:458:SER:O	1:D:459:GLU:HB3	2.10	0.51
1:J:289:SER:HB3	1:J:379:ILE:HG13	1.92	0.51
1:A:352:LEU:O	1:A:355:ASN:O	2.28	0.51
1:H:306:CYS:HB3	1:H:353:ILE:HD11	1.91	0.51
1:K:121:TYR:CD1	1:K:121:TYR:C	2.89	0.51
1:A:325:ALA:HA	1:A:326:GLN:HG3	1.93	0.51
1:B:231:PHE:HA	1:B:276:LYS:O	2.10	0.51
1:C:125:ASN:ND2	1:C:125:ASN:C	2.66	0.51
1:E:71:ASN:ND2	1:E:178:GLN:OE1	2.43	0.51
1:H:306:CYS:HB3	1:H:353:ILE:CD1	2.41	0.51
1:H:326:GLN:HB2	1:H:330:ALA:O	2.11	0.51
1:L:243:TYR:CD2	1:L:414:LYS:HG2	2.46	0.51
1:C:266:MET:HB3	1:D:215:PRO:HG3	1.93	0.51
1:D:464:ASP:OD2	1:D:465:THR:HG22	2.11	0.51
1:F:73:VAL:HG21	1:F:123:SER:O	2.11	0.51
1:H:105:GLY:N	1:H:108:GLU:OE1	2.42	0.51
1:K:401:ASP:N	1:K:402:GLY:HA2	2.26	0.51
1:K:428:GLY:N	1:K:465:THR:HG22	2.26	0.51
1:A:208:ILE:HG13	1:A:231:PHE:HB2	1.92	0.51
1:C:262:LYS:CD	1:D:259:GLY:HA2	2.41	0.51
1:H:147:THR:HB	2:H:485:HOH:O	2.10	0.51
1:I:247:VAL:O	1:I:248:SER:CB	2.58	0.51
1:E:46:GLU:CD	1:E:46:GLU:H	2.18	0.50
1:I:378:PHE:CG	1:I:379:ILE:N	2.79	0.50
1:D:6:VAL:HG23	1:D:423:ARG:HB2	1.93	0.50
1:G:164:VAL:HG22	1:G:167:TRP:CZ2	2.46	0.50
1:J:372:ASN:HD22	1:J:388:ASN:H	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ARG:HG2	1:A:159:PRO:HA	1.93	0.50
1:C:247:VAL:O	1:C:247:VAL:HG23	2.11	0.50
1:C:291:ASN:H	1:C:291:ASN:ND2	2.04	0.50
1:D:67:TRP:CE2	1:D:68:PRO:HB3	2.47	0.50
1:E:280:ASP:HA	1:E:323:ASN:HD22	1.75	0.50
1:K:70:GLY:HA2	2:K:485:HOH:O	2.11	0.50
1:L:262:LYS:O	1:L:266:MET:HG3	2.11	0.50
1:D:154:ARG:HG2	1:D:159:PRO:HA	1.93	0.50
1:D:243:TYR:CD2	1:D:414:LYS:HG3	2.46	0.50
1:F:314:LYS:HD2	1:F:395:ALA:HB2	1.93	0.50
1:L:378:PHE:CG	1:L:379:ILE:N	2.80	0.50
1:B:189:ARG:HH11	1:B:189:ARG:CG	2.21	0.50
1:C:122:ILE:HD13	1:C:137:TRP:CH2	2.47	0.50
1:E:240:SER:HB3	1:E:286:TYR:CG	2.46	0.50
1:F:8:ASP:O	1:F:362:VAL:HG12	2.11	0.50
1:J:66:ARG:HA	1:J:121:TYR:O	2.12	0.50
1:K:286:TYR:OH	1:K:300:LYS:NZ	2.39	0.50
1:A:236:PHE:O	1:A:282:TRP:HA	2.11	0.50
1:A:288:VAL:O	1:A:379:ILE:HD11	2.11	0.50
1:D:32:ILE:O	1:D:37:TYR:HB3	2.11	0.50
1:F:235:HIS:CE1	1:F:280:ASP:OD1	2.65	0.50
1:G:397:SER:O	1:G:405:LEU:HD12	2.11	0.50
1:C:142:ASN:ND2	1:C:164:VAL:H	2.06	0.50
1:H:225:ALA:HB1	1:H:229:ILE:HG23	1.93	0.50
1:H:280:ASP:HA	1:H:323:ASN:HB2	1.94	0.50
1:I:70:GLY:O	1:I:73:VAL:HG12	2.12	0.50
1:K:401:ASP:HB2	1:K:402:GLY:HA2	1.94	0.50
1:L:447:THR:H	1:L:451:PRO:HD3	1.75	0.50
1:B:451:PRO:HG2	1:B:452:ASN:ND2	2.25	0.50
1:E:370:THR:CG2	1:E:388:ASN:HA	2.41	0.50
1:G:341:LEU:C	1:G:341:LEU:HD12	2.37	0.50
1:H:131:LEU:HD23	1:H:194:TYR:HA	1.93	0.50
1:I:427:LEU:HB3	1:I:465:THR:H	1.76	0.50
1:D:140:TYR:O	1:D:153:ARG:HD3	2.11	0.49
1:K:372:ASN:O	1:K:373:ILE:HG23	2.11	0.49
1:A:347:TYR:HD2	1:A:348:LYS:HD3	1.77	0.49
1:C:121:TYR:CD1	1:C:121:TYR:C	2.89	0.49
1:C:189:ARG:NH2	1:E:186:GLU:OE1	2.45	0.49
1:D:24:PHE:O	1:D:326:GLN:HB3	2.12	0.49
1:E:206:LYS:HA	1:E:230:ASP:OD1	2.13	0.49
1:H:353:ILE:O	1:H:357:SER:HB3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:239:GLY:HA3	1:I:240:SER:OG	2.12	0.49
1:J:447:THR:O	1:J:448:MET:HB3	2.12	0.49
1:J:452:ASN:ND2	1:J:455:ASP:OD1	2.45	0.49
1:A:147:THR:HG22	1:A:149:TYR:H	1.77	0.49
1:H:135:LEU:HD21	1:L:94:LEU:HD11	1.94	0.49
1:H:380:ASN:HD22	1:H:381:LYS:N	2.10	0.49
1:L:214:ASP:O	1:L:217:TRP:HB3	2.12	0.49
1:F:126:MET:HE2	1:F:169:ILE:C	2.38	0.49
1:A:333:ALA:O	1:A:344:THR:OG1	2.26	0.49
1:I:61:LYS:HE2	1:I:355:ASN:OD1	2.11	0.49
1:J:251:TYR:HD1	1:J:254:LYS:HE3	1.77	0.49
1:K:113:CYS:HA	1:K:116:ILE:CD1	2.43	0.49
1:K:259:GLY:CA	1:L:262:LYS:HD3	2.42	0.49
1:L:241:GLU:HB2	2:L:486:HOH:O	2.12	0.49
1:L:442:VAL:HG23	1:L:443:ASN:ND2	2.27	0.49
1:C:423:ARG:HH12	1:C:425:GLU:CD	2.20	0.49
1:D:126:MET:CE	1:D:187:TYR:CE1	2.76	0.49
1:D:164:VAL:HG22	1:D:167:TRP:NE1	2.27	0.49
1:D:273:ARG:HG3	1:D:273:ARG:HH11	1.77	0.49
1:F:73:VAL:C	1:F:75:ASN:H	2.20	0.49
1:J:394:ALA:HB2	1:J:409:VAL:HB	1.94	0.49
1:G:45:ASP:C	1:G:47:ARG:H	2.21	0.49
1:G:88:ARG:NH1	1:G:102:ASN:O	2.44	0.49
1:I:4:ARG:NH2	1:I:423:ARG:HB2	2.28	0.49
1:I:26:GLU:HG2	1:I:69:GLY:HA2	1.95	0.49
1:A:238:THR:HG23	1:A:239:GLY:N	2.27	0.49
1:A:336:THR:HA	1:A:341:LEU:HA	1.95	0.49
1:H:234:TYR:OH	1:H:256:ARG:HD2	2.13	0.49
1:K:255:GLU:HA	1:K:255:GLU:OE2	2.13	0.49
1:L:299:LEU:O	1:L:303:ILE:HG12	2.13	0.49
1:D:31:CYS:HA	1:D:328:VAL:O	2.13	0.49
1:H:6:VAL:HG22	1:H:423:ARG:HB3	1.95	0.49
1:H:427:LEU:HD13	1:H:428:GLY:H	1.78	0.49
1:K:116:ILE:HD11	1:K:118:ALA:HB3	1.93	0.49
1:K:448:MET:O	1:K:449:GLU:CB	2.61	0.49
1:B:314:LYS:HE2	1:B:394:ALA:O	2.13	0.48
1:E:120:PRO:HG2	1:E:164:VAL:HB	1.95	0.48
1:H:60:ILE:O	1:H:354:VAL:HG11	2.13	0.48
1:K:236:PHE:CG	1:K:253:LEU:HD13	2.48	0.48
1:A:325:ALA:CA	1:A:326:GLN:HG3	2.43	0.48
1:B:285:TRP:CD1	1:B:379:ILE:HD11	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:399:SER:HB3	1:H:406:PHE:HE2	1.78	0.48
1:I:17:SER:O	1:I:20:ILE:HG12	2.13	0.48
1:K:183:THR:OG1	1:K:186:GLU:HG2	2.12	0.48
1:L:32:ILE:HG22	1:L:36:ILE:HD11	1.95	0.48
1:L:154:ARG:CG	1:L:159:PRO:HA	2.26	0.48
1:E:122:ILE:HG13	1:E:167:TRP:CZ3	2.49	0.48
1:G:463:VAL:HG12	1:G:464:ASP:N	2.28	0.48
1:I:173:MET:CE	1:I:182:MET:HG3	2.43	0.48
1:A:4:ARG:NH1	1:A:423:ARG:HG3	2.27	0.48
1:A:122:ILE:CD1	1:A:137:TRP:CE2	2.97	0.48
1:D:30:ARG:HH21	1:D:294:GLU:CD	2.20	0.48
1:D:145:GLY:O	1:D:154:ARG:NH2	2.36	0.48
1:E:174:TYR:CD1	1:E:175:GLY:N	2.81	0.48
1:F:450:ASN:C	1:F:452:ASN:H	2.22	0.48
1:G:23:HIS:CE1	1:G:350:PHE:CE1	3.01	0.48
1:H:77:HIS:CE1	1:H:128:THR:HG22	2.48	0.48
1:K:220:ARG:HA	1:K:220:ARG:HH11	1.77	0.48
1:K:401:ASP:HB2	1:K:402:GLY:C	2.38	0.48
1:A:126:MET:HE2	1:A:169:ILE:C	2.38	0.48
1:C:403:LYS:CB	1:C:484:GLU:HG3	2.43	0.48
1:H:233:SER:HB2	1:H:280:ASP:OD1	2.13	0.48
1:L:262:LYS:HE3	1:L:262:LYS:HA	1.95	0.48
1:F:9:PRO:HA	1:F:362:VAL:HG11	1.94	0.48
1:F:251:TYR:OH	1:F:393:ASP:OD2	2.28	0.48
1:F:427:LEU:HD22	1:F:428:GLY:H	1.78	0.48
1:G:32:ILE:HG23	1:G:33:TYR:H	1.78	0.48
1:G:340:GLY:HA3	2:G:496:HOH:O	2.14	0.48
1:K:394:ALA:HA	1:K:408:ALA:O	2.13	0.48
1:A:110:ILE:HG22	1:A:114:ARG:HD2	1.96	0.48
1:A:126:MET:HE2	1:A:170:GLY:HA3	1.96	0.48
1:A:184:ALA:HA	1:A:217:TRP:CE3	2.48	0.48
1:B:240:SER:OG	1:B:377:MET:HA	2.14	0.48
1:C:287:ARG:HD2	1:C:295:GLU:CD	2.38	0.48
1:E:131:LEU:HD22	1:E:135:LEU:HD22	1.95	0.48
1:J:329:ASN:ND2	1:J:335:HIS:HA	2.29	0.48
1:K:450:ASN:N	1:K:451:PRO:HD3	2.29	0.48
1:B:329:ASN:ND2	1:B:336:THR:H	2.11	0.48
1:D:73:VAL:C	1:D:75:ASN:H	2.22	0.48
1:F:370:THR:HG23	1:F:388:ASN:HA	1.96	0.48
1:H:110:ILE:HG13	1:H:162:TYR:CD1	2.49	0.48
1:I:32:ILE:HD13	1:I:32:ILE:C	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:226:GLY:O	1:K:273:ARG:HD3	2.14	0.48
1:C:122:ILE:HD13	1:C:137:TRP:CZ2	2.49	0.48
1:E:60:ILE:HD13	1:E:347:TYR:CZ	2.49	0.48
1:E:126:MET:HE1	1:E:190:ALA:HB1	1.96	0.48
1:F:428:GLY:HA3	1:F:464:ASP:HA	1.96	0.48
1:I:60:ILE:CD1	1:I:350:PHE:CB	2.80	0.48
1:L:350:PHE:O	1:L:354:VAL:HG23	2.14	0.48
1:A:60:ILE:O	1:A:60:ILE:HG22	2.14	0.47
1:E:295:GLU:HG2	1:E:297:TYR:CE1	2.49	0.47
1:I:90:VAL:HG22	1:I:101:THR:HA	1.95	0.47
1:J:5:ILE:HD11	1:J:392:LEU:HD21	1.97	0.47
1:L:141:CYS:C	1:L:142:ASN:HD22	2.22	0.47
1:F:56:ALA:O	1:F:347:TYR:OH	2.29	0.47
1:G:110:ILE:HG21	1:G:162:TYR:CD2	2.48	0.47
1:H:363:LYS:HB3	1:H:363:LYS:NZ	2.29	0.47
1:J:61:LYS:HB2	1:J:354:VAL:HG11	1.95	0.47
1:B:441:ASP:C	1:B:443:ASN:H	2.21	0.47
1:C:219:LEU:CD1	1:D:215:PRO:HB2	2.44	0.47
1:C:276:LYS:HE3	1:C:317:ASP:O	2.14	0.47
1:G:464:ASP:C	1:G:466:GLU:N	2.72	0.47
1:H:345:PRO:HA	1:H:348:LYS:HB2	1.96	0.47
1:L:238:THR:O	1:L:284:VAL:HA	2.15	0.47
1:D:464:ASP:C	1:D:466:GLU:N	2.66	0.47
1:E:150:ALA:O	1:E:151:GLN:C	2.56	0.47
1:F:130:THR:HG21	1:F:132:ASP:HB2	1.96	0.47
1:F:145:GLY:O	1:F:154:ARG:NH2	2.47	0.47
1:G:378:PHE:CG	1:G:379:ILE:N	2.81	0.47
1:L:327:LEU:HG	1:L:328:VAL:HG23	1.97	0.47
1:C:428:GLY:HA3	1:C:464:ASP:HA	1.97	0.47
1:C:434:VAL:HG22	1:C:479:ILE:HG12	1.96	0.47
1:E:217:TRP:CD1	1:E:217:TRP:C	2.92	0.47
1:E:287:ARG:HD3	1:E:295:GLU:OE2	2.14	0.47
1:G:147:THR:HB	2:G:485:HOH:O	2.14	0.47
1:J:112:TYR:O	1:J:116:ILE:HG12	2.14	0.47
1:B:239:GLY:HA3	1:B:240:SER:HG	1.78	0.47
1:C:319:VAL:HG22	1:C:319:VAL:O	2.15	0.47
1:H:448:MET:HE3	1:H:448:MET:HB3	1.84	0.47
1:J:248:SER:H	1:J:250:VAL:HG23	1.79	0.47
1:K:208:ILE:N	1:K:208:ILE:HD12	2.30	0.47
1:L:380:ASN:OD1	1:L:382:MET:HG3	2.14	0.47
1:A:160:GLU:HB3	2:A:506:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:435:TYR:HA	1:B:457:THR:O	2.15	0.47
1:C:291:ASN:HD22	1:C:291:ASN:N	2.05	0.47
1:D:50:ARG:NH2	1:D:340:GLY:O	2.47	0.47
1:E:74:SER:O	1:E:128:THR:HB	2.14	0.47
1:E:238:THR:HG21	1:E:304:PHE:CE1	2.50	0.47
1:F:130:THR:HG22	1:F:133:GLU:H	1.80	0.47
1:F:441:ASP:N	1:F:441:ASP:OD1	2.48	0.47
1:H:26:GLU:CG	1:H:27:HIS:H	2.28	0.47
1:I:420:VAL:HG22	1:I:471:PHE:HE2	1.80	0.47
1:L:22:GLY:HA3	1:L:64:ASN:HD22	1.80	0.47
1:L:25:THR:O	1:L:25:THR:CG2	2.62	0.47
1:L:45:ASP:OD1	1:L:47:ARG:NH1	2.48	0.47
1:B:45:ASP:OD1	1:B:47:ARG:NH1	2.46	0.47
1:B:52:ASP:O	1:B:55:GLU:HB3	2.14	0.47
1:B:280:ASP:HA	1:B:323:ASN:HD22	1.80	0.47
1:B:427:LEU:O	1:B:428:GLY:O	2.32	0.47
1:E:41:SER:HA	1:E:42:PRO:HD2	1.70	0.47
1:F:18:ARG:HG3	2:F:659:HOH:O	2.13	0.47
1:H:285:TRP:NE1	1:H:379:ILE:HD11	2.30	0.47
1:I:4:ARG:NH2	1:I:423:ARG:HD2	2.29	0.47
1:I:47:ARG:HH21	1:I:111:GLU:CD	2.21	0.47
1:A:318:ILE:HG22	1:A:319:VAL:HG12	1.96	0.47
1:C:183:THR:OG1	1:C:186:GLU:HG2	2.15	0.47
1:H:407:ILE:O	1:H:478:VAL:HA	2.15	0.47
1:I:3:TYR:CD1	1:I:418:LEU:HD21	2.50	0.47
1:I:479:ILE:HG22	1:I:481:VAL:HG13	1.97	0.47
1:J:239:GLY:HA3	1:J:240:SER:HG	1.80	0.47
1:K:309:LEU:O	1:K:313:GLN:HG3	2.15	0.47
1:A:126:MET:CE	1:A:170:GLY:HA3	2.45	0.47
1:A:206:LYS:HA	1:A:230:ASP:OD1	2.15	0.47
1:F:447:THR:O	1:F:448:MET:CB	2.63	0.47
1:I:24:PHE:CD1	1:I:25:THR:N	2.83	0.47
1:L:19:HIS:CD2	1:L:64:ASN:HB2	2.46	0.47
1:C:372:ASN:ND2	1:C:388:ASN:H	2.13	0.46
1:I:18:ARG:HG2	1:I:63:PRO:HB3	1.96	0.46
1:I:24:PHE:HD1	1:I:25:THR:H	1.62	0.46
1:L:375:GLY:O	1:L:383:PRO:HA	2.15	0.46
1:D:427:LEU:HD22	1:D:428:GLY:H	1.79	0.46
1:G:147:THR:HG22	1:G:150:ALA:H	1.80	0.46
1:G:244:TYR:O	1:G:248:SER:HB3	2.14	0.46
1:G:410:VAL:HG22	1:G:476:CYS:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:22:GLY:O	1:K:323:ASN:HA	2.15	0.46
1:K:24:PHE:CZ	1:K:26:GLU:HB3	2.50	0.46
1:E:212:CYS:SG	1:E:213:ASP:N	2.86	0.46
1:G:130:THR:HG22	1:G:133:GLU:CB	2.45	0.46
1:K:401:ASP:CB	1:K:402:GLY:HA2	2.46	0.46
1:J:144:LYS:HE3	1:J:161:PRO:HG3	1.97	0.46
1:L:126:MET:HE2	1:L:170:GLY:CA	2.37	0.46
1:B:126:MET:HE3	1:B:126:MET:HB3	1.59	0.46
1:L:74:SER:OG	1:L:178:GLN:NE2	2.36	0.46
1:A:238:THR:HG23	1:A:239:GLY:H	1.80	0.46
1:A:286:TYR:HA	1:A:379:ILE:HD12	1.98	0.46
1:D:13:VAL:HB	1:D:361:LEU:HD23	1.97	0.46
1:H:142:ASN:HD21	1:H:164:VAL:H	1.63	0.46
1:A:401:ASP:HB2	1:A:403:LYS:N	2.30	0.46
1:D:172:GLU:OE2	1:D:235:HIS:CD2	2.68	0.46
1:F:172:GLU:OE2	1:F:235:HIS:HD2	1.98	0.46
1:G:428:GLY:HA2	1:G:429:GLN:O	2.16	0.46
1:J:32:ILE:HD11	1:J:104:PHE:CD2	2.50	0.46
1:D:26:GLU:HG2	1:D:27:HIS:H	1.80	0.46
1:D:401:ASP:N	1:D:402:GLY:HA2	2.31	0.46
1:H:295:GLU:HG2	1:H:297:TYR:CE1	2.51	0.46
1:B:9:PRO:HB3	1:B:483:LEU:HD11	1.97	0.46
1:C:49:PHE:O	1:C:50:ARG:C	2.58	0.46
1:D:67:TRP:O	1:D:122:ILE:HA	2.15	0.46
1:D:372:ASN:ND2	1:D:388:ASN:H	2.13	0.46
1:F:300:LYS:HG3	1:F:301:ASP:N	2.31	0.46
1:I:32:ILE:HD11	1:I:104:PHE:CB	2.46	0.46
1:I:242:ASP:OD2	1:I:243:TYR:N	2.48	0.46
1:J:400:GLU:OE1	1:J:400:GLU:HA	2.16	0.46
1:K:345:PRO:HA	1:K:348:LYS:HB2	1.98	0.46
1:K:345:PRO:HG3	1:K:454:VAL:HG21	1.98	0.46
1:B:126:MET:HG3	1:B:170:GLY:HA2	1.98	0.46
1:E:74:SER:HB3	1:E:179:VAL:HG13	1.98	0.46
1:E:348:LYS:HD3	1:E:456:ILE:HD12	1.98	0.46
1:F:287:ARG:HD2	1:F:296:PRO:HD2	1.98	0.46
1:G:246:THR:C	1:G:247:VAL:O	2.59	0.46
1:K:16:ILE:O	1:K:16:ILE:HG22	2.16	0.46
1:D:238:THR:O	1:D:284:VAL:HA	2.16	0.45
1:F:260:VAL:HA	1:F:263:LEU:HD12	1.97	0.45
1:K:45:ASP:OD1	1:K:46:GLU:N	2.49	0.45
1:A:90:VAL:HB	1:D:146:ASN:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:22:GLY:HA2	1:C:64:ASN:HB2	1.97	0.45
1:C:163:ASN:C	1:C:163:ASN:HD22	2.24	0.45
1:C:290:ASP:OD1	1:C:293:LEU:N	2.46	0.45
1:F:122:ILE:HD12	1:F:123:SER:N	2.32	0.45
1:A:434:VAL:HG22	1:A:479:ILE:HG12	1.98	0.45
1:F:421:PRO:HA	1:F:468:GLU:HG3	1.99	0.45
1:H:106:THR:O	1:H:110:ILE:HG12	2.16	0.45
1:H:239:GLY:CA	1:H:378:PHE:H	2.29	0.45
1:B:126:MET:HG3	1:B:170:GLY:CA	2.47	0.45
1:B:189:ARG:NH2	1:C:186:GLU:OE1	2.50	0.45
1:B:196:LYS:HG2	1:B:197:TRP:N	2.31	0.45
1:C:4:ARG:NH2	1:C:466:GLU:OE2	2.41	0.45
1:I:358:GLY:HA3	1:I:398:ILE:O	2.17	0.45
1:L:4:ARG:NH2	1:L:423:ARG:HB2	2.31	0.45
1:A:37:TYR:OH	1:A:85:LYS:NZ	2.48	0.45
1:B:325:ALA:HA	1:B:326:GLN:HA	1.71	0.45
1:E:32:ILE:C	1:E:32:ILE:HD13	2.42	0.45
1:E:372:ASN:HD21	1:E:388:ASN:H	1.62	0.45
1:J:353:ILE:O	1:J:357:SER:HB3	2.17	0.45
1:C:298:ASP:C	1:C:345:PRO:HG2	2.42	0.45
1:D:183:THR:OG1	1:D:186:GLU:HG2	2.17	0.45
1:E:74:SER:HG	1:E:178:GLN:HE21	1.58	0.45
1:G:171:ASN:O	1:G:172:GLU:C	2.59	0.45
1:H:67:TRP:O	1:H:122:ILE:HA	2.16	0.45
1:H:75:ASN:ND2	1:H:75:ASN:O	2.49	0.45
1:H:128:THR:HG22	1:H:128:THR:O	2.16	0.45
1:I:24:PHE:CD1	1:I:66:ARG:HB3	2.52	0.45
1:I:255:GLU:HG3	1:J:262:LYS:NZ	2.31	0.45
1:I:304:PHE:O	1:I:308:VAL:HG23	2.17	0.45
1:K:235:HIS:HE1	1:K:280:ASP:OD1	1.98	0.45
1:L:136:HIS:CG	1:L:149:TYR:CE2	3.04	0.45
1:L:147:THR:HG22	1:L:150:ALA:H	1.80	0.45
1:L:448:MET:N	1:L:451:PRO:HD3	2.31	0.45
1:D:339:ASP:OD2	1:D:340:GLY:N	2.46	0.45
1:F:314:LYS:HE3	1:F:394:ALA:O	2.17	0.45
1:H:325:ALA:HA	1:H:326:GLN:HA	1.67	0.45
1:I:217:TRP:CD1	1:I:217:TRP:C	2.94	0.45
1:I:307:GLY:HA3	1:I:412:TYR:OH	2.17	0.45
1:L:32:ILE:HG12	1:L:33:TYR:N	2.31	0.45
1:A:139:GLU:HG2	1:A:201:PHE:CZ	2.51	0.45
1:A:240:SER:HB3	1:A:286:TYR:CD2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:TRP:CE3	1:A:378:PHE:HE1	2.34	0.45
1:B:160:GLU:CD	1:B:160:GLU:H	2.25	0.45
1:D:121:TYR:CD1	1:D:121:TYR:C	2.95	0.45
1:E:32:ILE:HD11	1:E:104:PHE:CG	2.52	0.45
1:F:88:ARG:NH1	1:F:102:ASN:O	2.46	0.45
1:G:70:GLY:H	1:G:171:ASN:ND2	2.15	0.45
1:H:148:TYR:C	1:H:148:TYR:CD2	2.94	0.45
1:J:29:GLY:H	1:J:98:GLN:HE22	1.64	0.45
1:J:141:CYS:C	1:J:142:ASN:HD22	2.24	0.45
1:C:259:GLY:CA	1:D:262:LYS:HD3	2.46	0.45
1:C:401:ASP:OD1	1:C:402:GLY:HA2	2.17	0.45
1:G:464:ASP:C	1:G:466:GLU:H	2.24	0.45
1:J:122:ILE:HD11	1:J:167:TRP:CH2	2.52	0.45
1:L:292:LYS:HE2	1:L:292:LYS:HB3	1.59	0.45
1:F:75:ASN:HD21	1:F:94:LEU:H	1.65	0.45
1:F:449:GLU:OE2	1:F:449:GLU:HA	2.17	0.45
1:G:452:ASN:O	1:G:453:VAL:C	2.59	0.45
1:H:268:ASP:HB3	1:H:271:ARG:HH12	1.80	0.45
1:H:449:GLU:O	1:H:450:ASN:HB2	2.17	0.45
1:I:26:GLU:HB3	1:I:28:LEU:HB2	1.99	0.45
1:J:51:LYS:HA	1:J:54:LEU:HB2	1.98	0.45
1:A:262:LYS:HG3	1:A:266:MET:HE3	1.98	0.44
1:A:131:LEU:HD13	1:A:135:LEU:HD11	1.99	0.44
1:A:436:THR:O	1:A:456:ILE:HA	2.17	0.44
1:C:24:PHE:CD1	1:C:25:THR:N	2.85	0.44
1:C:295:GLU:HG2	1:C:297:TYR:CE1	2.52	0.44
1:D:122:ILE:HD11	1:D:167:TRP:CH2	2.52	0.44
1:H:30:ARG:O	1:H:329:ASN:ND2	2.33	0.44
1:H:283:ASN:HD21	1:H:324:LEU:HD11	1.82	0.44
1:J:20:ILE:HD11	1:J:21:TYR:CZ	2.52	0.44
1:B:435:TYR:O	1:B:477:SER:HA	2.17	0.44
1:F:26:GLU:HG3	1:F:69:GLY:HA2	1.99	0.44
1:G:75:ASN:HB3	1:G:179:VAL:HG11	1.98	0.44
1:I:286:TYR:HA	1:I:379:ILE:HD12	1.99	0.44
1:K:401:ASP:H	1:K:402:GLY:HA2	1.82	0.44
1:A:9:PRO:HA	1:A:362:VAL:HG21	1.99	0.44
1:A:219:LEU:HD21	1:A:263:LEU:HD12	2.00	0.44
1:A:243:TYR:O	1:A:247:VAL:HG22	2.17	0.44
1:B:424:VAL:HG11	1:B:427:LEU:HD12	2.00	0.44
1:C:122:ILE:HD12	1:C:123:SER:N	2.32	0.44
1:E:209:ALA:HB2	1:E:229:ILE:HG21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:281:GLU:HG2	1:F:325:ALA:HB2	2.00	0.44
1:G:173:MET:HE3	1:G:182:MET:HG3	1.98	0.44
1:H:174:TYR:CE2	1:H:212:CYS:HB3	2.52	0.44
1:H:438:THR:HG21	1:H:472:LYS:HE3	1.98	0.44
1:K:295:GLU:HG2	1:K:297:TYR:CE1	2.53	0.44
1:B:73:VAL:C	1:B:75:ASN:H	2.25	0.44
1:C:11:LYS:O	1:C:362:VAL:CG2	2.65	0.44
1:C:127:GLY:HA3	1:C:179:VAL:O	2.16	0.44
1:C:131:LEU:HD22	1:C:135:LEU:CD2	2.46	0.44
1:D:238:THR:HG21	1:D:304:PHE:CE1	2.53	0.44
1:E:447:THR:CG2	1:E:449:GLU:H	2.30	0.44
1:G:139:GLU:HG2	1:G:201:PHE:CZ	2.53	0.44
1:H:220:ARG:HD2	1:H:220:ARG:HA	1.59	0.44
1:H:333:ALA:O	1:H:347:TYR:HB2	2.18	0.44
1:I:126:MET:HE2	1:I:170:GLY:HA3	2.00	0.44
1:K:253:LEU:HD21	1:K:279:LEU:HD11	1.99	0.44
1:K:423:ARG:HG2	1:K:466:GLU:OE1	2.17	0.44
1:L:447:THR:C	1:L:449:GLU:N	2.74	0.44
1:A:58:LYS:HE3	1:A:115:GLU:O	2.18	0.44
1:D:25:THR:HG23	1:D:25:THR:O	2.17	0.44
1:G:245:GLU:HG3	1:G:375:GLY:HA3	1.98	0.44
1:I:49:PHE:HB2	1:I:54:LEU:HD11	2.00	0.44
1:I:73:VAL:O	1:I:125:ASN:HB2	2.17	0.44
1:J:400:GLU:O	1:J:401:ASP:CG	2.60	0.44
1:C:284:VAL:O	1:C:297:TYR:HE1	2.00	0.44
1:I:325:ALA:HA	1:I:326:GLN:HA	1.73	0.44
1:K:401:ASP:HB2	1:K:403:LYS:N	2.32	0.44
1:A:242:ASP:OD2	1:A:243:TYR:N	2.50	0.44
1:C:171:ASN:HD22	1:C:178:GLN:NE2	2.15	0.44
1:E:452:ASN:O	1:E:453:VAL:C	2.60	0.44
1:F:235:HIS:CD2	1:F:281:GLU:HB2	2.52	0.44
1:F:447:THR:O	1:F:448:MET:HB3	2.18	0.44
1:G:122:ILE:HD11	1:G:137:TRP:CZ2	2.52	0.44
1:I:254:LYS:HG2	1:I:311:LEU:HD11	2.00	0.44
1:J:80:ASP:O	1:J:89:PRO:HD2	2.18	0.44
1:B:188:ALA:HB1	1:B:224:GLU:HB2	1.99	0.44
1:E:219:LEU:HD13	1:F:216:ILE:HD12	1.99	0.44
1:I:405:LEU:HB3	1:I:481:VAL:HG22	1.99	0.44
1:A:182:MET:HB3	1:A:186:GLU:HG3	2.00	0.43
1:B:238:THR:O	1:B:284:VAL:HA	2.18	0.43
1:C:401:ASP:OD1	1:C:401:ASP:N	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:192:LYS:HE3	1:D:224:GLU:O	2.17	0.43
1:F:39:GLU:CD	1:F:103:ARG:HH21	2.26	0.43
1:F:314:LYS:HA	1:F:361:LEU:HD11	2.00	0.43
1:H:240:SER:CB	1:H:377:MET:HA	2.42	0.43
1:J:341:LEU:HD12	1:J:341:LEU:C	2.42	0.43
1:K:60:ILE:O	1:K:61:LYS:C	2.62	0.43
1:L:5:ILE:HD12	1:L:420:VAL:HG11	1.99	0.43
1:A:66:ARG:HA	1:A:121:TYR:O	2.18	0.43
1:A:160:GLU:CD	1:A:160:GLU:H	2.26	0.43
1:B:261:LYS:HD3	1:B:318:ILE:HG23	1.99	0.43
1:C:298:ASP:OD1	1:C:300:LYS:HG2	2.18	0.43
1:D:226:GLY:O	1:D:273:ARG:HD3	2.18	0.43
1:H:248:SER:OG	1:H:373:ILE:HD11	2.16	0.43
1:H:251:TYR:CZ	1:H:390:PRO:HD2	2.53	0.43
1:H:382:MET:HA	1:H:383:PRO:HD3	1.88	0.43
1:H:425:GLU:HA	1:H:425:GLU:OE2	2.18	0.43
1:I:206:LYS:HA	1:I:230:ASP:OD1	2.17	0.43
1:L:71:ASN:HA	1:L:178:GLN:HE22	1.83	0.43
1:L:192:LYS:HD3	1:L:224:GLU:O	2.17	0.43
1:L:398:ILE:CG2	1:L:399:SER:O	2.61	0.43
1:A:132:ASP:OD2	1:F:77:HIS:NE2	2.48	0.43
1:C:122:ILE:HD12	1:C:122:ILE:C	2.43	0.43
1:G:142:ASN:HD21	1:G:164:VAL:N	2.05	0.43
1:G:142:ASN:ND2	1:G:163:ASN:HA	2.33	0.43
1:J:380:ASN:ND2	1:J:382:MET:HB2	2.34	0.43
1:A:45:ASP:OD1	1:A:47:ARG:HD3	2.19	0.43
1:A:50:ARG:NH2	1:A:52:ASP:OD2	2.44	0.43
1:B:84:PRO:HA	2:B:509:HOH:O	2.18	0.43
1:B:243:TYR:HD1	1:B:300:LYS:HB2	1.82	0.43
1:D:32:ILE:HD11	1:D:104:PHE:CG	2.53	0.43
1:E:9:PRO:HA	1:E:362:VAL:HG21	2.01	0.43
1:G:321:LEU:HD11	1:G:323:ASN:HD21	1.83	0.43
1:J:239:GLY:HA3	1:J:240:SER:OG	2.18	0.43
1:K:311:LEU:HA	1:K:314:LYS:HD2	2.01	0.43
1:D:32:ILE:HD11	1:D:104:PHE:CB	2.49	0.43
1:F:243:TYR:CE1	1:F:247:VAL:HG11	2.53	0.43
1:F:450:ASN:O	1:F:453:VAL:HG12	2.19	0.43
1:H:472:LYS:O	1:H:475:SER:OG	2.28	0.43
1:I:324:LEU:HD13	1:I:350:PHE:HE2	1.83	0.43
1:I:365:HIS:HE1	1:I:367:GLU:HG2	1.83	0.43
1:K:436:THR:O	1:K:456:ILE:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ARG:HA	1:A:89:PRO:HD3	1.80	0.43
1:B:401:ASP:HB2	1:B:403:LYS:H	1.83	0.43
1:C:20:ILE:HD12	1:C:312:LEU:HB3	2.00	0.43
1:C:235:HIS:HE1	1:C:280:ASP:OD1	2.01	0.43
1:E:32:ILE:HG23	1:E:33:TYR:H	1.82	0.43
1:E:411:ASN:OD1	1:E:413:ARG:HB2	2.19	0.43
1:G:27:HIS:HA	1:G:32:ILE:HG21	2.00	0.43
1:A:145:GLY:O	1:A:154:ARG:NH2	2.45	0.43
1:A:285:TRP:CD1	1:A:379:ILE:HD13	2.54	0.43
1:C:352:LEU:HD11	1:C:478:VAL:HG12	2.01	0.43
1:D:214:ASP:OD1	1:D:214:ASP:C	2.61	0.43
1:E:348:LYS:HD2	1:E:455:ASP:HA	2.01	0.43
1:F:126:MET:CE	1:F:169:ILE:C	2.92	0.43
1:H:169:ILE:HD12	1:H:169:ILE:HA	1.93	0.43
1:H:298:ASP:HA	1:H:345:PRO:HG3	2.01	0.43
1:I:75:ASN:HA	1:I:128:THR:OG1	2.18	0.43
1:I:233:SER:HA	1:I:278:ALA:O	2.19	0.43
1:I:407:ILE:O	1:I:478:VAL:HA	2.18	0.43
1:K:214:ASP:HB3	1:K:217:TRP:HB3	1.99	0.43
1:L:4:ARG:HG2	1:L:421:PRO:HG2	2.01	0.43
1:L:427:LEU:HD22	1:L:428:GLY:N	2.33	0.43
1:A:30:ARG:C	1:A:32:ILE:H	2.26	0.43
1:B:68:PRO:CG	1:B:73:VAL:HG23	2.44	0.43
1:C:309:LEU:O	1:C:313:GLN:HG3	2.18	0.43
1:D:4:ARG:HH22	1:D:423:ARG:HG3	1.84	0.43
1:D:81:GLY:O	1:D:105:GLY:HA3	2.19	0.43
1:E:167:TRP:O	1:E:207:ALA:HA	2.18	0.43
1:E:223:GLN:HE22	1:F:216:ILE:HD13	1.84	0.43
1:E:318:ILE:C	1:E:320:PRO:HD3	2.44	0.43
1:E:370:THR:HG21	1:E:388:ASN:OD1	2.19	0.43
1:F:71:ASN:O	1:F:95:ALA:HB2	2.19	0.43
1:F:174:TYR:CE2	1:F:212:CYS:HB3	2.54	0.43
1:H:32:ILE:HD11	1:H:104:PHE:CB	2.49	0.43
1:H:206:LYS:HA	1:H:230:ASP:OD1	2.19	0.43
1:J:8:ASP:HA	1:J:9:PRO:HD2	1.77	0.43
1:J:188:ALA:HB1	1:J:220:ARG:O	2.19	0.43
1:K:50:ARG:HH21	1:K:52:ASP:CG	2.27	0.43
1:K:404:LYS:HE2	1:K:480:GLU:OE2	2.18	0.43
1:K:436:THR:OG1	1:K:477:SER:HB3	2.18	0.43
1:C:125:ASN:OD1	1:C:128:THR:HG22	2.19	0.43
1:E:298:ASP:OD1	1:E:300:LYS:HG2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:202:ASP:OD1	1:G:204:THR:HB	2.19	0.43
1:A:233:SER:HA	1:A:278:ALA:O	2.18	0.43
1:A:341:LEU:HD12	1:A:341:LEU:C	2.43	0.43
1:D:32:ILE:HD11	1:D:104:PHE:HB3	2.01	0.43
1:D:60:ILE:HD13	1:D:60:ILE:HA	1.63	0.43
1:F:67:TRP:CE2	1:F:68:PRO:HB3	2.54	0.43
1:G:80:ASP:OD1	1:G:80:ASP:N	2.51	0.43
1:G:247:VAL:O	1:G:248:SER:HB3	2.18	0.43
1:J:73:VAL:C	1:J:75:ASN:N	2.75	0.43
1:K:428:GLY:HA2	1:K:429:GLN:HA	1.68	0.43
1:L:120:PRO:HG2	1:L:164:VAL:HB	2.01	0.43
1:B:73:VAL:HG21	1:B:123:SER:O	2.19	0.42
1:B:298:ASP:OD1	1:B:300:LYS:HG3	2.19	0.42
1:B:353:ILE:O	1:B:357:SER:HB3	2.18	0.42
1:C:423:ARG:NH1	1:C:425:GLU:CD	2.76	0.42
1:C:464:ASP:CG	1:C:465:THR:H	2.27	0.42
1:D:27:HIS:HA	1:D:32:ILE:HG21	2.01	0.42
1:D:473:PRO:O	1:D:474:PHE:C	2.62	0.42
1:E:313:GLN:HE22	1:E:357:SER:HB2	1.84	0.42
1:F:8:ASP:O	1:F:362:VAL:CG1	2.67	0.42
1:G:262:LYS:NZ	1:H:255:GLU:HG3	2.33	0.42
1:H:169:ILE:O	1:H:169:ILE:CG2	2.66	0.42
1:I:266:MET:HE2	1:J:215:PRO:HB3	2.01	0.42
1:K:154:ARG:CG	1:K:159:PRO:HA	2.49	0.42
1:L:325:ALA:HA	1:L:326:GLN:HA	1.56	0.42
1:A:262:LYS:O	1:A:266:MET:HG3	2.19	0.42
1:E:70:GLY:O	1:E:73:VAL:HG12	2.19	0.42
1:E:284:VAL:O	1:E:297:TYR:HE1	2.02	0.42
1:F:135:LEU:O	1:F:139:GLU:HG3	2.18	0.42
1:F:380:ASN:O	1:F:381:LYS:HB2	2.19	0.42
1:H:240:SER:HA	1:H:286:TYR:CD1	2.54	0.42
1:J:247:VAL:O	1:J:248:SER:HB3	2.19	0.42
1:K:158:HIS:HA	1:K:159:PRO:HD2	1.88	0.42
1:A:22:GLY:HA3	1:A:64:ASN:HB3	2.00	0.42
1:A:234:TYR:O	1:A:279:LEU:HD23	2.19	0.42
1:D:26:GLU:HG2	1:D:27:HIS:N	2.33	0.42
1:D:238:THR:HG21	1:D:304:PHE:CZ	2.53	0.42
1:E:45:ASP:OD2	1:E:45:ASP:C	2.63	0.42
1:G:32:ILE:HD13	1:G:32:ILE:C	2.44	0.42
1:G:64:ASN:C	1:G:64:ASN:HD22	2.28	0.42
1:L:110:ILE:O	1:L:114:ARG:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:399:SER:C	1:L:401:ASP:H	2.27	0.42
1:A:328:VAL:O	1:A:330:ALA:N	2.51	0.42
1:B:299:LEU:HD13	1:B:454:VAL:HG21	2.01	0.42
1:G:32:ILE:HD11	1:G:104:PHE:HB3	2.00	0.42
1:I:4:ARG:HG3	1:I:5:ILE:N	2.34	0.42
1:B:62:VAL:HA	1:B:63:PRO:HD3	1.90	0.42
1:B:105:GLY:H	1:B:108:GLU:HB2	1.85	0.42
1:B:220:ARG:HA	1:B:220:ARG:HD2	1.78	0.42
1:C:282:TRP:O	1:C:283:ASN:HB2	2.19	0.42
1:E:403:LYS:HB2	1:E:484:GLU:CA	2.48	0.42
1:H:124:ILE:HG21	1:H:198:MET:HE1	2.01	0.42
1:J:4:ARG:HB3	1:J:367:GLU:HB2	2.01	0.42
1:C:288:VAL:HG12	1:C:290:ASP:H	1.84	0.42
1:E:279:LEU:HD13	1:E:282:TRP:CD1	2.54	0.42
1:G:220[A]:ARG:HA	1:G:220[A]:ARG:HD2	1.88	0.42
1:I:174:TYR:CE2	1:I:212:CYS:HB3	2.55	0.42
1:J:121:TYR:CD1	1:J:121:TYR:C	2.98	0.42
1:L:88:ARG:HA	1:L:89:PRO:HD3	1.84	0.42
1:L:450:ASN:N	1:L:451:PRO:HD2	2.35	0.42
1:B:60:ILE:HD12	1:B:350:PHE:HB3	2.02	0.42
1:C:88:ARG:HA	1:C:89:PRO:HD3	1.91	0.42
1:C:235:HIS:CD2	1:C:281:GLU:HB2	2.55	0.42
1:E:437:LEU:HB2	1:E:456:ILE:HG13	2.01	0.42
1:G:434:VAL:HG22	1:G:479:ILE:HG12	2.02	0.42
1:I:9:PRO:HA	1:I:362:VAL:HG21	2.01	0.42
1:I:446:ASN:OD1	1:I:454:VAL:HG22	2.19	0.42
1:J:101:THR:O	1:J:102:ASN:HB2	2.20	0.42
1:K:73:VAL:C	1:K:75:ASN:N	2.74	0.42
1:L:135:LEU:O	1:L:139:GLU:HG3	2.20	0.42
1:A:36:ILE:HG23	1:A:328:VAL:HG21	2.02	0.42
1:A:430:LYS:NZ	1:A:484:GLU:OE1	2.53	0.42
1:C:125:ASN:HD22	1:C:126:MET:N	2.18	0.42
1:D:52:ASP:OD1	1:D:52:ASP:N	2.52	0.42
1:D:217:TRP:O	1:D:221:VAL:HG23	2.20	0.42
1:D:273:ARG:NH1	1:D:273:ARG:HG3	2.34	0.42
1:D:428:GLY:HA3	1:D:464:ASP:HA	2.01	0.42
1:E:239:GLY:HA3	1:E:240:SER:OG	2.20	0.42
1:E:309:LEU:O	1:E:313:GLN:HG3	2.20	0.42
1:G:22:GLY:HA3	1:G:64:ASN:HB3	2.02	0.42
1:G:463:VAL:CG1	1:G:464:ASP:N	2.83	0.42
1:I:380:ASN:OD1	1:I:382:MET:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:174:TYR:CE2	1:J:212:CYS:HB3	2.55	0.42
1:K:235:HIS:CE1	1:K:280:ASP:OD1	2.73	0.42
1:C:219:LEU:HD13	1:D:215:PRO:HB2	2.01	0.42
1:D:81:GLY:HA2	1:D:88:ARG:HD3	2.02	0.42
1:E:401:ASP:HB2	1:E:402:GLY:HA2	2.01	0.42
1:G:282:TRP:O	1:G:283:ASN:HB2	2.19	0.42
1:I:125:ASN:OD1	1:I:125:ASN:C	2.63	0.42
1:I:255:GLU:HG3	1:J:262:LYS:CE	2.50	0.42
1:J:4:ARG:NH2	1:J:423:ARG:HG3	2.35	0.42
1:K:448:MET:HB3	1:K:448:MET:HE2	1.60	0.42
1:L:467:PHE:CD1	1:L:468:GLU:N	2.88	0.42
1:B:239:GLY:CA	1:B:378:PHE:H	2.33	0.42
1:B:243:TYR:HD1	1:B:300:LYS:CB	2.33	0.42
1:D:60:ILE:HD11	1:D:351:GLU:CA	2.50	0.42
1:E:374:GLU:HG2	1:E:385:SER:CB	2.48	0.42
1:E:403:LYS:HZ2	1:E:403:LYS:H	1.67	0.42
1:G:9:PRO:HA	1:G:362:VAL:HG11	2.02	0.42
1:G:262:LYS:HG3	1:H:259:GLY:HA2	2.02	0.42
1:I:3:TYR:CD2	1:I:3:TYR:N	2.87	0.42
1:J:373:ILE:H	1:J:373:ILE:HG13	1.66	0.42
1:K:325:ALA:HA	1:K:326:GLN:HA	1.75	0.42
1:L:311:LEU:O	1:L:314:LYS:HB2	2.20	0.42
1:A:209:ALA:HB2	1:A:229:ILE:HG21	2.02	0.41
1:A:330:ALA:O	1:A:331:LEU:C	2.62	0.41
1:E:130:THR:HB	1:E:133:GLU:H	1.84	0.41
1:E:238:THR:OG1	1:E:239:GLY:N	2.53	0.41
1:H:154:ARG:HG2	1:H:159:PRO:HA	2.03	0.41
1:L:6:VAL:HG22	1:L:423:ARG:HB3	2.02	0.41
1:L:235:HIS:CE1	1:L:280:ASP:OD1	2.73	0.41
1:L:281:GLU:HG2	1:L:325:ALA:HB2	2.02	0.41
1:A:266:MET:HE1	1:B:263:LEU:HD13	2.02	0.41
1:A:378:PHE:CG	1:A:379:ILE:N	2.88	0.41
1:E:130:THR:HG22	1:E:131:LEU:N	2.35	0.41
1:E:141:CYS:HB3	1:E:164:VAL:CG1	2.49	0.41
1:E:192:LYS:O	1:E:196:LYS:HB2	2.20	0.41
1:E:372:ASN:HD22	1:E:388:ASN:H	1.65	0.41
1:G:403:LYS:HB2	1:G:484:GLU:HA	2.01	0.41
1:H:77:HIS:NE2	1:J:132:ASP:OD2	2.51	0.41
1:H:105:GLY:O	1:H:107:ASP:N	2.53	0.41
1:I:326:GLN:HB2	1:I:330:ALA:O	2.21	0.41
1:J:182:MET:HB3	1:J:186:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:398:ILE:HD13	1:J:398:ILE:HA	1.94	0.41
1:K:317:ASP:OD1	1:K:317:ASP:N	2.52	0.41
1:L:328:VAL:HG22	1:L:334:ILE:HB	2.02	0.41
1:B:157:GLY:O	1:B:159:PRO:HD3	2.20	0.41
1:D:24:PHE:HB3	1:D:324:LEU:O	2.21	0.41
1:D:85:LYS:HE2	1:D:108:GLU:OE2	2.20	0.41
1:D:122:ILE:HD11	1:D:167:TRP:CZ3	2.55	0.41
1:E:60:ILE:O	1:E:354:VAL:HG11	2.21	0.41
1:E:348:LYS:HB3	1:E:437:LEU:HD13	2.01	0.41
1:F:138:LEU:HD22	1:F:198:MET:HE3	2.02	0.41
1:F:460:THR:O	1:F:461:ILE:HD12	2.20	0.41
1:G:451:PRO:HB2	1:G:452:ASN:H	1.59	0.41
1:I:284:VAL:CG1	1:I:286:TYR:HE2	2.33	0.41
1:K:427:LEU:HD22	1:K:430:LYS:HD3	2.01	0.41
1:C:238:THR:O	1:C:285:TRP:N	2.44	0.41
1:D:319:VAL:O	1:D:319:VAL:HG22	2.19	0.41
1:E:225:ALA:O	1:E:229:ILE:HG12	2.21	0.41
1:H:239:GLY:HA2	1:H:286:TYR:HB3	2.01	0.41
1:H:359:GLU:O	1:H:360:LYS:HG3	2.20	0.41
1:K:262:LYS:O	1:K:266:MET:HG3	2.20	0.41
1:L:171:ASN:ND2	1:L:172:GLU:HG3	2.36	0.41
1:D:26:GLU:HG3	1:D:69:GLY:CA	2.45	0.41
1:D:359:GLU:HG3	1:D:400:GLU:CG	2.48	0.41
1:D:465:THR:O	1:D:466:GLU:HB2	2.19	0.41
1:E:125:ASN:OD1	1:E:125:ASN:C	2.62	0.41
1:L:282:TRP:CZ3	1:L:308:VAL:HG11	2.55	0.41
1:A:291:ASN:OD1	1:A:291:ASN:N	2.51	0.41
1:A:335:HIS:O	1:A:342:ILE:N	2.50	0.41
1:C:47:ARG:HE	1:C:47:ARG:HB2	1.65	0.41
1:C:122:ILE:CG1	1:C:167:TRP:CZ3	3.03	0.41
1:C:285:TRP:O	1:C:378:PHE:HA	2.21	0.41
1:D:359:GLU:CG	1:D:400:GLU:HG2	2.47	0.41
1:E:348:LYS:HB3	1:E:437:LEU:CD1	2.51	0.41
1:E:391:PHE:CD1	1:E:413:ARG:HG2	2.56	0.41
1:G:254:LYS:HG3	1:G:311:LEU:HD11	2.03	0.41
1:H:4:ARG:HG3	1:H:4:ARG:NH1	2.17	0.41
1:I:41:SER:HA	1:I:42:PRO:HD2	1.83	0.41
1:A:122:ILE:CD1	1:A:137:TRP:CZ2	3.04	0.41
1:B:451:PRO:HG2	1:B:452:ASN:HD21	1.86	0.41
1:C:202:ASP:HA	1:C:203:PRO:HD3	1.89	0.41
1:C:407:ILE:O	1:C:478:VAL:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:74:SER:HA	1:D:125:ASN:OD1	2.21	0.41
1:G:163:ASN:O	1:G:165:LYS:HD2	2.20	0.41
1:G:214:ASP:HA	1:G:215:PRO:HD2	1.88	0.41
1:G:398:ILE:HG13	1:G:404:LYS:O	2.21	0.41
1:I:283:ASN:HB2	1:I:325:ALA:O	2.20	0.41
1:K:32:ILE:HG22	1:K:33:TYR:N	2.35	0.41
1:K:450:ASN:HB3	1:K:453:VAL:HG23	2.02	0.41
1:L:192:LYS:O	1:L:196:LYS:HB3	2.20	0.41
1:L:330:ALA:O	1:L:331:LEU:C	2.62	0.41
1:A:262:LYS:NZ	1:A:262:LYS:CB	2.71	0.41
1:B:434:VAL:HG23	1:B:461:ILE:HG12	2.02	0.41
1:C:24:PHE:HD1	1:C:25:THR:H	1.68	0.41
1:C:314:LYS:HE2	1:C:394:ALA:O	2.21	0.41
1:C:406:PHE:CD2	1:C:406:PHE:N	2.88	0.41
1:G:472:LYS:HE3	1:G:472:LYS:HB2	1.94	0.41
1:A:28:LEU:HD23	1:A:29:GLY:N	2.36	0.41
1:A:160:GLU:HA	1:A:161:PRO:HD3	1.96	0.41
1:A:319:VAL:O	1:A:319:VAL:HG22	2.20	0.41
1:C:74:SER:HA	1:C:125:ASN:ND2	2.36	0.41
1:D:17:SER:O	1:D:18:ARG:C	2.64	0.41
1:D:219:LEU:HD23	1:D:219:LEU:HA	1.90	0.41
1:E:25:THR:O	1:E:25:THR:CG2	2.69	0.41
1:E:28:LEU:HD13	1:E:330:ALA:HB1	2.03	0.41
1:E:208:ILE:HG13	1:E:231:PHE:CD2	2.56	0.41
1:E:422:ILE:HB	1:E:467:PHE:CE2	2.56	0.41
1:E:428:GLY:HA3	1:E:429:GLN:C	2.45	0.41
1:F:24:PHE:CD2	1:F:326:GLN:HG2	2.55	0.41
1:F:283:ASN:CG	1:F:284:VAL:H	2.29	0.41
1:G:401:ASP:N	1:G:402:GLY:HA2	2.35	0.41
1:H:176:GLU:H	1:H:176:GLU:HG3	1.52	0.41
1:I:401:ASP:HB2	1:I:403:LYS:H	1.86	0.41
1:K:280:ASP:HA	1:K:323:ASN:HD22	1.86	0.41
1:L:26:GLU:HG3	1:L:28:LEU:HB2	2.02	0.41
1:D:147:THR:O	1:D:148:TYR:C	2.64	0.41
1:D:325:ALA:HA	1:D:326:GLN:HA	1.78	0.41
1:F:163:ASN:HD22	1:F:165:LYS:HE2	1.86	0.41
1:H:318:ILE:HG22	1:H:319:VAL:HG12	2.03	0.41
1:I:131:LEU:CD2	1:I:135:LEU:CD2	2.95	0.41
1:I:451:PRO:C	1:I:453:VAL:H	2.29	0.41
1:J:19:HIS:C	1:J:21:TYR:H	2.29	0.41
1:K:239:GLY:CA	1:K:240:SER:OG	2.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:THR:O	1:C:25:THR:HG23	2.20	0.40
1:C:217:TRP:O	1:C:218:ASN:C	2.64	0.40
1:D:246:THR:OG1	1:D:300:LYS:HE2	2.21	0.40
1:E:171:ASN:O	1:E:172:GLU:C	2.64	0.40
1:E:235:HIS:HD2	1:E:281:GLU:OE1	2.05	0.40
1:G:422:ILE:HB	1:G:467:PHE:CE2	2.56	0.40
1:H:236:PHE:CG	1:H:253:LEU:HD13	2.56	0.40
1:I:254:LYS:O	1:I:258:ILE:HG13	2.21	0.40
1:I:266:MET:HE1	1:J:263:LEU:HD22	2.02	0.40
1:J:401:ASP:OD1	1:J:401:ASP:C	2.64	0.40
1:K:16:ILE:HD12	1:K:361:LEU:HB2	2.03	0.40
1:K:208:ILE:HA	1:K:231:PHE:HB2	2.03	0.40
1:L:352:LEU:O	1:L:356:HIS:HB2	2.21	0.40
1:L:362:VAL:HG23	1:L:398:ILE:HG13	2.03	0.40
1:B:45:ASP:HB3	1:B:51:LYS:HD3	2.04	0.40
1:C:125:ASN:C	1:C:125:ASN:HD22	2.28	0.40
1:D:88:ARG:HA	1:D:89:PRO:HD3	1.91	0.40
1:E:268:ASP:O	1:E:269:THR:C	2.63	0.40
1:I:19:HIS:HD2	1:I:64:ASN:OD1	2.04	0.40
1:J:282:TRP:O	1:J:283:ASN:HB2	2.21	0.40
1:K:256:ARG:O	1:K:260:VAL:HG23	2.21	0.40
1:L:66:ARG:HA	1:L:121:TYR:O	2.21	0.40
1:L:199:LYS:HE2	1:L:205:ILE:O	2.20	0.40
1:L:295:GLU:HG2	1:L:297:TYR:CE1	2.56	0.40
1:A:219:LEU:HD11	1:B:215:PRO:HB2	2.03	0.40
1:A:243:TYR:CZ	1:A:247:VAL:HG21	2.56	0.40
1:B:310:VAL:O	1:B:311:LEU:C	2.64	0.40
1:D:231:PHE:HA	1:D:276:LYS:O	2.21	0.40
1:F:225:ALA:C	1:F:227:ASP:H	2.29	0.40
1:I:121:TYR:C	1:I:121:TYR:CD1	2.99	0.40
1:J:171:ASN:HD22	1:J:178:GLN:HE22	1.69	0.40
1:E:141:CYS:HB3	1:E:164:VAL:HG13	2.02	0.40
1:G:121:TYR:CD1	1:G:121:TYR:C	2.98	0.40
1:H:146:ASN:O	1:H:147:THR:C	2.64	0.40
1:I:32:ILE:HD11	1:I:104:PHE:CG	2.57	0.40
1:L:23:HIS:O	1:L:65:LEU:HA	2.22	0.40
1:L:235:HIS:CD2	1:L:281:GLU:HB2	2.57	0.40
1:A:428:GLY:HA2	1:A:429:GLN:HA	1.88	0.40
1:C:262:LYS:HD2	1:D:259:GLY:CA	2.51	0.40
1:E:183:THR:H	1:E:186:GLU:CD	2.29	0.40
1:F:77:HIS:NE2	1:F:128:THR:CG2	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:121:TYR:CD1	1:F:121:TYR:C	2.99	0.40
1:F:140:TYR:O	1:F:153:ARG:HD3	2.21	0.40
1:F:295:GLU:HG2	1:F:297:TYR:CZ	2.56	0.40
1:F:295:GLU:HA	1:F:296:PRO:HD3	1.89	0.40
1:G:67:TRP:CB	1:G:109:PHE:CE1	3.05	0.40
1:J:464:ASP:C	1:J:466:GLU:N	2.78	0.40
1:K:326:GLN:O	1:K:332:GLY:HA2	2.22	0.40
1:K:424:VAL:HG22	1:K:427:LEU:HB2	2.03	0.40
1:L:218:ASN:HB2	1:L:263:LEU:HD23	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	481/484 (99%)	434 (90%)	42 (9%)	5 (1%)	12	45
1	B	481/484 (99%)	435 (90%)	39 (8%)	7 (2%)	8	35
1	C	481/484 (99%)	433 (90%)	42 (9%)	6 (1%)	10	40
1	D	481/484 (99%)	434 (90%)	38 (8%)	9 (2%)	6	30
1	E	481/484 (99%)	431 (90%)	41 (8%)	9 (2%)	6	30
1	F	481/484 (99%)	433 (90%)	39 (8%)	9 (2%)	6	30
1	G	482/484 (100%)	424 (88%)	47 (10%)	11 (2%)	5	25
1	H	481/484 (99%)	418 (87%)	53 (11%)	10 (2%)	5	27
1	I	481/484 (99%)	426 (89%)	42 (9%)	13 (3%)	4	22
1	J	479/484 (99%)	416 (87%)	50 (10%)	13 (3%)	4	22
1	K	481/484 (99%)	433 (90%)	42 (9%)	6 (1%)	10	40
1	L	482/484 (100%)	420 (87%)	54 (11%)	8 (2%)	7	32
All	All	5772/5808 (99%)	5137 (89%)	529 (9%)	106 (2%)	6	31

All (106) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	450	ASN
1	B	227	ASP
1	B	428	GLY
1	D	450	ASN
1	D	465	THR
1	E	428	GLY
1	E	466	GLU
1	F	286	TYR
1	G	451	PRO
1	G	452	ASN
1	I	272	LYS
1	I	450	ASN
1	I	465	THR
1	J	279	LEU
1	J	374	GLU
1	K	428	GLY
1	L	283	ASN
1	A	247	VAL
1	A	283	ASN
1	C	248	SER
1	D	363	LYS
1	E	248	SER
1	E	329	ASN
1	F	247	VAL
1	G	474	PHE
1	H	29	GLY
1	H	106	THR
1	H	339	ASP
1	H	401	ASP
1	H	428	GLY
1	I	61	LYS
1	I	172	GLU
1	I	248	SER
1	K	449	GLU
1	L	172	GLU
1	L	356	HIS
1	A	172	GLU
1	B	27	HIS
1	B	248	SER
1	B	286	TYR
1	C	283	ASN
1	C	286	TYR

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Mol	Chain	Res	Type
1	D	466	GLU
1	E	196	LYS
1	F	74	SER
1	F	440	PRO
1	F	465	THR
1	G	172	GLU
1	G	247	VAL
1	H	400	GLU
1	I	247	VAL
1	I	286	TYR
1	I	329	ASN
1	I	466	GLU
1	J	32	ILE
1	J	305	ALA
1	J	440	PRO
1	J	450	ASN
1	L	47	ARG
1	A	329	ASN
1	C	4	ARG
1	C	50	ARG
1	D	227	ASP
1	D	459	GLU
1	F	283	ASN
1	F	329	ASN
1	F	448	MET
1	G	286	TYR
1	H	329	ASN
1	H	450	ASN
1	I	399	SER
1	J	74	SER
1	J	286	TYR
1	J	329	ASN
1	J	356	HIS
1	K	74	SER
1	K	286	TYR
1	L	248	SER
1	L	378	PHE
1	B	50	ARG
1	B	290	ASP
1	C	241	GLU
1	D	18	ARG
1	D	464	ASP

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Mol	Chain	Res	Type
1	E	18	ARG
1	E	331	LEU
1	F	449	GLU
1	G	329	ASN
1	I	85	LYS
1	I	451	PRO
1	J	248	SER
1	L	279	LEU
1	D	286	TYR
1	G	46	GLU
1	G	453	VAL
1	G	455	ASP
1	H	440	PRO
1	J	401	ASP
1	H	340	GLY
1	E	379	ILE
1	G	424	VAL
1	J	63	PRO
1	K	14	LYS
1	L	463	VAL
1	E	145	GLY
1	K	450	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	419/420 (100%)	370 (88%)	49 (12%)	5	23
1	B	419/420 (100%)	356 (85%)	63 (15%)	3	14
1	C	419/420 (100%)	362 (86%)	57 (14%)	3	17
1	D	419/420 (100%)	366 (87%)	53 (13%)	4	20
1	E	419/420 (100%)	361 (86%)	58 (14%)	3	17
1	F	419/420 (100%)	365 (87%)	54 (13%)	4	19
1	G	420/420 (100%)	355 (84%)	65 (16%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	419/420 (100%)	353 (84%)	66 (16%)	2	13
1	I	419/420 (100%)	367 (88%)	52 (12%)	4	20
1	J	417/420 (99%)	359 (86%)	58 (14%)	3	17
1	K	419/420 (100%)	361 (86%)	58 (14%)	3	17
1	L	420/420 (100%)	367 (87%)	53 (13%)	4	20
All	All	5028/5040 (100%)	4342 (86%)	686 (14%)	3	17

All (686) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	32	ILE
1	A	47	ARG
1	A	51	LYS
1	A	59	ARG
1	A	61	LYS
1	A	64	ASN
1	A	122	ILE
1	A	123	SER
1	A	131	LEU
1	A	144	LYS
1	A	160	GLU
1	A	163	ASN
1	A	164	VAL
1	A	176	GLU
1	A	179	VAL
1	A	199	LYS
1	A	206	LYS
1	A	216	ILE
1	A	261	LYS
1	A	262	LYS
1	A	263	LEU
1	A	279	LEU
1	A	287	ARG
1	A	291	ASN
1	A	292	LYS
1	A	319	VAL
1	A	328	VAL
1	A	353	ILE
1	A	359	GLU

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Mol	Chain	Res	Type
1	A	362	VAL
1	A	373	ILE
1	A	379	ILE
1	A	382	MET
1	A	403	LYS
1	A	409	VAL
1	A	415	GLU
1	A	418	LEU
1	A	424	VAL
1	A	425	GLU
1	A	427	LEU
1	A	430	LYS
1	A	454	VAL
1	A	456	ILE
1	A	460	THR
1	A	465	THR
1	A	478	VAL
1	A	481	VAL
1	A	484	GLU
1	B	25	THR
1	B	32	ILE
1	B	46	GLU
1	B	47	ARG
1	B	60	ILE
1	B	73	VAL
1	B	111	GLU
1	B	114	ARG
1	B	126	MET
1	B	128	THR
1	B	131	LEU
1	B	135	LEU
1	B	144	LYS
1	B	146	ASN
1	B	147	THR
1	B	155	LYS
1	B	164	VAL
1	B	165	LYS
1	B	179	VAL
1	B	189	ARG
1	B	196	LYS
1	B	199	LYS
1	B	200	VAL

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Mol	Chain	Res	Type
1	B	216	ILE
1	B	241	GLU
1	B	247	VAL
1	B	248	SER
1	B	262	LYS
1	B	277	ILE
1	B	279	LEU
1	B	287	ARG
1	B	288	VAL
1	B	291	ASN
1	B	292	LYS
1	B	293	LEU
1	B	295	GLU
1	B	300	LYS
1	B	319	VAL
1	B	353	ILE
1	B	359	GLU
1	B	362	VAL
1	B	364	THR
1	B	370	THR
1	B	401	ASP
1	B	403	LYS
1	B	409	VAL
1	B	415	GLU
1	B	419	LYS
1	B	422	ILE
1	B	424	VAL
1	B	427	LEU
1	B	430	LYS
1	B	431	LYS
1	B	433	THR
1	B	445	ARG
1	B	449	GLU
1	B	452	ASN
1	B	454	VAL
1	B	462	THR
1	B	465	THR
1	B	472	LYS
1	B	478	VAL
1	B	483	LEU
1	C	7	VAL
1	C	30	ARG

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Mol	Chain	Res	Type
1	C	32	ILE
1	C	47	ARG
1	C	60	ILE
1	C	64	ASN
1	C	86	ASP
1	C	87	GLN
1	C	121	TYR
1	C	122	ILE
1	C	128	THR
1	C	131	LEU
1	C	132	ASP
1	C	135	LEU
1	C	144	LYS
1	C	147	THR
1	C	164	VAL
1	C	171	ASN
1	C	176	GLU
1	C	179	VAL
1	C	185	ASP
1	C	189	ARG
1	C	199	LYS
1	C	204	THR
1	C	206	LYS
1	C	224	GLU
1	C	242	ASP
1	C	247	VAL
1	C	261	LYS
1	C	262	LYS
1	C	263	LEU
1	C	264	ILE
1	C	279	LEU
1	C	287	ARG
1	C	291	ASN
1	C	293	LEU
1	C	294	GLU
1	C	314	LYS
1	C	353	ILE
1	C	359	GLU
1	C	370	THR
1	C	373	ILE
1	C	397	SER
1	C	400	GLU

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Mol	Chain	Res	Type
1	C	401	ASP
1	C	404	LYS
1	C	409	VAL
1	C	415	GLU
1	C	418	LEU
1	C	424	VAL
1	C	427	LEU
1	C	452	ASN
1	C	454	VAL
1	C	465	THR
1	C	478	VAL
1	C	481	VAL
1	C	483	LEU
1	D	10	LYS
1	D	32	ILE
1	D	43	LEU
1	D	60	ILE
1	D	79	GLU
1	D	97	GLN
1	D	111	GLU
1	D	121	TYR
1	D	122	ILE
1	D	131	LEU
1	D	135	LEU
1	D	151	GLN
1	D	163	ASN
1	D	164	VAL
1	D	179	VAL
1	D	186	GLU
1	D	189	ARG
1	D	192	LYS
1	D	216	ILE
1	D	223	GLN
1	D	241	GLU
1	D	261	LYS
1	D	262	LYS
1	D	263	LEU
1	D	279	LEU
1	D	287	ARG
1	D	293	LEU
1	D	319	VAL
1	D	328	VAL

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Mol	Chain	Res	Type
1	D	341	LEU
1	D	353	ILE
1	D	359	GLU
1	D	362	VAL
1	D	367	GLU
1	D	370	THR
1	D	372	ASN
1	D	373	ILE
1	D	379	ILE
1	D	401	ASP
1	D	403	LYS
1	D	404	LYS
1	D	409	VAL
1	D	415	GLU
1	D	423	ARG
1	D	424	VAL
1	D	427	LEU
1	D	433	THR
1	D	458	SER
1	D	465	THR
1	D	477	SER
1	D	478	VAL
1	D	481	VAL
1	D	484	GLU
1	E	6	VAL
1	E	12	VAL
1	E	25	THR
1	E	28	LEU
1	E	32	ILE
1	E	46	GLU
1	E	54	LEU
1	E	55	GLU
1	E	59	ARG
1	E	60	ILE
1	E	79	GLU
1	E	86	ASP
1	E	87	GLN
1	E	121	TYR
1	E	122	ILE
1	E	126	MET
1	E	128	THR
1	E	130	THR

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Mol	Chain	Res	Type
1	E	131	LEU
1	E	135	LEU
1	E	151	GLN
1	E	164	VAL
1	E	165	LYS
1	E	179	VAL
1	E	216	ILE
1	E	254	LYS
1	E	262	LYS
1	E	279	LEU
1	E	286	TYR
1	E	287	ARG
1	E	288	VAL
1	E	291	ASN
1	E	293	LEU
1	E	319	VAL
1	E	348	LYS
1	E	355	ASN
1	E	356	HIS
1	E	359	GLU
1	E	363	LYS
1	E	370	THR
1	E	373	ILE
1	E	386	VAL
1	E	397	SER
1	E	398	ILE
1	E	401	ASP
1	E	403	LYS
1	E	409	VAL
1	E	415	GLU
1	E	419	LYS
1	E	420	VAL
1	E	422	ILE
1	E	427	LEU
1	E	433	THR
1	E	447	THR
1	E	449	GLU
1	E	454	VAL
1	E	459	GLU
1	E	481	VAL
1	F	28	LEU
1	F	47	ARG

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Mol	Chain	Res	Type
1	F	51	LYS
1	F	55	GLU
1	F	86	ASP
1	F	103	ARG
1	F	121	TYR
1	F	122	ILE
1	F	128	THR
1	F	130	THR
1	F	131	LEU
1	F	135	LEU
1	F	144	LYS
1	F	147	THR
1	F	155	LYS
1	F	160	GLU
1	F	164	VAL
1	F	179	VAL
1	F	196	LYS
1	F	198	MET
1	F	199	LYS
1	F	216	ILE
1	F	254	LYS
1	F	272	LYS
1	F	279	LEU
1	F	291	ASN
1	F	293	LEU
1	F	314	LYS
1	F	316	SER
1	F	319	VAL
1	F	353	ILE
1	F	359	GLU
1	F	362	VAL
1	F	367	GLU
1	F	370	THR
1	F	373	ILE
1	F	379	ILE
1	F	387	GLU
1	F	398	ILE
1	F	403	LYS
1	F	409	VAL
1	F	415	GLU
1	F	422	ILE
1	F	424	VAL

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Mol	Chain	Res	Type
1	F	427	LEU
1	F	441	ASP
1	F	443	ASN
1	F	450	ASN
1	F	453	VAL
1	F	454	VAL
1	F	457	THR
1	F	461	ILE
1	F	481	VAL
1	F	484	GLU
1	G	4	ARG
1	G	32	ILE
1	G	46	GLU
1	G	47	ARG
1	G	49	PHE
1	G	59	ARG
1	G	64	ASN
1	G	75	ASN
1	G	80	ASP
1	G	86	ASP
1	G	122	ILE
1	G	123	SER
1	G	128	THR
1	G	130	THR
1	G	131	LEU
1	G	135	LEU
1	G	147	THR
1	G	151	GLN
1	G	160	GLU
1	G	164	VAL
1	G	165	LYS
1	G	172	GLU
1	G	179	VAL
1	G	192	LYS
1	G	204	THR
1	G	241	GLU
1	G	248	SER
1	G	249	THR
1	G	258	ILE
1	G	262	LYS
1	G	263	LEU
1	G	271	ARG

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Mol	Chain	Res	Type
1	G	273	ARG
1	G	279	LEU
1	G	287	ARG
1	G	293	LEU
1	G	314	LYS
1	G	319	VAL
1	G	321	LEU
1	G	339	ASP
1	G	341	LEU
1	G	359	GLU
1	G	360	LYS
1	G	362	VAL
1	G	370	THR
1	G	373	ILE
1	G	381	LYS
1	G	398	ILE
1	G	403	LYS
1	G	409	VAL
1	G	415	GLU
1	G	423	ARG
1	G	424	VAL
1	G	427	LEU
1	G	430	LYS
1	G	452	ASN
1	G	457	THR
1	G	462	THR
1	G	466	GLU
1	G	468	GLU
1	G	472	LYS
1	G	476	CYS
1	G	478	VAL
1	G	482	GLU
1	G	483	LEU
1	H	4	ARG
1	H	32	ILE
1	H	58	LYS
1	H	106	THR
1	H	114	ARG
1	H	122	ILE
1	H	123	SER
1	H	130	THR
1	H	131	LEU

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Mol	Chain	Res	Type
1	H	135	LEU
1	H	147	THR
1	H	151	GLN
1	H	160	GLU
1	H	164	VAL
1	H	169	ILE
1	H	179	VAL
1	H	186	GLU
1	H	189	ARG
1	H	192	LYS
1	H	199	LYS
1	H	200	VAL
1	H	216	ILE
1	H	220	ARG
1	H	229	ILE
1	H	240	SER
1	H	241	GLU
1	H	252	LEU
1	H	262	LYS
1	H	263	LEU
1	H	272	LYS
1	H	279	LEU
1	H	293	LEU
1	H	294	GLU
1	H	300	LYS
1	H	306	CYS
1	H	314	LYS
1	H	319	VAL
1	H	338	LYS
1	H	339	ASP
1	H	344	THR
1	H	356	HIS
1	H	359	GLU
1	H	362	VAL
1	H	370	THR
1	H	373	ILE
1	H	380	ASN
1	H	397	SER
1	H	398	ILE
1	H	400	GLU
1	H	401	ASP
1	H	403	LYS

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Mol	Chain	Res	Type
1	H	407	ILE
1	H	409	VAL
1	H	418	LEU
1	H	422	ILE
1	H	424	VAL
1	H	427	LEU
1	H	433	THR
1	H	448	MET
1	H	458	SER
1	H	459	GLU
1	H	460	THR
1	H	466	GLU
1	H	468	GLU
1	H	478	VAL
1	H	481	VAL
1	I	3	TYR
1	I	32	ILE
1	I	53	VAL
1	I	79	GLU
1	I	91	ARG
1	I	121	TYR
1	I	128	THR
1	I	131	LEU
1	I	144	LYS
1	I	147	THR
1	I	164	VAL
1	I	179	VAL
1	I	192	LYS
1	I	199	LYS
1	I	206	LYS
1	I	213	ASP
1	I	216	ILE
1	I	227	ASP
1	I	254	LYS
1	I	261	LYS
1	I	262	LYS
1	I	263	LEU
1	I	273	ARG
1	I	279	LEU
1	I	287	ARG
1	I	293	LEU
1	I	319	VAL

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Mol	Chain	Res	Type
1	I	324	LEU
1	I	338	LYS
1	I	343	LEU
1	I	353	ILE
1	I	359	GLU
1	I	362	VAL
1	I	370	THR
1	I	386	VAL
1	I	401	ASP
1	I	405	LEU
1	I	415	GLU
1	I	418	LEU
1	I	424	VAL
1	I	427	LEU
1	I	447	THR
1	I	448	MET
1	I	449	GLU
1	I	450	ASN
1	I	455	ASP
1	I	460	THR
1	I	463	VAL
1	I	477	SER
1	I	478	VAL
1	I	479	ILE
1	I	481	VAL
1	J	7	VAL
1	J	39	GLU
1	J	47	ARG
1	J	49	PHE
1	J	51	LYS
1	J	53	VAL
1	J	60	ILE
1	J	79	GLU
1	J	121	TYR
1	J	122	ILE
1	J	126	MET
1	J	131	LEU
1	J	135	LEU
1	J	147	THR
1	J	160	GLU
1	J	164	VAL
1	J	171	ASN

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Mol	Chain	Res	Type
1	J	179	VAL
1	J	186	GLU
1	J	196	LYS
1	J	204	THR
1	J	206	LYS
1	J	220	ARG
1	J	227	ASP
1	J	261	LYS
1	J	262	LYS
1	J	263	LEU
1	J	272	LYS
1	J	279	LEU
1	J	287	ARG
1	J	291	ASN
1	J	292	LYS
1	J	338	LYS
1	J	359	GLU
1	J	362	VAL
1	J	363	LYS
1	J	370	THR
1	J	373	ILE
1	J	379	ILE
1	J	380	ASN
1	J	386	VAL
1	J	398	ILE
1	J	409	VAL
1	J	413	ARG
1	J	415	GLU
1	J	423	ARG
1	J	424	VAL
1	J	427	LEU
1	J	447	THR
1	J	449	GLU
1	J	454	VAL
1	J	457	THR
1	J	459	GLU
1	J	461	ILE
1	J	472	LYS
1	J	477	SER
1	J	478	VAL
1	J	481	VAL
1	K	2	SER

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Mol	Chain	Res	Type
1	K	4	ARG
1	K	5	ILE
1	K	25	THR
1	K	32	ILE
1	K	45	ASP
1	K	50	ARG
1	K	54	LEU
1	K	59	ARG
1	K	64	ASN
1	K	79	GLU
1	K	85	LYS
1	K	87	GLN
1	K	114	ARG
1	K	116	ILE
1	K	121	TYR
1	K	131	LEU
1	K	135	LEU
1	K	155	LYS
1	K	164	VAL
1	K	179	VAL
1	K	186	GLU
1	K	189	ARG
1	K	254	LYS
1	K	255	GLU
1	K	261	LYS
1	K	262	LYS
1	K	279	LEU
1	K	287	ARG
1	K	291	ASN
1	K	293	LEU
1	K	319	VAL
1	K	353	ILE
1	K	355	ASN
1	K	359	GLU
1	K	362	VAL
1	K	369	GLU
1	K	373	ILE
1	K	382	MET
1	K	392	LEU
1	K	398	ILE
1	K	400	GLU
1	K	403	LYS

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Mol	Chain	Res	Type
1	K	404	LYS
1	K	405	LEU
1	K	409	VAL
1	K	415	GLU
1	K	424	VAL
1	K	427	LEU
1	K	447	THR
1	K	448	MET
1	K	454	VAL
1	K	462	THR
1	K	465	THR
1	K	472	LYS
1	K	477	SER
1	K	478	VAL
1	K	481	VAL
1	L	5	ILE
1	L	11	LYS
1	L	18	ARG
1	L	32	ILE
1	L	46	GLU
1	L	51	LYS
1	L	79	GLU
1	L	97	GLN
1	L	101	THR
1	L	131	LEU
1	L	135	LEU
1	L	147	THR
1	L	164	VAL
1	L	179	VAL
1	L	185	ASP
1	L	189	ARG
1	L	196	LYS
1	L	206	LYS
1	L	214	ASP
1	L	220	ARG
1	L	241	GLU
1	L	247	VAL
1	L	250	VAL
1	L	254	LYS
1	L	262	LYS
1	L	266	MET
1	L	287	ARG

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Mol	Chain	Res	Type
1	L	289	SER
1	L	292	LYS
1	L	293	LEU
1	L	353	ILE
1	L	355	ASN
1	L	359	GLU
1	L	364	THR
1	L	373	ILE
1	L	374	GLU
1	L	379	ILE
1	L	381	LYS
1	L	386	VAL
1	L	400	GLU
1	L	405	LEU
1	L	415	GLU
1	L	424	VAL
1	L	425	GLU
1	L	427	LEU
1	L	430	LYS
1	L	441	ASP
1	L	449	GLU
1	L	452	ASN
1	L	478	VAL
1	L	481	VAL
1	L	482	GLU
1	L	484	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (150) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	97	GLN
1	A	146	ASN
1	A	151	GLN
1	A	163	ASN
1	A	178	GLN
1	A	223	GLN
1	A	235	HIS
1	A	326	GLN
1	A	355	ASN
1	A	365	HIS
1	A	372	ASN

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Mol	Chain	Res	Type
1	A	429	GLN
1	A	469	HIS
1	B	19	HIS
1	B	64	ASN
1	B	97	GLN
1	B	102	ASN
1	B	142	ASN
1	B	151	GLN
1	B	158	HIS
1	B	163	ASN
1	B	323	ASN
1	B	329	ASN
1	B	365	HIS
1	B	372	ASN
1	B	452	ASN
1	C	97	GLN
1	C	125	ASN
1	C	142	ASN
1	C	163	ASN
1	C	178	GLN
1	C	235	HIS
1	C	291	ASN
1	C	323	ASN
1	C	326	GLN
1	C	372	ASN
1	D	19	HIS
1	D	23	HIS
1	D	64	ASN
1	D	97	GLN
1	D	163	ASN
1	D	178	GLN
1	D	235	HIS
1	D	291	ASN
1	D	323	ASN
1	D	372	ASN
1	D	450	ASN
1	D	469	HIS
1	E	19	HIS
1	E	23	HIS
1	E	64	ASN
1	E	71	ASN
1	E	97	GLN

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Mol	Chain	Res	Type
1	E	163	ASN
1	E	178	GLN
1	E	223	GLN
1	E	235	HIS
1	E	313	GLN
1	E	323	ASN
1	E	329	ASN
1	E	335	HIS
1	E	372	ASN
1	E	469	HIS
1	F	19	HIS
1	F	23	HIS
1	F	64	ASN
1	F	71	ASN
1	F	75	ASN
1	F	98	GLN
1	F	142	ASN
1	F	163	ASN
1	F	178	GLN
1	F	235	HIS
1	F	291	ASN
1	F	323	ASN
1	F	326	GLN
1	F	429	GLN
1	G	23	HIS
1	G	64	ASN
1	G	71	ASN
1	G	97	GLN
1	G	142	ASN
1	G	171	ASN
1	G	223	GLN
1	G	235	HIS
1	G	291	ASN
1	G	323	ASN
1	G	329	ASN
1	G	372	ASN
1	G	429	GLN
1	G	452	ASN
1	H	19	HIS
1	H	142	ASN
1	H	151	GLN
1	H	178	GLN

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Mol	Chain	Res	Type
1	H	235	HIS
1	H	283	ASN
1	H	323	ASN
1	H	365	HIS
1	H	372	ASN
1	H	380	ASN
1	I	19	HIS
1	I	64	ASN
1	I	71	ASN
1	I	75	ASN
1	I	102	ASN
1	I	136	HIS
1	I	142	ASN
1	I	178	GLN
1	I	323	ASN
1	I	365	HIS
1	I	388	ASN
1	J	64	ASN
1	J	97	GLN
1	J	98	GLN
1	J	142	ASN
1	J	158	HIS
1	J	171	ASN
1	J	178	GLN
1	J	291	ASN
1	J	329	ASN
1	J	372	ASN
1	J	380	ASN
1	J	452	ASN
1	J	469	HIS
1	K	19	HIS
1	K	75	ASN
1	K	142	ASN
1	K	163	ASN
1	K	223	GLN
1	K	291	ASN
1	K	329	ASN
1	K	355	ASN
1	K	372	ASN
1	K	443	ASN
1	L	19	HIS
1	L	64	ASN

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Mol	Chain	Res	Type
1	L	97	GLN
1	L	142	ASN
1	L	163	ASN
1	L	178	GLN
1	L	223	GLN
1	L	291	ASN
1	L	323	ASN
1	L	329	ASN
1	L	335	HIS
1	L	365	HIS
1	L	372	ASN
1	L	443	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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	483/484 (99%)	-0.36	4 (0%) 82 64	17, 38, 55, 63	6 (1%)
1	B	483/484 (99%)	-0.41	0 100 100	23, 35, 50, 68	5 (1%)
1	C	483/484 (99%)	-0.31	7 (1%) 73 51	21, 37, 57, 71	8 (1%)
1	D	483/484 (99%)	-0.35	5 (1%) 79 59	22, 37, 55, 68	11 (2%)
1	E	483/484 (99%)	-0.28	7 (1%) 73 51	21, 37, 60, 72	8 (1%)
1	F	483/484 (99%)	-0.26	6 (1%) 76 55	19, 39, 59, 69	14 (2%)
1	G	483/484 (99%)	-0.23	6 (1%) 76 55	17, 45, 59, 72	12 (2%)
1	H	483/484 (99%)	0.04	6 (1%) 76 55	29, 55, 68, 81	8 (1%)
1	I	483/484 (99%)	0.05	19 (3%) 43 24	8, 48, 75, 86	22 (4%)
1	J	481/484 (99%)	0.08	14 (2%) 53 31	8, 55, 78, 87	22 (4%)
1	K	483/484 (99%)	-0.21	11 (2%) 61 38	25, 45, 60, 79	13 (2%)
1	L	483/484 (99%)	-0.07	9 (1%) 66 43	23, 50, 77, 86	13 (2%)
All	All	5794/5808 (99%)	-0.19	94 (1%) 70 47	8, 44, 67, 87	142 (2%)

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	468	GLU	20.2
1	I	428	GLY	12.5
1	J	428	GLY	11.5
1	H	46	GLU	7.5
1	F	400	GLU	7.0
1	F	472	LYS	6.9
1	I	429	GLN	6.8
1	G	431	LYS	6.5
1	L	61	LYS	6.4
1	C	431	LYS	6.2
1	J	415	GLU	5.7

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Mol	Chain	Res	Type	RSRZ
1	J	429	GLN	5.5
1	L	272	LYS	5.1
1	J	403	LYS	5.1
1	D	363	LYS	5.0
1	J	241	GLU	5.0
1	K	51	LYS	4.9
1	J	55	GLU	4.9
1	C	403	LYS	4.9
1	K	46	GLU	4.7
1	L	55	GLU	4.7
1	I	348	LYS	4.7
1	J	46	GLU	4.6
1	D	46	GLU	4.5
1	E	431	LYS	4.5
1	H	11	LYS	4.5
1	E	11	LYS	4.4
1	D	419	LYS	4.4
1	I	484	GLU	4.3
1	I	480	GLU	4.3
1	I	430	LYS	4.2
1	I	303	ILE	4.2
1	J	465	THR	4.2
1	A	363	LYS	4.2
1	I	51	LYS	4.2
1	E	468	GLU	4.2
1	L	155	LYS	4.0
1	I	482	GLU	4.0
1	I	419	LYS	4.0
1	F	241	GLU	4.0
1	K	338	LYS	4.0
1	E	464	ASP	3.9
1	D	431	LYS	3.9
1	H	55	GLU	3.8
1	J	292	LYS	3.7
1	I	437	LEU	3.7
1	A	268	ASP	3.6
1	J	61	LYS	3.6
1	K	47	ARG	3.6
1	G	448	MET	3.6
1	J	144	LYS	3.5
1	G	51	LYS	3.4
1	F	416	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	J	151	GLN	3.4
1	K	55	GLU	3.4
1	K	160	GLU	3.3
1	C	338	LYS	3.3
1	I	381	LYS	3.3
1	I	403	LYS	3.1
1	J	367	GLU	3.0
1	L	419	LYS	3.0
1	A	403	LYS	3.0
1	C	419	LYS	3.0
1	E	472	LYS	2.9
1	F	431	LYS	2.9
1	I	363	LYS	2.9
1	K	483	LEU	2.9
1	L	165	LYS	2.8
1	K	360	LYS	2.8
1	L	403	LYS	2.7
1	H	337	GLU	2.7
1	E	286	TYR	2.6
1	I	176	GLU	2.5
1	K	484	GLU	2.5
1	L	472	LYS	2.5
1	H	53	VAL	2.4
1	C	40	GLY	2.4
1	H	398	ILE	2.4
1	I	46	GLU	2.4
1	G	11	LYS	2.4
1	K	86	ASP	2.3
1	D	472	LYS	2.3
1	G	337	GLU	2.3
1	I	292	LYS	2.2
1	L	51	LYS	2.2
1	G	165	LYS	2.2
1	I	369	GLU	2.2
1	J	327	LEU	2.1
1	C	292	LYS	2.1
1	C	484	GLU	2.1
1	K	363	LYS	2.0
1	F	419	LYS	2.0
1	E	430	LYS	2.0
1	A	337	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.