



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:51 AM UTC

PDB ID : 1XTC / pdb_00001xtc
Title : CHOLERA TOXIN
Authors : Zhang, R.-G.; Westbrook, E.
Deposited on : 1996-01-10
Resolution : 2.40 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

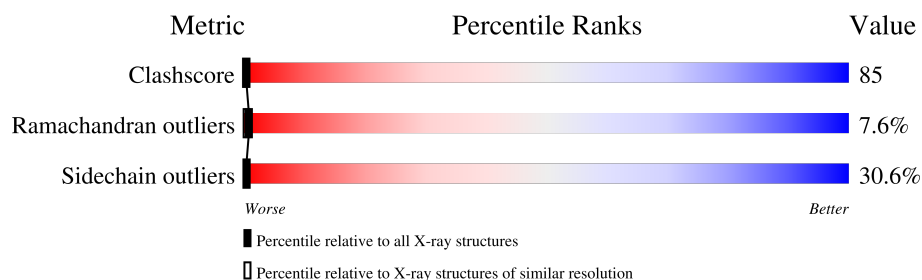
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	194	
2	C	46	
3	D	103	
3	E	103	
3	F	103	
3	G	103	
3	H	103	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6135 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 CHOLERA TOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	192	Total	C	N	O	S	0	0	0
			1532	961	279	288	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	85	LEU	ILE	conflict	UNP P01555
A	88	LEU	ILE	conflict	UNP P01555

- Molecule 2 is a protein called CHOLERA TOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	45	Total	C	N	O	S	0	0	0
			370	227	64	78	1			

- Molecule 3 is a protein called CHOLERA TOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	103	Total	C	N	O	S	0	0	0
			819	516	140	158	5			
3	E	103	Total	C	N	O	S	0	0	0
			819	516	140	158	5			
3	F	103	Total	C	N	O	S	0	0	0
			819	516	140	158	5			
3	G	103	Total	C	N	O	S	0	0	0
			819	516	140	158	5			
3	H	103	Total	C	N	O	S	0	0	0
			819	516	140	158	5			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	54	SER	GLY	conflict	UNP P01556
D	87	THR	VAL	conflict	UNP P01556
E	54	SER	GLY	conflict	UNP P01556
E	87	THR	VAL	conflict	UNP P01556
F	54	SER	GLY	conflict	UNP P01556
F	87	THR	VAL	conflict	UNP P01556
G	54	SER	GLY	conflict	UNP P01556
G	87	THR	VAL	conflict	UNP P01556
H	54	SER	GLY	conflict	UNP P01556
H	87	THR	VAL	conflict	UNP P01556

- Molecule 4 is water.

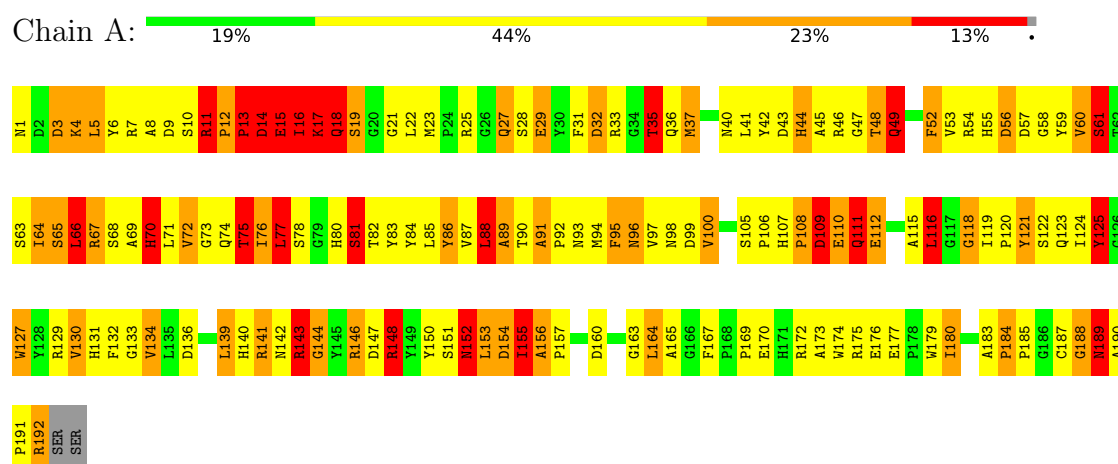
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	35	Total O 35 35	0	0
4	C	4	Total O 4 4	0	0
4	D	24	Total O 24 24	0	0
4	E	19	Total O 19 19	0	0
4	F	19	Total O 19 19	0	0
4	G	19	Total O 19 19	0	0
4	H	18	Total O 18 18	0	0

3 Residue-property plots

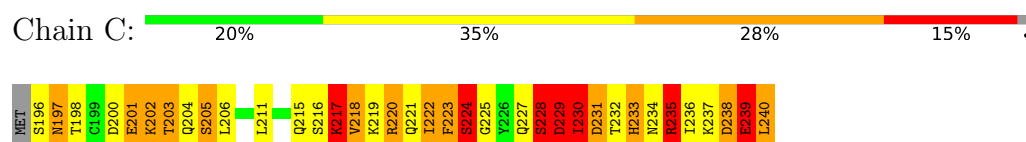
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

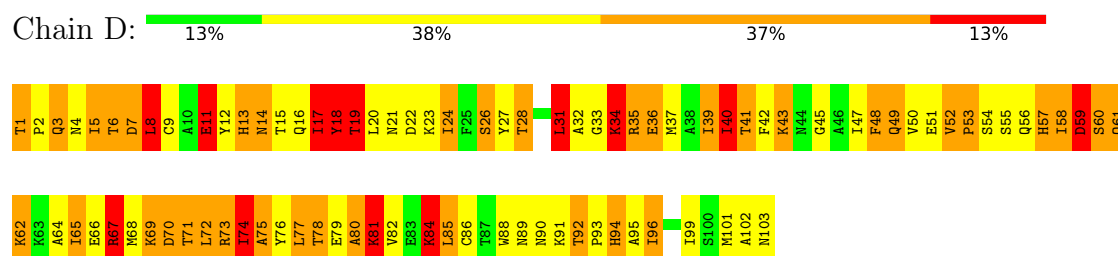
• Molecule 1: CHOLERA TOXIN



• Molecule 2: CHOLERA TOXIN

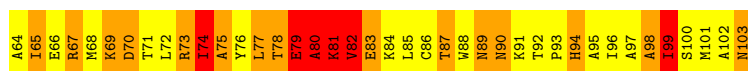
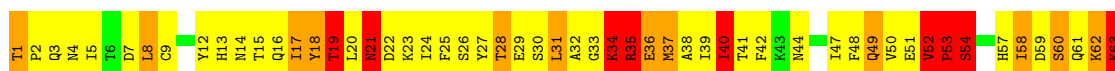


• Molecule 3: CHOLERA TOXIN

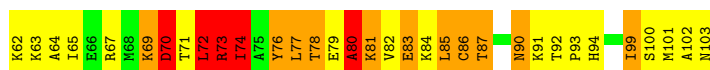
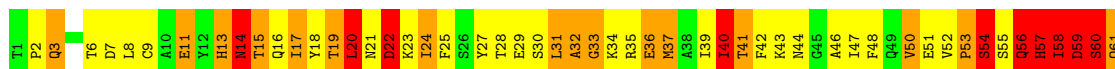
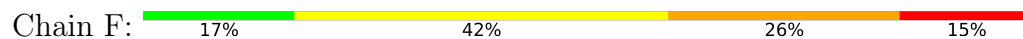


• Molecule 3: CHOLERA TOXIN

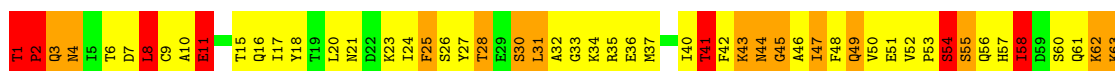
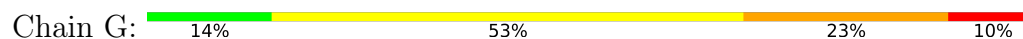




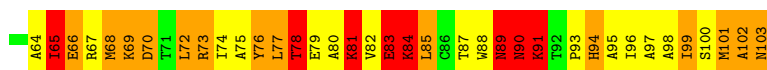
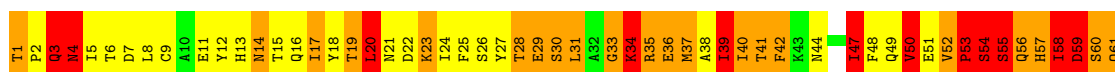
• Molecule 3: CHOLERA TOXIN



• Molecule 3: CHOLERA TOXIN



• Molecule 3: CHOLERA TOXIN



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.00Å 92.20Å 60.60Å 90.00° 106.40° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.40)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROFFT, X-PLOR	Depositor
R, R_{free}	0.185 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6135	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

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	1.27	8/1581 (0.5%)	2.45	92/2153 (4.3%)
2	C	1.34	2/374 (0.5%)	2.07	17/498 (3.4%)
3	D	1.25	1/833 (0.1%)	2.22	45/1125 (4.0%)
3	E	1.26	2/833 (0.2%)	2.25	42/1125 (3.7%)
3	F	1.23	0/833	2.20	38/1125 (3.4%)
3	G	1.39	1/833 (0.1%)	2.31	50/1125 (4.4%)
3	H	1.32	3/833 (0.4%)	2.69	45/1125 (4.0%)
All	All	1.29	17/6120 (0.3%)	2.35	329/8276 (4.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	15
2	C	0	2
3	D	0	8
3	E	0	2
3	F	0	4
3	G	0	9
3	H	0	10
All	All	0	50

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	19	SER	C-N	12.02	1.51	1.33
3	G	1	THR	C-N	10.57	1.58	1.33
1	A	16	ILE	C-N	-9.57	1.22	1.33
3	H	53	PRO	C-N	-8.88	1.21	1.33
3	H	54	SER	C-N	7.81	1.44	1.33
2	C	218	VAL	N-CA	7.39	1.55	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	15	GLU	C-N	6.32	1.41	1.33
3	E	80	ALA	N-CA	-5.98	1.38	1.46
1	A	96	ASN	N-CA	5.85	1.53	1.46
2	C	217	LYS	CA-C	5.62	1.59	1.52
1	A	155	ILE	N-CA	-5.39	1.39	1.46
3	H	4	ASN	CA-C	5.37	1.59	1.52
1	A	155	ILE	CA-CB	5.33	1.61	1.54
3	D	19	THR	CA-CB	5.30	1.59	1.52
3	E	54	SER	N-CA	-5.26	1.39	1.46
1	A	96	ASN	CA-CB	-5.14	1.46	1.53
1	A	14	ASP	C-N	5.04	1.40	1.33

All (329) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	53	PRO	CA-C-N	25.27	169.80	121.54
3	H	53	PRO	C-N-CA	25.27	169.80	121.54
3	H	54	SER	CA-C-N	24.26	167.88	121.54
3	H	54	SER	C-N-CA	24.26	167.88	121.54
1	A	15	GLU	O-C-N	-23.87	94.94	122.15
1	A	13	PRO	CA-C-N	19.03	157.89	121.54
1	A	13	PRO	C-N-CA	19.03	157.89	121.54
3	F	73	ARG	CD-NE-CZ	15.12	145.56	124.40
1	A	13	PRO	O-C-N	-14.26	106.05	122.17
3	E	79	GLU	CA-C-N	14.18	148.63	121.54
3	E	79	GLU	C-N-CA	14.18	148.63	121.54
3	G	1	THR	O-C-N	-13.62	101.21	123.00
1	A	3	ASP	CA-CB-CG	13.53	126.13	112.60
1	A	16	ILE	O-C-N	-13.21	107.69	121.96
3	D	14	ASN	CA-CB-CG	13.08	125.68	112.60
1	A	15	GLU	CA-C-N	12.64	137.33	120.77
1	A	15	GLU	C-N-CA	12.64	137.33	120.77
1	A	52	PHE	CA-CB-CG	12.31	126.11	113.80
3	H	53	PRO	O-C-N	-12.03	106.40	122.64
3	H	103	ASN	CA-CB-CG	11.96	124.56	112.60
1	A	99	ASP	CA-CB-CG	10.78	123.38	112.60
1	A	14	ASP	O-C-N	-10.77	108.27	122.59
3	E	53	PRO	CA-C-N	10.43	141.46	121.54
3	E	53	PRO	C-N-CA	10.43	141.46	121.54
1	A	16	ILE	CA-C-N	9.98	134.01	120.54
1	A	16	ILE	C-N-CA	9.98	134.01	120.54
3	E	73	ARG	CD-NE-CZ	9.87	138.22	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	GLU	CB-CG-CD	9.80	129.26	112.60
1	A	12	PRO	CA-C-N	9.30	128.64	118.97
1	A	12	PRO	C-N-CA	9.30	128.64	118.97
1	A	152	ASN	CA-CB-CG	-9.22	103.38	112.60
1	A	12	PRO	O-C-N	-8.94	116.95	121.15
1	A	172	ARG	CA-C-N	8.89	132.56	120.38
1	A	172	ARG	C-N-CA	8.89	132.56	120.38
3	G	84	LYS	CG-CD-CE	8.79	131.51	111.30
3	G	1	THR	CA-C-N	8.75	130.78	119.84
3	G	1	THR	C-N-CA	8.75	130.78	119.84
2	C	216	SER	O-C-N	-8.66	113.15	122.07
3	H	55	SER	CA-C-N	8.63	136.24	121.14
3	H	55	SER	C-N-CA	8.63	136.24	121.14
3	H	3	GLN	CA-C-N	8.48	135.95	122.21
3	H	3	GLN	C-N-CA	8.48	135.95	122.21
1	A	96	ASN	CA-CB-CG	8.48	121.08	112.60
1	A	155	ILE	N-CA-C	8.43	126.86	109.34
3	F	70	ASP	CA-C-N	8.28	131.20	120.44
3	F	70	ASP	C-N-CA	8.28	131.20	120.44
3	G	55	SER	N-CA-C	-8.25	98.27	110.48
3	G	2	PRO	CB-CA-C	8.22	125.13	111.56
1	A	109	ASP	CA-C-N	8.21	133.74	120.60
1	A	109	ASP	C-N-CA	8.21	133.74	120.60
3	E	36	GLU	N-CA-CB	8.11	121.97	110.46
3	D	60	SER	CA-C-N	7.97	130.96	120.28
3	D	60	SER	C-N-CA	7.97	130.96	120.28
1	A	93	ASN	CA-C-N	7.95	133.34	122.77
1	A	93	ASN	C-N-CA	7.95	133.34	122.77
1	A	17	LYS	O-C-N	-7.88	113.89	122.09
3	G	44	ASN	CA-C-N	7.80	136.70	121.41
3	G	44	ASN	C-N-CA	7.80	136.70	121.41
1	A	67	ARG	CD-NE-CZ	7.80	135.32	124.40
1	A	154	ASP	CA-CB-CG	7.77	120.37	112.60
3	F	72	LEU	N-CA-C	-7.76	99.55	110.50
3	D	84	LYS	N-CA-CB	7.72	122.63	111.05
1	A	17	LYS	N-CA-C	-7.72	101.84	111.11
1	A	154	ASP	CA-C-N	7.68	135.79	121.97
1	A	154	ASP	C-N-CA	7.68	135.79	121.97
3	G	45	GLY	N-CA-C	7.67	131.36	113.18
3	F	77	LEU	CA-C-N	7.63	131.91	120.31
3	F	77	LEU	C-N-CA	7.63	131.91	120.31
1	A	116	LEU	CB-CA-C	7.58	121.63	110.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	75	ALA	N-CA-C	-7.45	102.09	112.45
1	A	96	ASN	CB-CA-C	7.39	123.00	110.81
1	A	29	GLU	CB-CG-CD	7.37	125.12	112.60
3	G	41	THR	CA-CB-CG2	7.35	122.99	110.50
3	E	40	ILE	CB-CA-C	7.33	120.81	110.84
3	H	79	GLU	N-CA-CB	7.33	122.88	110.49
3	G	70	ASP	CA-C-N	7.29	133.07	120.68
3	G	70	ASP	C-N-CA	7.29	133.07	120.68
1	A	70	HIS	CA-CB-CG	7.28	121.08	113.80
3	F	62	LYS	CA-CB-CG	7.28	128.66	114.10
3	H	4	ASN	CA-C-O	-7.23	113.23	121.40
1	A	118	GLY	CA-C-O	-7.16	115.76	122.13
3	G	25	PHE	CA-CB-CG	7.14	120.94	113.80
3	E	4	ASN	CA-C-O	-7.08	113.70	121.28
1	A	189	ASN	CA-CB-CG	-7.01	105.58	112.60
1	A	17	LYS	CA-C-N	7.01	129.67	120.28
1	A	17	LYS	C-N-CA	7.01	129.67	120.28
3	D	17	ILE	CA-C-N	6.99	132.06	122.77
3	D	17	ILE	C-N-CA	6.99	132.06	122.77
1	A	163	GLY	CA-C-N	6.98	133.94	121.66
1	A	163	GLY	C-N-CA	6.98	133.94	121.66
2	C	218	VAL	CB-CA-C	-6.98	103.04	111.97
3	F	22	ASP	CA-CB-CG	6.97	119.57	112.60
1	A	172	ARG	N-CA-C	6.95	118.86	111.28
3	H	91	LYS	N-CA-CB	6.95	122.46	111.20
1	A	153	LEU	N-CA-CB	-6.87	99.34	111.08
3	E	7	ASP	CA-CB-CG	6.87	119.47	112.60
3	G	103	ASN	CA-CB-CG	6.85	119.45	112.60
1	A	144	GLY	N-CA-C	-6.85	105.74	114.37
3	E	54	SER	N-CA-C	6.82	125.33	110.80
3	G	83	GLU	CA-C-N	6.81	133.23	122.74
3	G	83	GLU	C-N-CA	6.81	133.23	122.74
3	H	94	HIS	CA-CB-CG	6.75	120.56	113.80
3	F	71	THR	CA-CB-CG2	6.74	121.95	110.50
3	D	61	GLN	O-C-N	6.73	129.25	122.12
2	C	229	ASP	CA-CB-CG	-6.72	105.88	112.60
3	H	4	ASN	CB-CA-C	-6.71	95.30	110.07
2	C	228	SER	O-C-N	-6.71	113.67	122.59
3	E	19	THR	O-C-N	6.70	130.49	122.85
2	C	205	SER	O-C-N	6.70	129.06	122.09
2	C	223	PHE	CA-CB-CG	-6.69	107.11	113.80
3	H	89	ASN	CA-CB-CG	6.64	119.24	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	76	TYR	CA-C-N	6.61	129.03	120.44
3	H	76	TYR	C-N-CA	6.61	129.03	120.44
3	D	24	ILE	CA-C-N	6.55	129.34	120.44
3	D	24	ILE	C-N-CA	6.55	129.34	120.44
3	G	49	GLN	CB-CG-CD	6.49	123.63	112.60
1	A	11	ARG	O-C-N	6.47	128.76	121.32
3	E	87	THR	CA-C-O	6.46	128.05	120.43
3	E	53	PRO	N-CA-C	6.45	125.76	112.47
3	F	40	ILE	CB-CA-C	6.42	120.18	110.62
1	A	164	LEU	CA-C-N	6.39	130.41	120.82
1	A	164	LEU	C-N-CA	6.39	130.41	120.82
3	D	49	GLN	CA-C-N	6.38	132.04	123.10
3	D	49	GLN	C-N-CA	6.38	132.04	123.10
3	G	2	PRO	O-C-N	-6.38	114.02	122.64
1	A	47	GLY	N-CA-C	-6.38	103.44	112.37
3	F	69	LYS	CA-C-N	6.35	129.31	120.29
3	F	69	LYS	C-N-CA	6.35	129.31	120.29
3	H	78	THR	CA-C-N	6.34	133.65	121.54
3	H	78	THR	C-N-CA	6.34	133.65	121.54
3	H	50	VAL	CB-CA-C	6.33	118.12	111.09
3	E	80	ALA	CA-C-O	6.33	129.56	120.51
3	G	72	LEU	CB-CA-C	6.30	120.71	110.95
3	G	90	ASN	N-CA-C	-6.29	105.66	113.15
1	A	11	ARG	CA-C-N	6.28	124.18	119.66
1	A	11	ARG	C-N-CA	6.28	124.18	119.66
3	D	78	THR	CA-C-O	6.27	126.11	119.03
1	A	154	ASP	CB-CA-C	6.25	124.60	110.67
1	A	143	ARG	N-CA-C	-6.24	101.04	110.28
3	D	40	ILE	CA-C-N	6.22	132.81	122.73
3	D	40	ILE	C-N-CA	6.22	132.81	122.73
3	D	80	ALA	N-CA-C	6.21	118.13	111.36
2	C	205	SER	N-CA-C	-6.19	103.68	111.11
3	D	57	HIS	CA-C-N	6.19	129.81	120.77
3	D	57	HIS	C-N-CA	6.19	129.81	120.77
3	E	63	LYS	N-CA-CB	6.19	119.83	110.30
1	A	100	VAL	CB-CA-C	6.18	119.10	111.80
3	G	6	THR	CA-CB-CG2	6.15	120.95	110.50
3	D	72	LEU	O-C-N	6.13	128.66	122.03
3	H	65	ILE	CA-C-N	6.13	128.50	120.28
3	H	65	ILE	C-N-CA	6.13	128.50	120.28
1	A	155	ILE	O-C-N	-6.09	114.95	122.57
2	C	228	SER	CA-C-N	-6.07	110.18	122.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	228	SER	C-N-CA	-6.07	110.18	122.31
3	F	62	LYS	N-CA-CB	6.04	119.63	109.78
3	D	11	GLU	N-CA-C	-6.03	104.70	111.28
3	D	22	ASP	CA-CB-CG	-6.02	106.58	112.60
3	G	75	ALA	N-CA-C	-6.02	104.83	111.82
1	A	35	THR	CA-C-N	-6.02	114.41	122.72
1	A	35	THR	C-N-CA	-6.02	114.41	122.72
3	H	19	THR	N-CA-CB	5.98	119.26	110.35
3	H	90	ASN	CA-CB-CG	5.96	118.56	112.60
3	G	54	SER	N-CA-CB	-5.93	101.72	110.97
3	F	56	GLN	N-CA-C	-5.92	106.04	113.20
2	C	220	ARG	NE-CZ-NH2	5.91	124.52	119.20
3	F	20	LEU	N-CA-C	-5.90	106.62	113.88
3	D	31	LEU	N-CA-C	-5.89	105.69	114.64
3	H	83	GLU	CA-C-O	5.89	127.68	120.56
1	A	91	ALA	CA-C-O	5.86	125.89	120.50
3	G	2	PRO	CA-N-CD	-5.85	103.81	112.00
1	A	86	TYR	O-C-N	5.85	129.89	123.22
3	E	28	THR	CB-CA-C	5.83	119.11	110.14
1	A	165	ALA	CA-C-N	5.83	130.90	121.00
1	A	165	ALA	C-N-CA	5.83	130.90	121.00
3	D	18	TYR	CA-C-O	-5.82	114.13	120.36
3	D	40	ILE	CB-CA-C	5.82	119.66	110.81
1	A	65	SER	N-CA-C	5.81	123.17	110.80
3	E	80	ALA	N-CA-C	5.80	123.16	110.80
3	G	58	ILE	CA-C-N	5.78	130.46	120.58
3	G	58	ILE	C-N-CA	5.78	130.46	120.58
3	E	60	SER	N-CA-C	-5.78	105.49	112.54
3	F	17	ILE	N-CA-CB	5.77	120.10	110.86
3	F	59	ASP	CB-CA-C	5.76	121.72	110.67
3	H	77	LEU	N-CA-C	5.75	117.22	111.07
3	E	70	ASP	CA-C-N	5.74	130.32	121.19
3	E	70	ASP	C-N-CA	5.74	130.32	121.19
3	E	74	ILE	N-CA-CB	5.73	120.57	112.15
3	H	85	LEU	O-C-N	5.71	130.77	123.11
3	D	36	GLU	CA-C-N	5.71	132.41	122.82
3	D	36	GLU	C-N-CA	5.71	132.41	122.82
3	D	13	HIS	CA-CB-CG	-5.70	108.10	113.80
3	D	86	CYS	CA-C-O	-5.70	114.55	121.05
3	F	74	ILE	CB-CA-C	5.68	119.24	111.97
1	A	18	GLN	O-C-N	5.68	128.14	122.12
1	A	44	HIS	CA-C-N	5.67	128.66	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	HIS	C-N-CA	5.67	128.66	120.38
3	F	3	GLN	N-CA-C	-5.67	106.24	114.12
3	D	75	ALA	N-CA-C	-5.66	105.19	111.36
3	G	44	ASN	CB-CA-C	5.66	120.37	111.72
3	E	4	ASN	O-C-N	5.65	128.94	123.29
3	E	90	ASN	N-CA-C	-5.64	106.44	113.15
3	G	49	GLN	O-C-N	5.64	130.00	123.17
3	G	55	SER	CA-C-O	-5.64	114.98	121.47
3	F	60	SER	CA-C-N	5.63	128.28	120.29
3	F	60	SER	C-N-CA	5.63	128.28	120.29
3	H	34	LYS	CG-CD-CE	5.62	124.24	111.30
3	E	74	ILE	O-C-N	5.62	127.15	122.09
3	G	49	GLN	CA-CB-CG	5.62	125.34	114.10
3	G	6	THR	CA-C-N	5.62	127.81	120.28
3	G	6	THR	C-N-CA	5.62	127.81	120.28
3	E	94	HIS	CA-CB-CG	-5.60	108.20	113.80
1	A	112	GLU	CB-CA-C	-5.59	100.06	109.50
2	C	230	ILE	N-CA-C	-5.57	105.29	110.53
1	A	81	SER	N-CA-C	-5.53	105.26	112.23
2	C	217	LYS	O-C-N	-5.53	116.38	122.07
1	A	95	PHE	CA-CB-CG	-5.52	108.28	113.80
3	G	73	ARG	CA-CB-CG	5.52	125.15	114.10
1	A	75	THR	N-CA-C	-5.52	106.48	113.43
2	C	239	GLU	O-C-N	-5.50	114.41	121.83
3	D	18	TYR	CB-CA-C	-5.50	101.29	110.19
3	G	2	PRO	CA-C-N	5.48	129.91	122.07
3	G	2	PRO	C-N-CA	5.48	129.91	122.07
3	G	74	ILE	CA-CB-CG2	5.48	119.81	110.50
3	E	82	VAL	N-CA-CB	5.47	120.26	111.23
3	G	28	THR	N-CA-CB	5.47	119.55	110.52
3	H	30	SER	N-CA-CB	5.46	119.53	110.63
1	A	28	SER	CB-CA-C	5.46	119.83	110.23
1	A	35	THR	N-CA-C	-5.45	99.19	110.80
1	A	32	ASP	CA-CB-CG	-5.43	107.17	112.60
3	E	87	THR	CA-CB-CG2	5.43	119.74	110.50
3	H	57	HIS	N-CA-C	5.43	118.22	108.17
1	A	90	THR	CA-C-O	5.42	126.34	120.43
3	G	68	MET	O-C-N	5.42	129.80	122.59
1	A	160	ASP	N-CA-C	-5.41	105.41	112.23
3	G	54	SER	N-CA-C	5.41	115.39	108.24
3	D	70	ASP	CA-CB-CG	-5.41	107.19	112.60
1	A	147	ASP	CA-C-O	-5.40	114.77	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	11	GLU	N-CA-C	-5.40	105.95	112.54
3	D	67	ARG	NE-CZ-NH2	-5.40	114.34	119.20
3	D	71	THR	N-CA-C	-5.40	105.43	112.23
2	C	237	LYS	N-CA-C	-5.39	105.51	111.71
3	E	49	GLN	CA-C-N	5.39	130.56	123.11
3	E	49	GLN	C-N-CA	5.39	130.56	123.11
3	H	103	ASN	N-CA-CB	5.39	119.66	110.50
3	E	94	HIS	CA-C-N	5.38	130.06	121.66
3	E	94	HIS	C-N-CA	5.38	130.06	121.66
3	D	5	ILE	CA-C-N	5.38	128.26	120.79
3	D	5	ILE	C-N-CA	5.38	128.26	120.79
3	G	8	LEU	CA-C-N	5.37	127.74	120.44
3	G	8	LEU	C-N-CA	5.37	127.74	120.44
3	D	43	LYS	O-C-N	5.37	127.60	122.07
3	F	17	ILE	CA-C-N	5.37	131.23	123.13
3	F	17	ILE	C-N-CA	5.37	131.23	123.13
3	F	90	ASN	CA-CB-CG	-5.36	107.24	112.60
3	E	99	ILE	N-CA-CB	-5.35	101.45	111.62
3	D	31	LEU	CB-CA-C	5.35	117.36	109.29
1	A	109	ASP	CA-CB-CG	5.33	117.93	112.60
1	A	47	GLY	CA-C-O	-5.33	115.60	121.94
3	F	58	ILE	CA-C-O	-5.32	117.48	121.68
3	G	88	TRP	CA-C-O	-5.31	115.25	120.98
3	H	69	LYS	CA-C-N	5.31	129.70	120.68
3	H	69	LYS	C-N-CA	5.31	129.70	120.68
3	E	19	THR	N-CA-C	-5.30	103.39	110.55
3	G	44	ASN	CA-CB-CG	5.30	117.91	112.60
3	G	90	ASN	CB-CA-C	5.30	120.17	110.36
2	C	224	SER	CA-C-N	5.30	125.83	119.94
2	C	224	SER	C-N-CA	5.30	125.83	119.94
1	A	48	THR	N-CA-C	5.29	119.81	112.45
2	C	201	GLU	CB-CA-C	-5.29	102.57	110.88
1	A	97	VAL	CB-CA-C	5.28	118.95	112.04
3	H	39	ILE	CB-CA-C	5.27	118.94	110.82
3	E	35	ARG	N-CA-C	5.27	119.30	111.87
3	H	37	MET	CA-CB-CG	-5.26	103.58	114.10
3	D	33	GLY	CA-C-N	5.26	131.59	121.54
3	D	33	GLY	C-N-CA	5.26	131.59	121.54
1	A	58	GLY	N-CA-C	5.25	122.98	114.90
3	F	11	GLU	CA-CB-CG	5.23	124.56	114.10
3	F	59	ASP	CA-C-N	5.23	127.81	120.28
3	F	59	ASP	C-N-CA	5.23	127.81	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	86	CYS	CB-CA-C	5.23	118.38	109.80
1	A	57	ASP	CA-C-N	5.21	131.12	120.80
1	A	57	ASP	C-N-CA	5.21	131.12	120.80
1	A	148	ARG	CA-C-N	5.20	127.52	120.65
1	A	148	ARG	C-N-CA	5.20	127.52	120.65
1	A	61	SER	CB-CA-C	5.20	118.11	109.53
3	H	35	ARG	CA-C-O	-5.20	116.34	121.02
3	G	3	GLN	N-CA-C	5.19	118.59	111.54
3	F	40	ILE	CA-CB-CG2	5.18	119.31	110.50
3	E	28	THR	CA-CB-CG2	5.18	119.30	110.50
3	D	84	LYS	CA-CB-CG	5.17	124.45	114.10
3	E	52	VAL	N-CA-CB	-5.17	103.98	111.21
3	G	2	PRO	N-CD-CG	-5.16	95.46	103.20
3	H	20	LEU	CA-C-N	-5.16	115.20	122.63
3	H	20	LEU	C-N-CA	-5.16	115.20	122.63
1	A	37	MET	O-C-N	5.14	130.12	122.97
3	H	58	ILE	N-CA-CB	5.14	119.72	111.23
3	H	72	LEU	CB-CA-C	5.14	119.59	110.85
3	H	42	PHE	CB-CA-C	5.14	119.45	109.33
3	E	98	ALA	O-C-N	5.14	128.09	123.26
1	A	27	GLN	N-CA-C	-5.13	101.03	109.40
3	G	72	LEU	O-C-N	-5.13	116.49	122.03
3	H	85	LEU	CA-CB-CG	5.12	134.22	116.30
3	D	31	LEU	CA-C-O	5.12	124.83	118.43
3	D	74	ILE	N-CA-C	-5.11	107.44	113.42
1	A	88	LEU	CA-C-O	-5.11	114.81	120.33
3	G	55	SER	O-C-N	5.11	128.73	122.96
3	E	18	TYR	CA-C-O	-5.10	113.12	120.11
3	F	39	ILE	CA-C-O	5.10	125.30	120.25
3	D	19	THR	CA-CB-OG1	-5.09	101.97	109.60
3	D	86	CYS	N-CA-C	-5.09	102.16	110.20
3	F	57	HIS	CA-CB-CG	-5.08	108.72	113.80
3	G	7	ASP	O-C-N	5.08	127.50	122.12
1	A	19	SER	CA-C-N	5.07	130.56	122.25
1	A	19	SER	C-N-CA	5.07	130.56	122.25
3	E	67	ARG	NE-CZ-NH1	-5.06	116.44	121.50
3	F	32	ALA	CA-C-N	5.06	131.34	121.41
3	F	32	ALA	C-N-CA	5.06	131.34	121.41
3	D	57	HIS	N-CA-C	5.06	117.31	108.76
1	A	167	PHE	O-C-N	5.05	127.08	121.53
1	A	60	VAL	CB-CA-C	5.04	117.69	110.33
3	E	34	LYS	N-CA-CB	-5.04	109.06	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	80	ALA	CA-C-N	5.04	129.47	122.77
3	F	80	ALA	C-N-CA	5.04	129.47	122.77
3	H	84	LYS	O-C-N	5.03	128.98	123.25
3	F	54	SER	CB-CA-C	5.02	120.41	110.42
3	E	50	VAL	N-CA-CB	5.00	118.51	112.10
3	H	102	ALA	N-CA-C	5.00	116.78	108.02
3	D	40	ILE	CA-CB-CG2	5.00	119.00	110.50
3	G	81	LYS	CA-C-O	5.00	125.71	120.36

There are no chirality outliers.

All (50) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	109	ASP	Mainchain
1	A	11	ARG	Sidechain
1	A	121	TYR	Sidechain
1	A	125	TYR	Sidechain
1	A	127	TRP	Mainchain
1	A	13	PRO	Peptide
1	A	14	ASP	Mainchain
1	A	148	ARG	Sidechain
1	A	152	ASN	Sidechain
1	A	16	ILE	Mainchain
1	A	17	LYS	Mainchain
1	A	18	GLN	Mainchain
1	A	35	THR	Mainchain
1	A	52	PHE	Mainchain
1	A	88	LEU	Mainchain
2	C	235	ARG	Sidechain
2	C	239	GLU	Mainchain
3	D	18	TYR	Mainchain
3	D	35	ARG	Mainchain
3	D	40	ILE	Mainchain
3	D	48	PHE	Mainchain
3	D	67	ARG	Sidechain
3	D	71	THR	Mainchain
3	D	81	LYS	Mainchain
3	D	85	LEU	Mainchain
3	E	65	ILE	Mainchain
3	E	81	LYS	Mainchain
3	F	13	HIS	Mainchain
3	F	61	GLN	Mainchain

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Mol	Chain	Res	Type	Group
3	F	70	ASP	Mainchain
3	F	76	TYR	Sidechain
3	G	1	THR	Mainchain
3	G	11	GLU	Sidechain
3	G	27	TYR	Mainchain
3	G	44	ASN	Mainchain
3	G	50	VAL	Mainchain
3	G	66	GLU	Mainchain
3	G	8	LEU	Mainchain
3	G	80	ALA	Mainchain
3	G	94	HIS	Mainchain
3	H	39	ILE	Mainchain
3	H	4	ASN	Mainchain
3	H	47	ILE	Mainchain
3	H	50	VAL	Mainchain
3	H	53	PRO	Peptide,Mainchain
3	H	54	SER	Mainchain
3	H	70	ASP	Mainchain
3	H	73	ARG	Sidechain
3	H	81	LYS	Mainchain

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	1532	0	1421	210	2
2	C	370	0	355	93	0
3	D	819	0	823	214	0
3	E	819	0	822	230	2
3	F	819	0	823	161	0
3	G	819	0	823	121	0
3	H	819	0	822	138	0
4	A	35	0	0	6	0
4	C	4	0	0	1	0
4	D	24	0	0	6	0
4	E	19	0	0	1	0
4	F	19	0	0	1	0
4	G	19	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	18	0	0	0	0
All	All	6135	0	5889	1011	2

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 85.

All (1011) 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:A:129:ARG:NH2	1:A:131:HIS:HB3	1.25	1.47
2:C:235:ARG:HH22	2:C:239:GLU:CB	1.35	1.37
3:F:70:ASP:O	3:F:74:ILE:HG23	1.20	1.32
2:C:235:ARG:NH2	2:C:239:GLU:CB	1.90	1.30
1:A:170:GLU:HB3	1:A:192:ARG:NH2	1.47	1.29
3:H:1:THR:CG2	3:H:2:PRO:HD2	1.64	1.27
3:G:55:SER:O	3:G:56:GLN:HG2	1.30	1.26
2:C:235:ARG:NH2	2:C:239:GLU:HB2	0.94	1.24
1:A:143:ARG:NH1	1:A:146:ARG:HH21	1.36	1.22
3:E:22:ASP:O	3:E:81:LYS:HA	1.03	1.19
1:A:76:ILE:O	1:A:78:SER:N	1.76	1.19
2:C:228:SER:OG	3:D:74:ILE:HG13	1.01	1.18
3:H:1:THR:HG22	3:H:2:PRO:CD	1.74	1.17
1:A:32:ASP:HB3	1:A:35:THR:HB	1.21	1.17
3:E:22:ASP:O	3:E:81:LYS:CA	1.93	1.16
1:A:175:ARG:HA	1:A:180:ILE:CD1	1.77	1.14
3:D:5:ILE:HG23	3:D:84:LYS:HZ2	0.98	1.14
1:A:189:ASN:HB3	1:A:191:PRO:HD2	1.18	1.14
1:A:143:ARG:NH1	1:A:146:ARG:NH2	1.95	1.13
1:A:185:PRO:CD	2:C:202:LYS:HG2	1.78	1.13
3:F:56:GLN:HG2	3:F:57:HIS:CE1	1.82	1.13
3:E:42:PHE:HZ	3:E:82:VAL:CG1	1.63	1.12
2:C:224:SER:OG	3:E:77:LEU:HB3	1.51	1.11
1:A:129:ARG:NH2	1:A:131:HIS:CB	2.12	1.11
2:C:228:SER:OG	3:D:74:ILE:CG1	1.98	1.10
3:E:83:GLU:HG2	3:E:84:LYS:HG3	1.29	1.10
3:E:89:ASN:C	3:E:89:ASN:HD22	1.58	1.10
1:A:68:SER:O	1:A:72:VAL:HG13	1.52	1.09
2:C:227:GLN:HA	2:C:230:ILE:HG12	1.33	1.09
3:D:48:PHE:CE2	3:D:85:LEU:HD23	1.87	1.09
3:F:56:GLN:HG2	3:F:57:HIS:ND1	1.69	1.08
3:E:5:ILE:CG2	3:E:84:LYS:HZ3	1.66	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:25:PHE:HE1	3:G:103:ASN:OXT	1.37	1.07
1:A:185:PRO:HD2	2:C:202:LYS:CG	1.85	1.06
3:F:29:GLU:OE2	3:G:71:THR:HG21	1.54	1.05
3:G:55:SER:O	3:G:56:GLN:CG	2.04	1.05
2:C:234:ASN:O	2:C:238:ASP:HB2	1.56	1.04
3:E:5:ILE:CG2	3:E:84:LYS:NZ	2.20	1.04
3:F:25:PHE:CE1	3:G:103:ASN:OXT	2.10	1.04
3:G:85:LEU:HD23	3:G:99:ILE:HD13	1.35	1.03
1:A:40:ASN:ND2	1:A:43:ASP:H	1.56	1.02
1:A:131:HIS:CE1	1:A:136:ASP:HB2	1.93	1.02
1:A:155:ILE:O	1:A:156:ALA:HB3	1.58	1.02
3:D:20:LEU:HD23	3:D:42:PHE:CZ	1.94	1.02
3:E:42:PHE:CZ	3:E:82:VAL:CG1	2.43	1.01
3:H:39:ILE:HD13	3:H:39:ILE:C	1.84	1.01
3:E:77:LEU:CD1	3:F:78:THR:HG21	1.91	1.01
3:D:5:ILE:HG23	3:D:84:LYS:NZ	1.74	1.01
3:F:33:GLY:O	3:F:34:LYS:HG2	1.58	1.00
2:C:227:GLN:HA	2:C:230:ILE:CG1	1.91	1.00
3:E:25:PHE:HA	3:F:103:ASN:ND2	1.78	0.98
3:H:8:LEU:HD23	3:H:8:LEU:C	1.88	0.98
1:A:175:ARG:HA	1:A:180:ILE:HD13	1.45	0.98
3:E:80:ALA:C	3:E:81:LYS:HG2	1.88	0.98
3:E:5:ILE:HG22	3:E:84:LYS:NZ	1.79	0.97
3:F:70:ASP:O	3:F:74:ILE:CG2	2.11	0.97
3:F:24:ILE:HG21	3:F:40:ILE:HG13	1.44	0.96
3:G:74:ILE:O	3:G:78:THR:HB	1.66	0.96
3:D:65:ILE:HD12	3:H:31:LEU:HD11	1.47	0.96
2:C:235:ARG:HH21	2:C:239:GLU:HB2	1.21	0.95
3:D:31:LEU:HD22	3:E:97:ALA:HA	1.46	0.95
1:A:185:PRO:HD2	2:C:202:LYS:HG2	0.96	0.95
3:E:42:PHE:CZ	3:E:82:VAL:HG13	2.02	0.95
1:A:175:ARG:HA	1:A:180:ILE:HD12	1.46	0.94
3:G:24:ILE:HG22	3:G:76:TYR:HD1	1.31	0.94
1:A:170:GLU:CB	1:A:192:ARG:NH2	2.31	0.94
2:C:218:VAL:O	2:C:222:ILE:HG22	1.68	0.94
3:E:42:PHE:HZ	3:E:82:VAL:HG11	1.29	0.94
3:F:58:ILE:HD13	3:F:60:SER:OG	1.68	0.94
3:G:103:ASN:ND2	3:G:103:ASN:O	2.01	0.94
2:C:217:LYS:NZ	4:C:106:HOH:O	2.00	0.93
3:D:14:ASN:HB3	3:D:90:ASN:ND2	1.83	0.93
3:D:58:ILE:HG22	3:D:60:SER:OG	1.68	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:56:GLN:CG	3:F:57:HIS:CE1	2.52	0.93
3:G:86:CYS:HB3	3:G:98:ALA:HB3	1.49	0.93
3:D:2:PRO:HG2	3:D:8:LEU:HD12	1.51	0.92
3:E:49:GLN:O	3:E:96:ILE:HD12	1.68	0.92
1:A:15:GLU:HA	1:A:18:GLN:HG2	1.50	0.92
3:E:14:ASN:HB3	3:E:90:ASN:HB3	1.47	0.92
3:E:34:LYS:C	3:E:35:ARG:HD2	1.93	0.92
2:C:240:LEU:HD12	3:F:63:LYS:NZ	1.85	0.91
3:E:22:ASP:O	3:E:81:LYS:HE2	1.69	0.91
1:A:76:ILE:C	1:A:78:SER:H	1.77	0.91
3:F:30:SER:OG	3:F:35:ARG:O	1.87	0.91
3:E:83:GLU:CG	3:E:84:LYS:HG3	1.99	0.91
3:D:20:LEU:CD2	3:D:42:PHE:CZ	2.53	0.91
1:A:129:ARG:HH22	1:A:131:HIS:HB3	1.25	0.91
1:A:189:ASN:HB3	1:A:191:PRO:CD	2.00	0.90
3:D:74:ILE:O	3:D:78:THR:HG22	1.72	0.90
3:D:65:ILE:HD12	3:H:31:LEU:CD1	1.99	0.90
1:A:40:ASN:HD22	1:A:43:ASP:H	1.19	0.90
3:D:67:ARG:O	3:D:70:ASP:HB2	1.71	0.90
1:A:32:ASP:CB	1:A:35:THR:HB	2.01	0.90
3:E:5:ILE:HG22	3:E:84:LYS:HZ3	1.33	0.90
1:A:131:HIS:HE1	1:A:136:ASP:HB2	1.36	0.89
3:D:74:ILE:O	3:D:78:THR:CG2	2.20	0.89
3:E:33:GLY:O	3:E:34:LYS:HB2	1.67	0.89
3:G:18:TYR:HE1	3:G:87:THR:HG1	1.21	0.89
2:C:228:SER:HG	3:D:74:ILE:HG13	1.10	0.88
1:A:13:PRO:HD3	1:A:84:TYR:CE2	2.07	0.88
2:C:229:ASP:OD2	3:D:73:ARG:NH1	2.06	0.88
3:D:50:VAL:HG11	3:D:69:LYS:HG3	1.54	0.88
1:A:143:ARG:HH12	1:A:146:ARG:HH21	1.21	0.88
3:D:13:HIS:O	3:D:14:ASN:HB2	1.72	0.88
3:D:18:TYR:OH	3:D:94:HIS:HD2	1.57	0.88
3:F:51:GLU:OE2	3:F:91:LYS:HE2	1.72	0.88
3:D:58:ILE:O	3:D:61:GLN:HB2	1.75	0.87
1:A:22:LEU:C	1:A:23:MET:HE2	1.98	0.87
3:E:89:ASN:C	3:E:89:ASN:ND2	2.31	0.87
3:E:14:ASN:HD22	3:E:90:ASN:CB	1.86	0.87
3:G:102:ALA:O	3:G:103:ASN:HB3	1.72	0.87
3:D:5:ILE:CG2	3:D:84:LYS:HZ2	1.84	0.86
3:F:58:ILE:CD1	3:F:60:SER:OG	2.23	0.86
3:G:31:LEU:C	3:G:31:LEU:HD23	2.00	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:43:LYS:HE2	3:G:43:LYS:H	1.40	0.86
3:D:5:ILE:CG2	3:D:84:LYS:NZ	2.39	0.86
2:C:220:ARG:O	2:C:224:SER:HB2	1.74	0.86
3:E:25:PHE:HA	3:F:103:ASN:HD21	1.38	0.86
3:D:91:LYS:NZ	3:E:1:THR:OG1	2.07	0.86
3:E:87:THR:CG2	3:E:94:HIS:HB3	2.06	0.85
3:F:74:ILE:O	3:F:78:THR:HB	1.76	0.85
3:D:2:PRO:HG3	3:D:11:GLU:OE1	1.76	0.85
3:E:77:LEU:HD12	3:F:78:THR:HG21	1.56	0.84
1:A:187:CYS:O	1:A:189:ASN:N	2.10	0.84
1:A:175:ARG:HD3	1:A:189:ASN:O	1.77	0.84
3:G:24:ILE:HG22	3:G:76:TYR:CD1	2.11	0.84
3:H:51:GLU:OE2	3:H:91:LYS:HE2	1.78	0.83
3:G:1:THR:HA	4:G:104:HOH:O	1.79	0.83
3:D:18:TYR:OH	3:D:94:HIS:CD2	2.32	0.83
3:D:49:GLN:HG2	3:D:93:PRO:O	1.79	0.83
3:D:54:SER:O	3:D:57:HIS:CD2	2.32	0.83
3:G:42:PHE:CD2	3:G:46:ALA:HB3	2.14	0.83
3:E:59:ASP:CG	3:E:62:LYS:HZ1	1.85	0.82
3:G:82:VAL:CG1	3:G:99:ILE:HD11	2.10	0.82
1:A:33:ARG:HH12	3:F:23:LYS:NZ	1.77	0.82
3:F:36:GLU:O	3:F:52:VAL:HG22	1.79	0.82
3:E:59:ASP:HA	3:E:62:LYS:HE2	1.59	0.82
3:G:58:ILE:O	3:G:62:LYS:HG3	1.79	0.82
3:G:99:ILE:HD12	3:G:100:SER:H	1.42	0.82
1:A:170:GLU:HB3	1:A:192:ARG:HH21	1.40	0.82
3:H:48:PHE:CE1	3:H:87:THR:HG21	2.14	0.82
2:C:228:SER:HG	3:D:74:ILE:CG1	1.88	0.81
2:C:230:ILE:HG13	2:C:231:ASP:H	1.42	0.81
3:D:73:ARG:O	3:D:73:ARG:HG3	1.80	0.81
3:D:96:ILE:HG22	3:D:96:ILE:O	1.78	0.81
1:A:72:VAL:O	1:A:76:ILE:HD12	1.79	0.81
1:A:139:LEU:O	1:A:141:ARG:NH2	2.14	0.81
3:D:76:TYR:O	3:D:78:THR:N	2.14	0.81
3:G:85:LEU:CD2	3:G:99:ILE:HD13	2.11	0.81
3:G:18:TYR:OH	3:G:94:HIS:CD2	2.34	0.81
1:A:18:GLN:HG3	1:A:19:SER:N	1.96	0.80
1:A:91:ALA:HB1	1:A:92:PRO:HD2	1.64	0.80
1:A:15:GLU:CA	1:A:18:GLN:HG2	2.11	0.80
2:C:227:GLN:O	2:C:230:ILE:HG13	1.82	0.80
3:D:20:LEU:HD23	3:D:42:PHE:CE2	2.16	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:2:PRO:HB2	3:G:8:LEU:HD23	1.63	0.80
1:A:48:THR:O	1:A:49:GLN:HB2	1.80	0.80
3:D:28:THR:OG1	3:D:39:ILE:CG2	2.30	0.80
3:F:15:THR:HG21	3:F:86:CYS:SG	2.21	0.80
1:A:143:ARG:HH11	1:A:146:ARG:HH21	1.28	0.79
3:E:15:THR:OG1	3:E:86:CYS:SG	2.41	0.79
2:C:198:THR:O	2:C:202:LYS:HB2	1.82	0.79
3:H:68:MET:HE1	3:H:99:ILE:HG21	1.62	0.79
3:H:36:GLU:CD	3:H:36:GLU:H	1.89	0.79
3:D:56:GLN:HE21	3:D:57:HIS:CE1	2.00	0.79
3:E:83:GLU:HG2	3:E:84:LYS:N	1.96	0.79
1:A:15:GLU:O	1:A:18:GLN:CG	2.31	0.79
3:H:24:ILE:HG22	3:H:26:SER:O	1.82	0.79
1:A:88:LEU:HD23	1:A:119:ILE:HG21	1.63	0.79
1:A:129:ARG:HH22	1:A:131:HIS:CB	1.86	0.78
2:C:197:ASN:O	2:C:201:GLU:HB2	1.84	0.78
1:A:27:GLN:OE1	1:A:35:THR:CG2	2.31	0.78
1:A:143:ARG:HH21	3:D:80:ALA:HA	1.46	0.78
3:E:67:ARG:HG3	3:E:67:ARG:HH11	1.49	0.78
3:D:28:THR:CB	3:D:39:ILE:CG2	2.63	0.77
2:C:240:LEU:HD12	3:F:63:LYS:HZ2	1.49	0.77
3:E:28:THR:O	3:E:38:ALA:HA	1.84	0.77
3:F:27:TYR:HD1	3:F:40:ILE:HD11	1.47	0.77
3:E:47:ILE:HG21	3:F:3:GLN:HB3	1.65	0.77
3:D:41:THR:HG23	4:D:125:HOH:O	1.85	0.77
3:E:9:CYS:SG	3:E:15:THR:OG1	2.42	0.77
3:G:18:TYR:OH	3:G:94:HIS:NE2	2.18	0.77
3:E:59:ASP:OD1	3:E:62:LYS:NZ	2.17	0.77
3:E:65:ILE:O	3:E:69:LYS:HG3	1.85	0.76
1:A:129:ARG:HH21	1:A:131:HIS:HB3	0.96	0.76
3:G:33:GLY:N	3:H:61:GLN:NE2	2.34	0.76
3:D:8:LEU:O	3:D:11:GLU:HB2	1.86	0.76
3:F:50:VAL:HG12	3:F:65:ILE:CG2	2.15	0.76
3:D:2:PRO:CG	3:D:8:LEU:HD12	2.15	0.76
3:D:26:SER:OG	3:D:41:THR:CG2	2.33	0.76
1:A:175:ARG:CA	1:A:180:ILE:HD13	2.15	0.76
1:A:70:HIS:CD2	1:A:74:GLN:OE1	2.39	0.76
3:F:27:TYR:HD1	3:F:40:ILE:CD1	1.99	0.75
2:C:235:ARG:HD2	3:F:67:ARG:HB2	1.67	0.75
1:A:190:ALA:N	1:A:191:PRO:CD	2.48	0.75
2:C:227:GLN:NE2	3:F:74:ILE:HA	2.00	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:35:ARG:NH2	3:E:2:PRO:HD3	2.02	0.75
3:D:28:THR:CB	3:D:39:ILE:HG22	2.16	0.75
3:D:47:ILE:HD13	3:E:3:GLN:HG2	1.69	0.75
1:A:98:ASN:OD1	1:A:111:GLN:HG2	1.87	0.75
3:D:32:ALA:O	3:D:35:ARG:O	2.04	0.75
2:C:235:ARG:HH22	2:C:239:GLU:HB3	1.50	0.74
3:F:84:LYS:HB2	3:F:100:SER:OG	1.85	0.74
3:E:5:ILE:HG21	3:E:84:LYS:NZ	2.01	0.74
3:E:59:ASP:HA	3:E:62:LYS:CE	2.17	0.74
3:H:18:TYR:HB3	3:H:20:LEU:CD2	2.18	0.74
3:E:14:ASN:HD22	3:E:90:ASN:HB2	1.52	0.74
3:E:54:SER:HA	3:E:57:HIS:HB2	1.68	0.74
3:D:47:ILE:O	3:D:48:PHE:CD1	2.41	0.74
3:D:67:ARG:NH1	3:H:69:LYS:HB2	2.03	0.74
3:E:20:LEU:O	3:E:21:ASN:C	2.30	0.74
3:D:14:ASN:HB3	3:D:90:ASN:HD22	1.53	0.73
3:E:62:LYS:O	3:E:66:GLU:HG2	1.88	0.73
3:E:61:GLN:O	3:E:64:ALA:N	2.18	0.73
1:A:148:ARG:CZ	3:E:79:GLU:O	2.36	0.73
2:C:230:ILE:HG13	2:C:231:ASP:N	2.04	0.73
3:F:19:THR:HG23	3:F:84:LYS:NZ	2.02	0.73
3:F:56:GLN:CG	3:F:57:HIS:HE1	2.00	0.73
2:C:234:ASN:O	2:C:238:ASP:CB	2.33	0.72
3:D:67:ARG:NH2	3:H:70:ASP:OD1	2.22	0.72
1:A:33:ARG:HH12	3:F:23:LYS:HZ3	1.37	0.72
3:F:69:LYS:CB	3:G:67:ARG:NH2	2.52	0.72
2:C:228:SER:HB2	3:D:77:LEU:HD23	1.71	0.72
3:E:13:HIS:C	3:E:13:HIS:CD2	2.67	0.72
3:G:46:ALA:HB1	3:G:48:PHE:CE1	2.25	0.72
1:A:15:GLU:O	1:A:18:GLN:HG2	1.88	0.72
1:A:129:ARG:NH2	1:A:131:HIS:CG	2.56	0.72
3:D:5:ILE:HG12	3:D:17:ILE:HD11	1.71	0.72
2:C:224:SER:OG	3:E:77:LEU:CB	2.35	0.72
2:C:227:GLN:HE22	3:F:74:ILE:HA	1.53	0.72
2:C:230:ILE:CG2	3:H:74:ILE:HD13	2.18	0.72
3:E:89:ASN:HA	3:E:94:HIS:ND1	2.04	0.72
3:H:39:ILE:C	3:H:39:ILE:CD1	2.62	0.72
1:A:86:TYR:O	1:A:88:LEU:HD12	1.89	0.72
2:C:219:LYS:O	2:C:223:PHE:HB2	1.90	0.72
3:D:68:MET:C	3:D:70:ASP:H	1.98	0.72
3:F:37:MET:HE1	3:G:1:THR:OG1	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:18:TYR:HB3	3:H:20:LEU:HD21	1.71	0.72
3:H:18:TYR:O	3:H:84:LYS:HA	1.90	0.71
1:A:76:ILE:HG22	1:A:77:LEU:N	2.03	0.71
3:D:16:GLN:OE1	3:D:89:ASN:HB3	1.90	0.71
3:D:28:THR:HB	3:D:39:ILE:CG2	2.20	0.71
1:A:4:LYS:HG2	1:A:87:VAL:CG1	2.20	0.71
3:F:33:GLY:O	3:F:34:LYS:CG	2.37	0.71
3:E:14:ASN:CB	3:E:90:ASN:HB3	2.20	0.71
3:E:48:PHE:HE1	3:E:87:THR:HG21	1.55	0.71
3:H:8:LEU:HD23	3:H:8:LEU:O	1.89	0.71
3:D:47:ILE:HG21	3:E:3:GLN:HG3	1.72	0.71
3:E:76:TYR:CZ	3:F:101:MET:O	2.43	0.71
1:A:96:ASN:O	1:A:100:VAL:HG23	1.91	0.71
3:D:47:ILE:CD1	3:E:3:GLN:HG2	2.21	0.71
3:E:74:ILE:C	3:E:74:ILE:HD13	2.15	0.71
1:A:14:ASP:OD2	4:A:197:HOH:O	2.09	0.71
3:D:58:ILE:CG2	3:D:60:SER:OG	2.38	0.71
1:A:9:ASP:HB3	1:A:86:TYR:HE2	1.55	0.71
1:A:27:GLN:OE1	1:A:35:THR:HG22	1.91	0.71
3:D:28:THR:OG1	3:D:39:ILE:HG21	1.89	0.71
1:A:7:ARG:HH12	1:A:55:HIS:HB3	1.55	0.70
2:C:227:GLN:HB2	2:C:231:ASP:OD1	1.91	0.70
3:G:4:ASN:O	3:G:8:LEU:HB2	1.91	0.70
1:A:129:ARG:HH22	1:A:131:HIS:CG	2.08	0.70
2:C:227:GLN:CA	2:C:230:ILE:HG12	2.17	0.70
3:D:47:ILE:HG21	3:E:3:GLN:CG	2.21	0.70
3:F:93:PRO:HD2	3:G:1:THR:H3	1.56	0.70
3:D:14:ASN:O	3:D:88:TRP:HD1	1.74	0.70
3:E:42:PHE:CE2	3:E:82:VAL:HG13	2.26	0.70
1:A:155:ILE:O	1:A:156:ALA:CB	2.27	0.70
3:E:5:ILE:HG12	3:E:5:ILE:O	1.92	0.70
3:E:58:ILE:HG22	3:E:60:SER:H	1.57	0.70
3:H:29:GLU:CG	3:H:29:GLU:O	2.40	0.70
1:A:190:ALA:H	1:A:191:PRO:HD3	1.56	0.70
3:F:53:PRO:HA	3:F:57:HIS:CD2	2.26	0.69
3:E:77:LEU:HD11	3:F:78:THR:HG21	1.74	0.69
3:F:69:LYS:HB2	3:G:67:ARG:NH2	2.07	0.69
1:A:129:ARG:HH21	1:A:131:HIS:CB	1.87	0.69
3:G:74:ILE:HD12	3:G:77:LEU:HB2	1.74	0.69
3:H:37:MET:HG3	3:H:38:ALA:N	2.06	0.69
3:H:68:MET:O	3:H:68:MET:HG3	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:PRO:HA	1:A:84:TYR:CE2	2.27	0.69
3:H:36:GLU:CD	3:H:36:GLU:N	2.49	0.69
1:A:88:LEU:O	1:A:89:ALA:O	2.11	0.69
3:E:33:GLY:O	3:E:34:LYS:CB	2.41	0.69
3:F:31:LEU:O	3:F:31:LEU:HG	1.93	0.69
1:A:188:GLY:O	1:A:189:ASN:HB2	1.91	0.69
2:C:227:GLN:O	2:C:228:SER:O	2.10	0.69
3:D:20:LEU:HD22	3:D:82:VAL:HG11	1.75	0.69
3:D:26:SER:OG	3:D:41:THR:HG21	1.92	0.69
3:E:14:ASN:HD22	3:E:90:ASN:HB3	1.57	0.69
3:G:54:SER:OG	3:G:57:HIS:HD2	1.74	0.68
1:A:107:HIS:O	1:A:110:GLU:HB2	1.93	0.68
3:H:65:ILE:HG22	3:H:66:GLU:OE1	1.93	0.68
3:D:23:LYS:HB3	3:D:81:LYS:HG3	1.73	0.68
3:H:29:GLU:O	3:H:29:GLU:HG3	1.91	0.68
1:A:76:ILE:HG22	1:A:77:LEU:H	1.58	0.68
3:F:87:THR:CG2	3:F:94:HIS:HB3	2.23	0.68
1:A:82:THR:HA	1:A:130:VAL:O	1.93	0.68
3:D:36:GLU:O	3:D:52:VAL:HA	1.94	0.68
3:F:69:LYS:CB	3:G:67:ARG:HH21	2.07	0.68
1:A:132:PHE:HD1	1:A:132:PHE:H	1.42	0.68
2:C:239:GLU:OE1	2:C:239:GLU:HA	1.94	0.68
3:D:2:PRO:CB	3:D:8:LEU:HD12	2.23	0.68
3:F:67:ARG:HG3	3:F:67:ARG:HH11	1.59	0.68
3:H:5:ILE:HD11	3:H:98:ALA:HB3	1.76	0.68
2:C:223:PHE:O	2:C:227:GLN:HG2	1.94	0.67
2:C:239:GLU:O	2:C:240:LEU:HB2	1.94	0.67
3:H:5:ILE:CD1	3:H:98:ALA:HB3	2.24	0.67
3:E:80:ALA:O	3:E:81:LYS:HG2	1.95	0.67
3:D:48:PHE:CD2	3:D:85:LEU:HD23	2.30	0.67
3:F:83:GLU:HG3	3:F:84:LYS:N	2.09	0.67
3:G:23:LYS:O	3:G:43:LYS:NZ	2.27	0.67
3:D:19:THR:HG21	4:D:106:HOH:O	1.95	0.67
3:H:8:LEU:C	3:H:8:LEU:CD2	2.67	0.67
3:D:32:ALA:HB1	3:E:12:TYR:CE2	2.29	0.67
3:D:48:PHE:HE2	3:D:85:LEU:HD23	1.56	0.67
3:F:70:ASP:OD1	3:G:67:ARG:NH1	2.27	0.67
3:G:33:GLY:N	3:H:61:GLN:HE21	1.93	0.66
1:A:15:GLU:O	1:A:18:GLN:HG3	1.95	0.66
3:E:5:ILE:HG21	3:E:84:LYS:HZ2	1.60	0.66
3:E:23:LYS:HA	3:E:80:ALA:HB3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:67:ARG:HG3	3:E:67:ARG:NH1	2.10	0.66
3:F:83:GLU:HG3	3:F:100:SER:OG	1.95	0.66
3:E:58:ILE:O	3:E:61:GLN:HB2	1.94	0.66
3:F:52:VAL:O	3:F:54:SER:N	2.22	0.66
3:G:54:SER:OG	3:G:57:HIS:CD2	2.47	0.66
3:H:88:TRP:CZ3	3:H:97:ALA:HB2	2.31	0.66
3:F:87:THR:HG23	3:F:94:HIS:HB3	1.76	0.66
3:D:70:ASP:OD1	3:E:67:ARG:NH1	2.28	0.66
2:C:233:HIS:CE1	3:D:67:ARG:HG3	2.30	0.66
1:A:143:ARG:HH12	1:A:146:ARG:NH2	1.81	0.66
3:G:9:CYS:C	3:G:11:GLU:H	2.04	0.66
3:G:46:ALA:HB1	3:G:48:PHE:HE1	1.60	0.66
1:A:106:PRO:O	1:A:107:HIS:CD2	2.49	0.65
1:A:174:TRP:HA	1:A:174:TRP:CE3	2.31	0.65
3:D:81:LYS:NZ	3:D:103:ASN:O	2.29	0.65
1:A:4:LYS:HG2	1:A:87:VAL:HG13	1.77	0.65
3:E:48:PHE:CE1	3:E:87:THR:HG21	2.31	0.65
3:E:76:TYR:OH	3:F:101:MET:O	2.14	0.65
1:A:69:ALA:O	1:A:72:VAL:HG22	1.97	0.65
3:E:26:SER:HB2	3:E:41:THR:HB	1.78	0.65
1:A:190:ALA:HB3	1:A:191:PRO:HD3	1.77	0.65
3:F:29:GLU:OE2	3:G:71:THR:CG2	2.40	0.65
1:A:12:PRO:HA	1:A:84:TYR:HE2	1.62	0.65
2:C:227:GLN:NE2	3:F:74:ILE:HB	2.11	0.65
3:D:2:PRO:HD3	3:H:35:ARG:HH21	1.62	0.65
3:F:54:SER:HB2	3:F:56:GLN:OE1	1.96	0.65
3:G:2:PRO:HB2	3:G:8:LEU:CD2	2.27	0.65
3:E:83:GLU:CG	3:E:84:LYS:N	2.60	0.65
3:F:46:ALA:HB1	3:F:48:PHE:CZ	2.31	0.65
3:H:1:THR:CG2	3:H:2:PRO:CD	2.53	0.65
3:E:42:PHE:CZ	3:E:82:VAL:HG11	2.21	0.65
3:E:89:ASN:HD22	3:E:90:ASN:N	1.95	0.65
3:E:58:ILE:CG2	3:E:60:SER:OG	2.44	0.65
3:D:28:THR:HB	3:D:39:ILE:HG22	1.78	0.64
3:F:78:THR:HG22	3:F:80:ALA:H	1.61	0.64
3:E:44:ASN:OD1	3:E:44:ASN:O	2.14	0.64
3:D:47:ILE:HD12	3:E:3:GLN:OE1	1.96	0.64
3:E:35:ARG:HD2	3:E:35:ARG:N	2.11	0.64
3:D:52:VAL:O	3:D:54:SER:N	2.31	0.64
3:E:20:LEU:HD22	3:E:42:PHE:CD2	2.32	0.64
3:F:90:ASN:N	3:F:90:ASN:OD1	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:15:THR:CG2	3:D:88:TRP:NE1	2.61	0.64
3:F:15:THR:CG2	3:F:86:CYS:SG	2.86	0.64
3:F:21:ASN:HA	3:F:83:GLU:HA	1.80	0.64
3:E:67:ARG:HH11	3:E:67:ARG:CG	2.08	0.64
3:H:66:GLU:OE1	3:H:69:LYS:NZ	2.25	0.64
3:E:89:ASN:HA	3:E:94:HIS:CE1	2.33	0.64
3:G:48:PHE:CE2	3:G:87:THR:HG21	2.32	0.64
3:E:72:LEU:HA	3:E:75:ALA:HB3	1.78	0.64
3:G:99:ILE:HD12	3:G:100:SER:N	2.13	0.64
3:H:57:HIS:O	3:H:58:ILE:C	2.41	0.64
1:A:190:ALA:H	1:A:191:PRO:CD	2.08	0.63
3:E:54:SER:OG	3:E:62:LYS:NZ	2.30	0.63
3:F:69:LYS:HB3	3:G:67:ARG:HH21	1.63	0.63
3:G:42:PHE:HB2	3:G:46:ALA:HB3	1.80	0.63
1:A:31:PHE:CE1	2:C:219:LYS:HG3	2.32	0.63
3:D:28:THR:CB	3:D:39:ILE:HG21	2.28	0.63
3:H:51:GLU:OE2	3:H:91:LYS:CE	2.46	0.63
3:G:32:ALA:C	3:H:61:GLN:HE21	2.07	0.63
3:F:19:THR:HG23	3:F:84:LYS:HZ2	1.62	0.63
3:F:24:ILE:HD13	3:F:42:PHE:CZ	2.34	0.63
3:D:2:PRO:HB2	3:D:8:LEU:HD12	1.81	0.63
3:D:20:LEU:HD21	3:D:42:PHE:CZ	2.33	0.63
1:A:33:ARG:NH1	3:F:23:LYS:NZ	2.47	0.63
2:C:227:GLN:CA	2:C:230:ILE:CG1	2.72	0.63
1:A:143:ARG:HD3	1:A:144:GLY:N	2.13	0.63
3:G:61:GLN:O	3:G:65:ILE:HG13	1.98	0.63
3:D:32:ALA:HB1	3:E:12:TYR:CZ	2.34	0.62
3:F:50:VAL:HG12	3:F:65:ILE:HG23	1.81	0.62
3:H:1:THR:HG22	3:H:2:PRO:HD2	0.77	0.62
2:C:233:HIS:CE1	3:H:73:ARG:HH22	2.17	0.62
3:E:68:MET:O	3:E:70:ASP:N	2.32	0.62
3:F:92:THR:O	3:G:1:THR:N	2.32	0.62
1:A:15:GLU:C	1:A:18:GLN:HG2	2.23	0.62
3:E:77:LEU:HD12	3:F:78:THR:CG2	2.30	0.62
3:G:3:GLN:O	3:G:4:ASN:HB3	2.00	0.62
3:G:40:ILE:HG13	3:G:40:ILE:O	1.98	0.62
3:H:87:THR:HB	3:H:94:HIS:HB3	1.82	0.62
4:D:109:HOH:O	3:E:1:THR:HG21	2.00	0.62
3:E:24:ILE:HD13	3:E:40:ILE:HG13	1.81	0.62
1:A:59:TYR:CZ	1:A:116:LEU:HD22	2.34	0.62
3:D:1:THR:HG22	3:D:2:PRO:HD2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:73:ARG:HA	3:F:76:TYR:HB3	1.80	0.62
3:G:58:ILE:O	3:G:62:LYS:CG	2.47	0.62
3:E:80:ALA:O	3:E:81:LYS:CG	2.47	0.61
1:A:143:ARG:NH2	3:D:80:ALA:HA	2.14	0.61
3:D:8:LEU:HD21	3:H:30:SER:HB2	1.83	0.61
3:G:31:LEU:C	3:G:31:LEU:CD2	2.73	0.61
1:A:106:PRO:O	1:A:107:HIS:CG	2.53	0.61
1:A:143:ARG:HD3	1:A:144:GLY:H	1.65	0.61
3:F:27:TYR:CD1	3:F:40:ILE:HD11	2.34	0.61
1:A:1:ASN:ND2	1:A:3:ASP:CG	2.59	0.61
1:A:40:ASN:CG	1:A:43:ASP:OD2	2.43	0.61
3:F:67:ARG:HG3	3:F:67:ARG:NH1	2.13	0.61
3:D:96:ILE:O	3:D:96:ILE:CG2	2.47	0.61
3:E:14:ASN:ND2	3:E:90:ASN:HB3	2.15	0.61
3:E:58:ILE:HG22	3:E:60:SER:OG	2.01	0.61
3:E:58:ILE:CG2	3:E:60:SER:H	2.13	0.61
3:E:82:VAL:HG23	3:E:99:ILE:HD13	1.83	0.61
3:D:15:THR:HG22	3:D:88:TRP:CD1	2.35	0.60
3:E:89:ASN:C	3:E:91:LYS:H	2.09	0.60
1:A:40:ASN:ND2	1:A:43:ASP:OD2	2.34	0.60
3:H:68:MET:HE1	3:H:99:ILE:CG2	2.31	0.60
3:H:5:ILE:CD1	3:H:98:ALA:CB	2.79	0.60
1:A:175:ARG:HD2	1:A:180:ILE:HD11	1.83	0.60
3:D:48:PHE:CE2	3:D:85:LEU:CD2	2.75	0.60
1:A:173:ALA:O	1:A:179:TRP:HB2	2.01	0.60
3:D:65:ILE:HD12	3:H:31:LEU:HD12	1.81	0.60
3:H:58:ILE:O	3:H:60:SER:N	2.35	0.60
1:A:77:LEU:H	1:A:77:LEU:HD22	1.67	0.60
1:A:185:PRO:CG	2:C:202:LYS:HG2	2.32	0.60
3:E:76:TYR:O	3:E:77:LEU:C	2.45	0.60
3:E:58:ILE:HG22	3:E:60:SER:N	2.17	0.59
2:C:227:GLN:HA	2:C:230:ILE:CD1	2.32	0.59
3:E:54:SER:OG	3:E:62:LYS:HD2	2.03	0.59
3:G:35:ARG:HE	3:H:11:GLU:CD	2.10	0.59
1:A:13:PRO:HD3	1:A:84:TYR:CZ	2.36	0.59
3:E:24:ILE:CG2	3:E:26:SER:O	2.51	0.59
3:E:27:TYR:OH	3:E:29:GLU:HG3	2.02	0.59
3:H:14:ASN:OD1	3:H:14:ASN:N	2.36	0.59
1:A:175:ARG:C	1:A:180:ILE:HD13	2.28	0.59
1:A:190:ALA:N	1:A:191:PRO:HD3	2.16	0.59
3:H:41:THR:HG22	3:H:47:ILE:HG23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:4:ASN:OD1	3:D:4:ASN:C	2.45	0.59
3:D:39:ILE:CG2	3:D:39:ILE:O	2.49	0.59
3:G:58:ILE:HD12	3:G:60:SER:OG	2.02	0.59
3:G:91:LYS:HD2	4:G:107:HOH:O	2.02	0.59
3:G:16:GLN:CD	3:G:89:ASN:HD22	2.11	0.59
1:A:132:PHE:CD1	1:A:132:PHE:N	2.70	0.59
1:A:143:ARG:HH11	1:A:146:ARG:NH2	1.89	0.59
1:A:174:TRP:CE3	1:A:183:ALA:HB2	2.37	0.59
3:F:58:ILE:HD11	3:F:60:SER:OG	2.02	0.59
3:E:20:LEU:O	3:E:22:ASP:N	2.36	0.58
3:F:83:GLU:OE1	3:F:84:LYS:HD2	2.03	0.58
3:D:35:ARG:CZ	3:E:2:PRO:HD3	2.32	0.58
3:D:56:GLN:HE21	3:D:57:HIS:HE1	1.47	0.58
3:F:79:GLU:O	3:F:80:ALA:C	2.46	0.58
2:C:227:GLN:O	2:C:231:ASP:HB2	2.03	0.58
3:E:49:GLN:O	3:E:96:ILE:CD1	2.49	0.58
3:F:56:GLN:CD	3:F:57:HIS:CE1	2.81	0.58
3:F:58:ILE:HG12	3:F:59:ASP:N	2.17	0.58
1:A:98:ASN:HD21	1:A:108:PRO:HA	1.67	0.58
2:C:229:ASP:OD1	3:D:73:ARG:HG2	2.04	0.58
3:F:9:CYS:SG	3:F:15:THR:CG2	2.92	0.58
1:A:170:GLU:CB	1:A:192:ARG:HH21	2.05	0.58
3:D:14:ASN:HB3	3:D:90:ASN:HD21	1.65	0.58
3:D:78:THR:HG23	3:D:80:ALA:HB2	1.86	0.58
1:A:88:LEU:CD2	1:A:119:ILE:HG21	2.34	0.58
3:D:27:TYR:HD1	3:D:40:ILE:HD11	1.66	0.58
3:E:83:GLU:CD	3:E:84:LYS:HE3	2.29	0.58
2:C:227:GLN:HE21	3:F:74:ILE:HB	1.69	0.58
3:E:15:THR:HA	3:E:87:THR:O	2.04	0.58
1:A:35:THR:HG22	1:A:35:THR:O	2.03	0.57
2:C:229:ASP:HB2	3:D:74:ILE:HB	1.86	0.57
3:D:50:VAL:HG11	3:D:69:LYS:CG	2.29	0.57
3:G:42:PHE:HD2	3:G:46:ALA:HB3	1.67	0.57
1:A:148:ARG:NH1	3:E:79:GLU:O	2.38	0.57
2:C:203:THR:O	2:C:206:LEU:HB2	2.05	0.57
3:F:57:HIS:ND1	3:F:57:HIS:N	2.51	0.57
3:H:74:ILE:O	3:H:78:THR:HB	2.04	0.57
3:H:37:MET:CG	3:H:38:ALA:N	2.62	0.57
3:H:68:MET:O	3:H:72:LEU:HG	2.03	0.57
3:H:75:ALA:O	3:H:80:ALA:N	2.38	0.57
3:D:54:SER:O	3:D:57:HIS:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:76:TYR:C	3:D:78:THR:H	2.12	0.57
1:A:5:LEU:HD23	1:A:94:MET:HE3	1.86	0.57
3:D:34:LYS:HE2	3:E:58:ILE:HG13	1.87	0.57
3:E:87:THR:HG23	3:E:94:HIS:HB3	1.85	0.57
3:D:5:ILE:HB	3:H:28:THR:HG21	1.87	0.57
3:E:65:ILE:O	3:E:65:ILE:HG22	2.05	0.57
3:F:27:TYR:CD1	3:F:40:ILE:CD1	2.86	0.56
3:G:31:LEU:HD23	3:G:32:ALA:N	2.20	0.56
2:C:231:ASP:OD2	3:F:74:ILE:CG2	2.54	0.56
3:D:67:ARG:NH1	3:H:70:ASP:OD1	2.38	0.56
3:E:73:ARG:O	3:E:77:LEU:HD23	2.05	0.56
3:E:83:GLU:HG2	3:E:84:LYS:CG	2.19	0.56
3:F:20:LEU:HD23	3:F:85:LEU:HD23	1.87	0.56
3:D:82:VAL:HG22	3:D:99:ILE:HD11	1.88	0.56
3:F:31:LEU:O	3:F:31:LEU:CG	2.52	0.56
3:G:2:PRO:CB	3:G:8:LEU:HD23	2.35	0.56
1:A:1:ASN:HD21	1:A:3:ASP:CG	2.14	0.56
2:C:232:THR:HG21	3:D:73:ARG:HH22	1.69	0.56
3:D:103:ASN:OD1	3:H:25:PHE:HE1	1.89	0.56
2:C:230:ILE:HG21	3:H:74:ILE:HD13	1.88	0.56
3:F:8:LEU:HD23	3:F:8:LEU:C	2.31	0.56
3:F:31:LEU:HB2	3:G:64:ALA:HB1	1.88	0.56
3:E:74:ILE:HD12	3:E:74:ILE:H	1.69	0.56
1:A:16:ILE:HD13	1:A:22:LEU:HD23	1.88	0.56
2:C:230:ILE:HG23	3:H:74:ILE:HD13	1.87	0.56
3:E:82:VAL:CG2	3:E:99:ILE:HD13	2.35	0.56
3:G:54:SER:HB2	3:G:55:SER:O	2.05	0.56
1:A:108:PRO:O	1:A:109:ASP:C	2.49	0.56
3:H:27:TYR:CD1	3:H:27:TYR:C	2.82	0.56
3:E:13:HIS:CD2	3:E:13:HIS:O	2.59	0.56
1:A:109:ASP:HB2	1:A:110:GLU:OE1	2.06	0.55
3:E:31:LEU:C	3:E:31:LEU:HD23	2.31	0.55
3:E:89:ASN:ND2	3:E:90:ASN:N	2.53	0.55
1:A:110:GLU:HG3	4:A:217:HOH:O	2.05	0.55
1:A:63:SER:HB2	1:A:69:ALA:HB2	1.88	0.55
1:A:66:LEU:O	1:A:67:ARG:C	2.49	0.55
3:E:25:PHE:O	3:F:102:ALA:HA	2.06	0.55
3:G:31:LEU:HA	3:H:64:ALA:HB1	1.89	0.55
3:H:90:ASN:HD22	3:H:91:LYS:HD3	1.72	0.55
1:A:92:PRO:HD3	1:A:153:LEU:HG	1.88	0.55
3:F:32:ALA:O	3:F:35:ARG:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:56:GLN:OE1	3:F:57:HIS:CE1	2.60	0.55
1:A:54:ARG:HG3	1:A:61:SER:HB3	1.89	0.55
1:A:64:ILE:HG13	1:A:64:ILE:O	2.05	0.55
1:A:81:SER:O	1:A:130:VAL:O	2.24	0.55
3:E:27:TYR:HD1	3:E:40:ILE:HD11	1.71	0.55
3:G:82:VAL:HG11	3:G:99:ILE:HD11	1.87	0.55
3:D:73:ARG:O	3:D:73:ARG:CG	2.52	0.55
3:G:26:SER:HA	3:H:101:MET:O	2.07	0.55
1:A:12:PRO:HB2	1:A:14:ASP:OD2	2.07	0.55
1:A:91:ALA:O	1:A:94:MET:HG2	2.07	0.55
1:A:150:TYR:C	1:A:152:ASN:H	2.15	0.55
3:D:68:MET:O	3:D:70:ASP:N	2.40	0.55
3:D:99:ILE:O	3:H:28:THR:HA	2.06	0.55
1:A:176:GLU:O	1:A:180:ILE:HB	2.07	0.55
3:H:4:ASN:HB3	3:H:6:THR:H	1.72	0.55
1:A:119:ILE:HG23	1:A:123:GLN:HB3	1.88	0.54
3:D:14:ASN:O	3:D:88:TRP:CD1	2.59	0.54
3:D:73:ARG:HH11	3:D:73:ARG:HB3	1.72	0.54
3:F:46:ALA:HB1	3:F:48:PHE:CE2	2.41	0.54
3:G:2:PRO:CB	3:G:8:LEU:CD2	2.85	0.54
1:A:129:ARG:NH2	1:A:131:HIS:ND1	2.56	0.54
3:D:11:GLU:HB3	3:D:12:TYR:CD1	2.43	0.54
3:E:82:VAL:CG2	3:E:99:ILE:CD1	2.85	0.54
3:F:84:LYS:CB	3:F:100:SER:OG	2.53	0.54
3:F:69:LYS:HB3	3:G:67:ARG:NH2	2.20	0.54
1:A:170:GLU:HB3	1:A:192:ARG:CZ	2.33	0.54
3:G:20:LEU:O	3:G:21:ASN:C	2.50	0.54
1:A:16:ILE:CD1	1:A:22:LEU:CD2	2.86	0.54
3:D:48:PHE:CD2	3:D:85:LEU:CD2	2.91	0.54
3:E:22:ASP:O	3:E:81:LYS:CE	2.52	0.54
3:F:37:MET:HA	3:F:69:LYS:NZ	2.23	0.54
3:G:20:LEU:HD11	3:G:85:LEU:HD12	1.89	0.54
3:H:88:TRP:CE3	3:H:97:ALA:HB2	2.42	0.54
1:A:40:ASN:HD22	1:A:43:ASP:N	1.96	0.54
1:A:88:LEU:O	1:A:89:ALA:C	2.50	0.54
3:D:26:SER:HG	3:D:41:THR:HG21	1.71	0.54
3:G:25:PHE:CD2	3:G:41:THR:HG22	2.43	0.54
1:A:16:ILE:CD1	1:A:22:LEU:HD23	2.38	0.53
3:D:68:MET:C	3:D:70:ASP:N	2.61	0.53
3:E:19:THR:HG22	3:E:21:ASN:OD1	2.07	0.53
3:E:30:SER:O	3:E:36:GLU:OE1	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:58:ILE:HG21	3:E:60:SER:OG	2.08	0.53
1:A:119:ILE:CG2	1:A:123:GLN:HB3	2.39	0.53
3:H:58:ILE:HG22	3:H:59:ASP:OD1	2.08	0.53
3:F:24:ILE:HG21	3:F:40:ILE:CG1	2.28	0.53
3:E:17:ILE:HG22	3:E:18:TYR:N	2.22	0.53
3:H:87:THR:HA	3:H:95:ALA:O	2.07	0.53
1:A:13:PRO:HB3	1:A:127:TRP:CZ2	2.44	0.53
1:A:33:ARG:NH1	3:F:23:LYS:HZ3	2.06	0.53
2:C:202:LYS:O	2:C:206:LEU:HG	2.08	0.53
3:D:3:GLN:OE1	3:H:47:ILE:HD13	2.08	0.53
1:A:174:TRP:HA	1:A:174:TRP:HE3	1.70	0.53
3:D:31:LEU:CD2	3:E:97:ALA:HA	2.28	0.53
3:D:73:ARG:HH11	3:D:73:ARG:CB	2.22	0.53
2:C:204:GLN:O	2:C:205:SER:C	2.52	0.53
3:E:47:ILE:HD13	3:F:3:GLN:HB3	1.91	0.53
2:C:231:ASP:HB3	3:E:73:ARG:HH22	1.73	0.53
1:A:10:SER:O	1:A:11:ARG:C	2.51	0.53
1:A:9:ASP:OD1	1:A:10:SER:N	2.42	0.52
1:A:131:HIS:CE1	1:A:136:ASP:CB	2.80	0.52
3:F:19:THR:HG23	3:F:84:LYS:HZ1	1.75	0.52
3:F:83:GLU:HG3	3:F:84:LYS:H	1.74	0.52
3:H:5:ILE:HD13	3:H:98:ALA:HB1	1.91	0.52
2:C:234:ASN:N	2:C:234:ASN:HD22	2.06	0.52
1:A:131:HIS:HE1	1:A:136:ASP:CB	2.13	0.52
1:A:175:ARG:HD2	1:A:180:ILE:CD1	2.40	0.52
3:D:15:THR:HG22	3:D:88:TRP:NE1	2.23	0.52
3:F:76:TYR:CD1	3:F:76:TYR:C	2.87	0.52
3:G:24:ILE:HG21	3:G:76:TYR:HB2	1.90	0.52
3:D:39:ILE:HA	3:D:48:PHE:O	2.09	0.52
3:F:2:PRO:HB3	3:F:7:ASP:HB2	1.92	0.52
3:F:8:LEU:O	3:F:11:GLU:HB3	2.10	0.52
1:A:40:ASN:HD21	1:A:43:ASP:H	1.53	0.52
1:A:59:TYR:CZ	1:A:116:LEU:CD2	2.93	0.52
3:E:14:ASN:HB3	3:E:90:ASN:CB	2.32	0.52
3:E:81:LYS:NZ	3:E:81:LYS:HB3	2.25	0.52
3:H:9:CYS:SG	3:H:15:THR:HB	2.49	0.52
3:H:15:THR:HA	3:H:87:THR:O	2.09	0.52
3:E:13:HIS:HB2	4:E:109:HOH:O	2.09	0.52
3:E:68:MET:O	3:E:69:LYS:C	2.53	0.52
3:F:73:ARG:NH1	3:G:71:THR:OG1	2.43	0.52
3:G:9:CYS:C	3:G:11:GLU:N	2.67	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:18:TYR:O	3:H:84:LYS:HB3	2.10	0.52
3:G:32:ALA:O	3:G:36:GLU:HG3	2.09	0.52
3:E:47:ILE:HG21	3:F:3:GLN:CB	2.36	0.51
3:F:24:ILE:HD11	3:F:82:VAL:HG21	1.92	0.51
3:F:93:PRO:CD	3:G:1:THR:H3	2.22	0.51
3:D:65:ILE:CD1	3:H:31:LEU:HD11	2.29	0.51
3:E:2:PRO:HB2	3:E:8:LEU:HD23	1.92	0.51
3:F:82:VAL:HG22	3:F:99:ILE:HD11	1.93	0.51
3:H:24:ILE:CG2	3:H:26:SER:O	2.54	0.51
1:A:91:ALA:CB	1:A:92:PRO:HD2	2.37	0.51
3:D:5:ILE:CG2	3:D:84:LYS:HZ1	2.21	0.51
3:D:15:THR:CG2	3:D:88:TRP:CD1	2.94	0.51
3:H:50:VAL:HG21	3:H:72:LEU:HD12	1.91	0.51
1:A:188:GLY:O	1:A:189:ASN:CB	2.57	0.51
2:C:235:ARG:HH22	2:C:239:GLU:HB2	0.68	0.51
3:D:20:LEU:HD11	3:D:48:PHE:CE2	2.45	0.51
3:F:53:PRO:HB3	3:F:65:ILE:HD12	1.93	0.51
1:A:21:GLY:C	1:A:23:MET:CE	2.84	0.51
3:E:31:LEU:HD23	3:E:32:ALA:N	2.25	0.51
3:F:22:ASP:HA	3:F:81:LYS:HG3	1.92	0.51
1:A:60:VAL:CG2	1:A:118:GLY:HA2	2.41	0.51
2:C:227:GLN:NE2	3:F:74:ILE:CA	2.73	0.51
3:D:47:ILE:O	3:D:48:PHE:HD1	1.89	0.51
1:A:74:GLN:HB3	1:A:83:TYR:OH	2.11	0.50
1:A:12:PRO:HG2	4:A:197:HOH:O	2.11	0.50
2:C:227:GLN:C	2:C:230:ILE:HG13	2.36	0.50
3:D:65:ILE:HA	3:H:31:LEU:CD1	2.41	0.50
3:D:66:GLU:O	3:E:67:ARG:NH2	2.45	0.50
3:F:9:CYS:SG	3:F:15:THR:HG21	2.52	0.50
1:A:70:HIS:NE2	1:A:74:GLN:OE1	2.44	0.50
1:A:169:PRO:O	1:A:188:GLY:HA2	2.11	0.50
1:A:185:PRO:HG2	2:C:202:LYS:HE2	1.92	0.50
3:E:77:LEU:CD1	3:F:78:THR:CG2	2.80	0.50
3:G:26:SER:OG	3:G:41:THR:HB	2.11	0.50
1:A:42:TYR:O	1:A:46:ARG:HG2	2.11	0.50
3:E:57:HIS:HD2	3:E:61:GLN:OE1	1.94	0.50
3:G:41:THR:HA	3:G:46:ALA:O	2.11	0.50
1:A:88:LEU:CD2	1:A:119:ILE:HG12	2.41	0.50
2:C:228:SER:CB	3:D:77:LEU:HD23	2.41	0.50
3:F:53:PRO:HA	3:F:57:HIS:NE2	2.26	0.50
3:H:5:ILE:O	3:H:9:CYS:N	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:233:HIS:CE1	3:D:67:ARG:HA	2.47	0.50
3:D:16:GLN:CD	3:D:89:ASN:HB3	2.37	0.50
3:F:28:THR:HA	3:G:99:ILE:O	2.12	0.50
3:H:24:ILE:HG21	3:H:40:ILE:HB	1.93	0.50
1:A:107:HIS:O	1:A:108:PRO:C	2.55	0.50
3:D:14:ASN:CB	3:D:90:ASN:HD22	2.23	0.50
3:E:2:PRO:HG2	3:E:8:LEU:HD22	1.94	0.50
3:G:55:SER:C	3:G:56:GLN:CG	2.84	0.50
1:A:125:TYR:CD1	1:A:125:TYR:C	2.89	0.50
3:D:7:ASP:O	3:D:8:LEU:C	2.54	0.50
1:A:174:TRP:CZ3	1:A:179:TRP:HB3	2.46	0.49
1:A:59:TYR:CE2	1:A:116:LEU:HB2	2.47	0.49
1:A:174:TRP:O	1:A:180:ILE:HD12	2.12	0.49
3:F:40:ILE:O	3:F:47:ILE:HA	2.11	0.49
3:G:74:ILE:CD1	3:G:77:LEU:HB2	2.39	0.49
3:H:27:TYR:HD1	3:H:27:TYR:O	1.95	0.49
3:H:73:ARG:O	3:H:76:TYR:HB3	2.12	0.49
3:E:83:GLU:HB2	3:E:102:ALA:CB	2.43	0.49
3:E:83:GLU:HB2	3:E:102:ALA:HB3	1.94	0.49
3:F:93:PRO:CD	3:G:1:THR:N	2.75	0.49
3:G:43:LYS:HE2	3:G:43:LYS:N	2.19	0.49
3:D:58:ILE:O	3:D:61:GLN:N	2.43	0.49
3:D:58:ILE:N	3:D:58:ILE:HD13	2.27	0.49
1:A:184:PRO:HG2	1:A:187:CYS:SG	2.52	0.49
3:E:71:THR:O	3:E:74:ILE:HD13	2.13	0.49
3:H:37:MET:HB2	3:H:50:VAL:O	2.13	0.49
3:G:18:TYR:HH	3:G:94:HIS:HE2	1.59	0.49
1:A:25:ARG:HD2	1:A:56:ASP:OD1	2.13	0.49
3:D:2:PRO:HB3	3:D:8:LEU:CA	2.42	0.49
3:D:6:THR:O	3:D:7:ASP:O	2.31	0.49
3:D:19:THR:CG2	4:D:106:HOH:O	2.58	0.49
3:D:24:ILE:HG21	3:D:40:ILE:HG13	1.93	0.49
3:E:53:PRO:HB3	3:E:62:LYS:HG3	1.94	0.49
3:F:58:ILE:HG12	3:F:59:ASP:H	1.77	0.49
3:G:87:THR:OG1	3:G:94:HIS:HD2	1.96	0.49
3:H:91:LYS:O	3:H:94:HIS:HA	2.13	0.49
3:E:2:PRO:HB2	3:E:8:LEU:CD2	2.42	0.49
3:H:4:ASN:ND2	3:H:7:ASP:OD2	2.46	0.49
3:H:14:ASN:O	3:H:88:TRP:HD1	1.96	0.49
1:A:21:GLY:C	1:A:23:MET:HE3	2.38	0.49
3:D:66:GLU:OE1	3:E:63:LYS:NZ	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:75:ALA:CA	3:D:78:THR:HG22	2.43	0.49
3:F:87:THR:HG21	3:F:94:HIS:HB3	1.94	0.49
3:G:18:TYR:CD1	3:G:87:THR:HG23	2.48	0.49
3:G:42:PHE:CG	3:G:46:ALA:HB3	2.46	0.49
3:H:83:GLU:HB3	3:H:100:SER:OG	2.13	0.49
2:C:219:LYS:O	2:C:223:PHE:CB	2.58	0.49
3:G:30:SER:HB3	3:G:35:ARG:O	2.12	0.49
2:C:211:LEU:O	2:C:215:GLN:HG3	2.13	0.48
3:F:24:ILE:HG22	3:F:41:THR:O	2.13	0.48
3:F:69:LYS:C	3:G:67:ARG:HH22	2.20	0.48
2:C:219:LYS:O	2:C:223:PHE:N	2.40	0.48
3:F:72:LEU:O	3:F:73:ARG:HB3	2.13	0.48
1:A:108:PRO:O	1:A:110:GLU:N	2.46	0.48
3:D:2:PRO:CG	3:D:11:GLU:OE1	2.56	0.48
3:E:24:ILE:HG22	3:E:26:SER:O	2.13	0.48
2:C:220:ARG:NE	3:E:77:LEU:O	2.46	0.48
3:E:25:PHE:CD1	3:F:103:ASN:ND2	2.81	0.48
3:E:57:HIS:CD2	3:E:61:GLN:OE1	2.66	0.48
3:H:93:PRO:O	3:H:94:HIS:C	2.55	0.48
2:C:227:GLN:O	2:C:228:SER:C	2.56	0.48
2:C:239:GLU:OE1	2:C:239:GLU:CA	2.61	0.48
1:A:98:ASN:HB2	1:A:111:GLN:NE2	2.28	0.48
1:A:106:PRO:C	1:A:107:HIS:CG	2.92	0.48
1:A:174:TRP:CE3	1:A:179:TRP:HB3	2.48	0.48
3:D:39:ILE:O	3:D:40:ILE:HD12	2.12	0.48
3:E:92:THR:HA	3:E:93:PRO:C	2.38	0.48
3:F:15:THR:HG22	3:F:16:GLN:H	1.78	0.48
3:G:42:PHE:CD2	3:G:46:ALA:CB	2.91	0.48
3:D:66:GLU:HG3	3:E:67:ARG:NH2	2.28	0.48
3:D:67:ARG:NH1	3:H:69:LYS:CB	2.74	0.48
3:D:91:LYS:CG	4:D:117:HOH:O	2.60	0.48
1:A:76:ILE:CG2	1:A:77:LEU:N	2.72	0.48
1:A:120:PRO:O	1:A:122:SER:N	2.47	0.48
3:E:36:GLU:HG2	3:F:64:ALA:HB2	1.96	0.48
3:G:41:THR:O	3:G:42:PHE:CD2	2.67	0.48
2:C:230:ILE:CG1	2:C:231:ASP:N	2.75	0.48
3:E:20:LEU:O	3:E:22:ASP:HB2	2.14	0.48
1:A:170:GLU:CB	1:A:192:ARG:CZ	2.92	0.48
3:D:2:PRO:HD3	3:H:35:ARG:NH2	2.27	0.48
3:D:43:LYS:HE2	3:D:43:LYS:HB3	1.51	0.48
3:H:39:ILE:HD13	3:H:40:ILE:N	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:13:HIS:C	3:E:13:HIS:HD2	2.17	0.47
3:E:48:PHE:HD1	3:E:94:HIS:O	1.97	0.47
3:F:19:THR:HA	3:F:83:GLU:O	2.14	0.47
1:A:143:ARG:NH2	3:D:78:THR:O	2.26	0.47
2:C:229:ASP:CG	3:D:73:ARG:HG2	2.39	0.47
3:D:93:PRO:CD	3:E:1:THR:HB	2.44	0.47
3:H:68:MET:HE2	3:H:72:LEU:HD21	1.96	0.47
3:D:66:GLU:CD	3:E:63:LYS:HZ2	2.21	0.47
3:D:75:ALA:HA	3:D:78:THR:HG22	1.95	0.47
3:F:40:ILE:HG22	3:F:48:PHE:HB2	1.97	0.47
3:F:93:PRO:HD2	3:G:1:THR:N	2.25	0.47
2:C:231:ASP:OD2	3:F:74:ILE:HG22	2.13	0.47
3:D:73:ARG:HE	3:E:71:THR:HA	1.79	0.47
3:E:76:TYR:O	3:E:78:THR:N	2.48	0.47
3:E:62:LYS:H	3:E:62:LYS:HD3	1.79	0.47
3:E:92:THR:N	3:E:93:PRO:O	2.48	0.47
3:G:1:THR:HB	3:G:2:PRO:HD2	1.97	0.47
3:G:66:GLU:OE1	3:G:66:GLU:HA	2.15	0.47
3:D:92:THR:O	3:E:1:THR:OG1	2.19	0.47
1:A:191:PRO:O	1:A:192:ARG:HB2	2.14	0.47
3:E:82:VAL:HG21	3:E:99:ILE:CD1	2.45	0.47
3:F:73:ARG:C	3:F:76:TYR:H	2.23	0.47
3:G:18:TYR:O	3:G:84:LYS:HA	2.14	0.47
3:G:89:ASN:C	3:G:91:LYS:H	2.22	0.47
3:E:91:LYS:O	3:E:92:THR:OG1	2.27	0.47
1:A:154:ASP:CB	4:A:222:HOH:O	2.62	0.47
3:D:49:GLN:OE1	3:D:91:LYS:HE3	2.15	0.47
3:E:20:LEU:C	3:E:22:ASP:N	2.71	0.47
3:D:28:THR:HB	3:D:39:ILE:HG21	1.91	0.47
3:H:51:GLU:OE1	3:H:57:HIS:HE1	1.97	0.47
3:H:58:ILE:C	3:H:60:SER:N	2.73	0.47
1:A:8:ALA:HB2	1:A:85:LEU:HD11	1.96	0.46
3:D:12:TYR:O	3:D:13:HIS:ND1	2.49	0.46
3:D:49:GLN:O	3:D:95:ALA:HA	2.15	0.46
3:D:53:PRO:HG3	3:E:63:LYS:NZ	2.30	0.46
3:F:72:LEU:O	3:F:73:ARG:CB	2.63	0.46
3:D:102:ALA:HB1	3:D:103:ASN:ND2	2.30	0.46
3:E:72:LEU:O	3:E:75:ALA:HB3	2.15	0.46
1:A:183:ALA:O	1:A:184:PRO:O	2.34	0.46
3:D:15:THR:HG23	3:D:88:TRP:NE1	2.29	0.46
3:E:82:VAL:HG21	3:E:99:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:78:THR:O	3:G:79:GLU:HB2	2.14	0.46
2:C:233:HIS:HE1	3:H:73:ARG:HH22	1.59	0.46
1:A:75:THR:HG21	4:A:216:HOH:O	2.15	0.46
3:E:72:LEU:HA	3:E:75:ALA:CB	2.46	0.46
3:E:71:THR:O	3:E:75:ALA:HB2	2.16	0.46
3:E:103:ASN:HD22	3:E:103:ASN:HA	1.50	0.46
3:H:52:VAL:HA	3:H:53:PRO:HD3	1.84	0.46
3:H:75:ALA:O	3:H:80:ALA:HB2	2.15	0.46
2:C:227:GLN:CB	2:C:230:ILE:HD11	2.45	0.46
3:D:5:ILE:HB	3:H:28:THR:CG2	2.45	0.46
3:E:54:SER:OG	3:E:62:LYS:CE	2.64	0.46
3:G:41:THR:HG23	3:G:42:PHE:H	1.81	0.46
1:A:91:ALA:HB3	1:A:123:GLN:NE2	2.31	0.46
3:D:92:THR:O	3:D:92:THR:HG22	2.16	0.46
3:E:65:ILE:HG22	3:E:69:LYS:HE2	1.98	0.46
3:F:61:GLN:O	3:F:65:ILE:HG13	2.16	0.46
3:F:90:ASN:ND2	4:F:111:HOH:O	2.14	0.46
3:D:34:LYS:NZ	3:E:60:SER:OG	2.36	0.46
3:D:39:ILE:O	3:D:39:ILE:HG23	2.15	0.45
3:E:17:ILE:CG2	3:E:84:LYS:HB3	2.46	0.45
3:E:68:MET:C	3:E:70:ASP:N	2.72	0.45
3:F:2:PRO:HG2	3:F:8:LEU:HA	1.98	0.45
3:G:51:GLU:HG3	3:G:95:ALA:CB	2.45	0.45
3:D:34:LYS:HZ1	3:E:58:ILE:HG21	1.82	0.45
3:D:101:MET:O	3:H:26:SER:HA	2.16	0.45
3:E:88:TRP:HB3	3:E:90:ASN:OD1	2.16	0.45
3:G:36:GLU:OE2	3:H:61:GLN:HG2	2.16	0.45
3:G:66:GLU:OE1	3:G:69:LYS:NZ	2.35	0.45
3:H:58:ILE:C	3:H:60:SER:H	2.24	0.45
1:A:98:ASN:ND2	1:A:105:SER:OG	2.50	0.45
2:C:239:GLU:OE2	3:G:63:LYS:HD2	2.16	0.45
3:D:39:ILE:C	3:D:40:ILE:HD12	2.41	0.45
3:D:53:PRO:HG3	3:E:63:LYS:HZ3	1.82	0.45
3:F:52:VAL:C	3:F:54:SER:N	2.75	0.45
3:H:27:TYR:CD1	3:H:27:TYR:O	2.69	0.45
1:A:154:ASP:HB2	4:A:222:HOH:O	2.15	0.45
2:C:231:ASP:OD2	3:F:74:ILE:HG21	2.15	0.45
3:D:59:ASP:O	3:D:62:LYS:HB2	2.17	0.45
3:F:9:CYS:SG	3:F:15:THR:HG22	2.56	0.45
3:H:33:GLY:O	3:H:34:LYS:HB3	2.16	0.45
1:A:45:ALA:HB1	1:A:106:PRO:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:26:SER:OG	3:D:41:THR:HG22	2.13	0.45
3:D:47:ILE:HG21	3:E:3:GLN:HG2	1.97	0.45
3:E:19:THR:O	3:E:20:LEU:HG	2.16	0.45
3:H:54:SER:O	3:H:56:GLN:NE2	2.50	0.45
1:A:85:LEU:HD13	1:A:130:VAL:HG21	1.98	0.45
1:A:184:PRO:O	1:A:187:CYS:HB2	2.16	0.45
3:D:8:LEU:CD2	3:H:30:SER:HB2	2.47	0.45
3:D:67:ARG:CZ	3:H:70:ASP:OD1	2.64	0.45
3:E:65:ILE:O	3:E:65:ILE:CG2	2.65	0.45
3:F:36:GLU:CD	3:G:60:SER:HB2	2.42	0.45
1:A:9:ASP:HB3	1:A:86:TYR:CE2	2.45	0.45
2:C:229:ASP:OD2	3:D:73:ARG:CZ	2.65	0.45
3:H:85:LEU:CD1	3:H:96:ILE:HG12	2.47	0.45
3:E:48:PHE:HB3	3:E:96:ILE:HD11	1.99	0.45
3:F:18:TYR:HB2	3:F:85:LEU:HB2	1.99	0.45
3:G:42:PHE:CB	3:G:46:ALA:HB3	2.46	0.45
3:E:54:SER:HG	3:E:62:LYS:HD2	1.80	0.45
3:H:39:ILE:HA	3:H:48:PHE:O	2.17	0.45
2:C:228:SER:OG	2:C:229:ASP:N	2.50	0.44
3:E:54:SER:HG	3:E:62:LYS:NZ	2.13	0.44
3:E:76:TYR:HD1	3:E:77:LEU:HD22	1.83	0.44
3:E:91:LYS:HG3	3:E:95:ALA:CB	2.48	0.44
3:H:83:GLU:HG3	3:H:102:ALA:CB	2.47	0.44
1:A:88:LEU:HD23	1:A:119:ILE:HG12	1.98	0.44
3:D:65:ILE:HG23	3:D:69:LYS:HE2	1.99	0.44
3:H:85:LEU:HD12	3:H:96:ILE:HG12	1.97	0.44
2:C:217:LYS:H	2:C:217:LYS:HG2	1.69	0.44
3:D:93:PRO:HD3	3:E:1:THR:HB	1.99	0.44
3:E:14:ASN:ND2	3:E:90:ASN:CB	2.66	0.44
3:H:20:LEU:O	3:H:21:ASN:HB2	2.16	0.44
3:H:61:GLN:O	3:H:65:ILE:HD12	2.18	0.44
1:A:120:PRO:O	1:A:123:GLN:N	2.42	0.44
3:D:2:PRO:HB2	3:D:8:LEU:CD1	2.47	0.44
3:E:92:THR:CA	3:E:93:PRO:C	2.90	0.44
3:G:103:ASN:ND2	3:G:103:ASN:C	2.72	0.44
3:D:23:LYS:HD2	3:D:79:GLU:HB3	2.00	0.44
1:A:86:TYR:O	1:A:88:LEU:CD1	2.61	0.44
1:A:119:ILE:HG23	1:A:123:GLN:CB	2.47	0.44
2:C:225:GLY:O	2:C:228:SER:CB	2.66	0.44
3:D:20:LEU:HD21	3:D:42:PHE:CE1	2.53	0.44
3:D:67:ARG:O	3:D:70:ASP:CB	2.54	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:22:ASP:C	3:E:81:LYS:HA	2.14	0.44
3:F:19:THR:CG2	3:F:84:LYS:HZ1	2.31	0.44
3:H:22:ASP:CG	3:H:23:LYS:H	2.25	0.44
3:D:12:TYR:CD1	3:D:12:TYR:N	2.86	0.44
3:D:16:GLN:HG3	3:D:18:TYR:CE1	2.53	0.44
3:D:91:LYS:HD2	4:D:119:HOH:O	2.18	0.44
3:E:85:LEU:CD1	3:E:99:ILE:HG12	2.48	0.44
3:F:13:HIS:O	3:F:14:ASN:HB2	2.17	0.44
1:A:49:GLN:HB2	1:A:49:GLN:HE21	1.35	0.43
3:E:86:CYS:SG	3:E:87:THR:N	2.90	0.43
3:F:14:ASN:ND2	3:F:90:ASN:HB3	2.33	0.43
3:G:15:THR:HG23	3:G:88:TRP:CD1	2.53	0.43
3:H:16:GLN:N	3:H:87:THR:O	2.46	0.43
3:D:64:ALA:HB1	3:H:31:LEU:HA	2.00	0.43
3:E:32:ALA:O	3:E:35:ARG:HB2	2.17	0.43
1:A:76:ILE:CG2	1:A:77:LEU:H	2.23	0.43
3:F:69:LYS:C	3:G:67:ARG:NH2	2.76	0.43
3:G:93:PRO:HD3	3:H:1:THR:HB	2.00	0.43
1:A:175:ARG:CD	1:A:180:ILE:HD11	2.49	0.43
3:F:50:VAL:CG1	3:F:65:ILE:CG2	2.92	0.43
3:H:41:THR:C	3:H:42:PHE:CD1	2.97	0.43
3:E:5:ILE:O	3:E:5:ILE:CG1	2.65	0.43
3:E:52:VAL:H	3:E:52:VAL:HG23	1.45	0.43
3:E:58:ILE:O	3:E:61:GLN:N	2.45	0.43
3:E:88:TRP:O	3:E:91:LYS:HB2	2.19	0.43
2:C:233:HIS:CD2	3:D:67:ARG:HH21	2.37	0.43
3:D:6:THR:HA	3:D:17:ILE:HD12	2.00	0.43
3:D:101:MET:C	3:H:76:TYR:OH	2.61	0.43
3:E:14:ASN:O	3:E:88:TRP:HA	2.19	0.43
3:E:17:ILE:HG22	3:E:18:TYR:H	1.82	0.43
3:H:20:LEU:HD12	3:H:44:ASN:HD21	1.82	0.43
2:C:233:HIS:HE1	3:D:67:ARG:HG3	1.78	0.43
3:E:30:SER:OG	3:E:31:LEU:N	2.51	0.43
3:G:18:TYR:HE1	3:G:87:THR:OG1	1.90	0.43
3:H:12:TYR:CD1	3:H:12:TYR:N	2.87	0.43
3:H:81:LYS:HG2	3:H:103:ASN:OD1	2.19	0.43
2:C:221:GLN:NE2	3:E:78:THR:O	2.52	0.43
3:D:74:ILE:O	3:D:78:THR:HB	2.19	0.43
3:E:48:PHE:CE1	3:E:94:HIS:HB2	2.54	0.43
2:C:227:GLN:C	2:C:230:ILE:CG1	2.92	0.42
3:D:47:ILE:C	3:D:48:PHE:CD1	2.96	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:18:TYR:HE2	3:H:94:HIS:HD2	1.67	0.42
3:D:61:GLN:HE21	3:H:33:GLY:H	1.66	0.42
3:E:17:ILE:CG2	3:E:18:TYR:N	2.82	0.42
3:E:18:TYR:O	3:E:84:LYS:HA	2.20	0.42
3:E:76:TYR:CD1	3:E:77:LEU:HD22	2.54	0.42
3:E:78:THR:O	3:E:79:GLU:HB2	2.19	0.42
3:G:42:PHE:HD2	3:G:46:ALA:CB	2.30	0.42
3:D:43:LYS:C	3:D:45:GLY:H	2.26	0.42
3:E:37:MET:HB2	3:E:37:MET:HE3	1.62	0.42
1:A:40:ASN:ND2	1:A:43:ASP:CG	2.76	0.42
1:A:176:GLU:O	1:A:180:ILE:HG22	2.19	0.42
2:C:225:GLY:O	2:C:228:SER:HB3	2.19	0.42
3:D:15:THR:HG23	3:D:88:TRP:HE1	1.84	0.42
3:D:20:LEU:HD22	3:D:82:VAL:CG1	2.47	0.42
3:D:80:ALA:O	3:D:81:LYS:HB2	2.17	0.42
2:C:235:ARG:HB2	3:E:70:ASP:OD2	2.20	0.42
3:D:43:LYS:C	3:D:45:GLY:N	2.77	0.42
3:F:56:GLN:CD	3:F:56:GLN:H	2.27	0.42
3:F:84:LYS:N	3:F:100:SER:OG	2.52	0.42
3:H:81:LYS:O	3:H:101:MET:HG3	2.19	0.42
3:D:7:ASP:O	3:D:9:CYS:N	2.53	0.42
3:D:74:ILE:O	3:D:78:THR:CB	2.68	0.42
3:F:22:ASP:N	3:F:82:VAL:O	2.53	0.42
3:F:33:GLY:O	3:F:34:LYS:CB	2.65	0.42
3:G:28:THR:HG23	3:H:99:ILE:O	2.20	0.42
3:H:13:HIS:CD2	3:H:14:ASN:ND2	2.87	0.42
3:D:65:ILE:O	3:D:69:LYS:HE2	2.20	0.42
3:E:17:ILE:CG2	3:E:18:TYR:H	2.33	0.42
3:G:41:THR:O	3:G:42:PHE:CG	2.73	0.42
3:H:83:GLU:HG3	3:H:102:ALA:HB3	2.01	0.42
3:E:88:TRP:HB2	3:E:95:ALA:HB3	2.01	0.42
3:F:55:SER:C	3:F:57:HIS:H	2.28	0.42
3:H:2:PRO:O	3:H:2:PRO:HG2	2.20	0.42
1:A:139:LEU:HD23	1:A:140:HIS:N	2.35	0.42
3:G:3:GLN:O	3:G:4:ASN:CB	2.66	0.42
1:A:105:SER:O	1:A:108:PRO:HD3	2.20	0.41
1:A:156:ALA:HA	1:A:157:PRO:HD2	1.72	0.41
3:E:1:THR:HA	3:E:2:PRO:HD3	1.90	0.41
3:G:77:LEU:HD22	3:H:78:THR:HG21	2.03	0.41
1:A:11:ARG:HA	1:A:12:PRO:HD3	1.82	0.41
1:A:134:VAL:O	1:A:134:VAL:CG1	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:56:GLN:HG3	3:D:57:HIS:CE1	2.54	0.41
3:D:78:THR:O	3:D:79:GLU:C	2.62	0.41
3:E:18:TYR:HE1	3:E:87:THR:HB	1.84	0.41
3:E:91:LYS:HG3	3:E:95:ALA:HB2	2.01	0.41
3:F:58:ILE:HG23	3:F:61:GLN:HG3	2.01	0.41
3:H:40:ILE:HD13	3:H:72:LEU:HD13	2.02	0.41
1:A:95:PHE:CE2	1:A:164:LEU:HD12	2.55	0.41
2:C:234:ASN:N	2:C:234:ASN:ND2	2.66	0.41
3:D:8:LEU:HD21	3:H:30:SER:CB	2.48	0.41
3:D:57:HIS:HB3	3:D:61:GLN:OE1	2.20	0.41
3:E:25:PHE:CA	3:F:103:ASN:ND2	2.67	0.41
3:E:83:GLU:HG2	3:E:84:LYS:H	1.80	0.41
3:F:20:LEU:HD12	3:F:44:ASN:HD21	1.85	0.41
3:H:75:ALA:O	3:H:80:ALA:CA	2.69	0.41
1:A:94:MET:SD	1:A:115:ALA:HB2	2.61	0.41
3:F:57:HIS:CD2	3:F:65:ILE:HD11	2.54	0.41
1:A:119:ILE:HA	1:A:120:PRO:HD2	1.80	0.41
1:A:150:TYR:C	1:A:152:ASN:N	2.78	0.41
3:D:14:ASN:CB	3:D:90:ASN:ND2	2.70	0.41
3:F:53:PRO:O	3:F:54:SER:O	2.38	0.41
3:G:47:ILE:HG21	3:H:3:GLN:HB3	2.02	0.41
4:G:112:HOH:O	3:H:67:ARG:HD2	2.20	0.41
3:H:49:GLN:NE2	3:H:91:LYS:HG3	2.36	0.41
1:A:66:LEU:C	1:A:68:SER:N	2.78	0.41
1:A:91:ALA:HB1	1:A:92:PRO:CD	2.43	0.41
3:D:24:ILE:HG22	3:D:26:SER:O	2.19	0.41
3:D:47:ILE:HD12	3:E:3:GLN:HG2	1.97	0.41
3:F:15:THR:CG2	3:F:87:THR:O	2.68	0.41
3:F:18:TYR:HB2	3:F:85:LEU:CB	2.50	0.41
3:G:53:PRO:HG2	4:G:115:HOH:O	2.19	0.41
3:G:56:GLN:HG3	3:G:57:HIS:CD2	2.56	0.41
3:E:42:PHE:CE2	3:E:82:VAL:CG1	2.93	0.41
1:A:6:TYR:CD1	1:A:66:LEU:HD23	2.55	0.41
1:A:73:GLY:C	1:A:75:THR:H	2.26	0.41
2:C:227:GLN:HA	2:C:230:ILE:HD11	2.01	0.41
3:E:86:CYS:HB3	3:E:98:ALA:HB3	2.02	0.41
3:E:89:ASN:C	3:E:91:LYS:N	2.76	0.41
3:F:67:ARG:O	3:F:70:ASP:HB2	2.20	0.41
3:G:68:MET:O	3:G:68:MET:HG3	2.21	0.41
3:D:40:ILE:HD13	3:D:72:LEU:HD13	2.03	0.41
3:E:74:ILE:N	3:E:74:ILE:CD1	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:2:PRO:HG2	3:F:8:LEU:CA	2.50	0.41
3:F:36:GLU:H	3:F:36:GLU:HG3	1.55	0.41
3:H:5:ILE:HD11	3:H:98:ALA:CB	2.44	0.41
3:H:14:ASN:C	3:H:89:ASN:OD1	2.63	0.41
3:E:59:ASP:CG	3:E:62:LYS:NZ	2.66	0.41
3:D:99:ILE:HG22	3:H:29:GLU:HG2	2.03	0.40
3:E:5:ILE:HD11	3:E:86:CYS:H	1.86	0.40
3:E:20:LEU:N	3:E:83:GLU:O	2.53	0.40
3:F:30:SER:CB	3:F:35:ARG:O	2.68	0.40
3:G:48:PHE:CD2	3:G:87:THR:HG21	2.56	0.40
3:H:17:ILE:HD13	3:H:17:ILE:HA	1.76	0.40
1:A:69:ALA:C	1:A:72:VAL:HG22	2.46	0.40
1:A:83:TYR:HE2	1:A:85:LEU:CD1	2.34	0.40
1:A:155:ILE:O	1:A:156:ALA:O	2.39	0.40
3:H:24:ILE:CG2	3:H:40:ILE:HB	2.52	0.40
1:A:185:PRO:C	1:A:187:CYS:H	2.28	0.40
2:C:219:LYS:HG2	2:C:223:PHE:CE2	2.56	0.40
3:D:20:LEU:HD11	3:D:48:PHE:HE2	1.85	0.40
3:D:73:ARG:O	3:D:77:LEU:HB2	2.22	0.40
3:E:62:LYS:O	3:E:66:GLU:CG	2.66	0.40
3:F:20:LEU:O	3:F:21:ASN:C	2.65	0.40
3:F:50:VAL:CG1	3:F:65:ILE:HG23	2.49	0.40
3:F:56:GLN:CD	3:F:57:HIS:HE1	2.26	0.40
3:F:78:THR:O	3:F:79:GLU:HB2	2.20	0.40
3:G:1:THR:O	3:G:3:GLN:N	2.53	0.40
3:D:58:ILE:HD12	3:D:58:ILE:HA	1.72	0.40
3:E:94:HIS:N	3:E:94:HIS:CD2	2.89	0.40
3:G:9:CYS:SG	3:G:17:ILE:HG12	2.61	0.40
3:G:25:PHE:CD2	3:G:41:THR:CG2	3.04	0.40
1:A:43:ASP:O	1:A:44:HIS:C	2.65	0.40
1:A:83:TYR:CZ	1:A:130:VAL:HG11	2.57	0.40
1:A:124:ILE:O	1:A:142:ASN:ND2	2.55	0.40
3:D:23:LYS:HA	3:D:81:LYS:HA	2.03	0.40
3:E:54:SER:OG	3:E:62:LYS:CD	2.68	0.40
3:E:80:ALA:O	3:E:81:LYS:CB	2.69	0.40
3:H:4:ASN:HB2	3:H:7:ASP:H	1.86	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:ARG:O	3:E:14:ASN:ND2[1_655]	1.74	0.46
1:A:192:ARG:CD	3:E:13:HIS:NE2[1_655]	2.11	0.09

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	190/194 (98%)	149 (78%)	22 (12%)	19 (10%)	0	0
2	C	43/46 (94%)	40 (93%)	2 (5%)	1 (2%)	5	6
3	D	101/103 (98%)	81 (80%)	11 (11%)	9 (9%)	0	0
3	E	101/103 (98%)	73 (72%)	18 (18%)	10 (10%)	0	0
3	F	101/103 (98%)	87 (86%)	8 (8%)	6 (6%)	1	0
3	G	101/103 (98%)	80 (79%)	15 (15%)	6 (6%)	1	0
3	H	101/103 (98%)	83 (82%)	13 (13%)	5 (5%)	1	1
All	All	738/755 (98%)	593 (80%)	89 (12%)	56 (8%)	1	0

All (56) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	THR
1	A	49	GLN
1	A	77	LEU
1	A	111	GLN
1	A	155	ILE
1	A	188	GLY
1	A	189	ASN
2	C	228	SER
3	D	7	ASP
3	D	8	LEU
3	E	54	SER
3	E	62	LYS

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Mol	Chain	Res	Type
3	E	80	ALA
3	F	33	GLY
3	F	54	SER
3	G	2	PRO
3	H	54	SER
3	H	59	ASP
3	H	81	LYS
1	A	66	LEU
1	A	89	ALA
1	A	109	ASP
1	A	121	TYR
3	D	34	LYS
3	D	55	SER
3	D	59	ASP
3	D	77	LEU
3	E	21	ASN
3	E	69	LYS
3	E	79	GLU
3	E	81	LYS
3	E	83	GLU
3	F	80	ALA
3	G	4	ASN
3	G	45	GLY
3	G	80	ALA
3	H	55	SER
1	A	14	ASP
1	A	65	SER
1	A	76	ILE
3	D	53	PRO
3	D	69	LYS
3	D	94	HIS
3	F	14	ASN
3	F	73	ARG
3	G	10	ALA
1	A	108	PRO
1	A	151	SER
1	A	156	ALA
3	H	33	GLY
1	A	184	PRO
3	F	53	PRO
3	G	58	ILE
3	E	77	LEU

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Mol	Chain	Res	Type
1	A	133	GLY
3	E	53	PRO

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	158/160 (99%)	118 (75%)	40 (25%)	0	1
2	C	43/44 (98%)	26 (60%)	17 (40%)	0	0
3	D	90/90 (100%)	63 (70%)	27 (30%)	0	0
3	E	90/90 (100%)	65 (72%)	25 (28%)	0	0
3	F	90/90 (100%)	60 (67%)	30 (33%)	0	0
3	G	90/90 (100%)	67 (74%)	23 (26%)	0	0
3	H	90/90 (100%)	53 (59%)	37 (41%)	0	0
All	All	651/654 (100%)	452 (69%)	199 (31%)	0	0

All (199) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	5	LEU
1	A	15	GLU
1	A	16	ILE
1	A	17	LYS
1	A	18	GLN
1	A	29	GLU
1	A	35	THR
1	A	36	GLN
1	A	37	MET
1	A	41	LEU
1	A	49	GLN
1	A	53	VAL
1	A	56	ASP
1	A	61	SER

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Mol	Chain	Res	Type
1	A	64	ILE
1	A	66	LEU
1	A	70	HIS
1	A	71	LEU
1	A	72	VAL
1	A	75	THR
1	A	77	LEU
1	A	80	HIS
1	A	81	SER
1	A	111	GLN
1	A	112	GLU
1	A	116	LEU
1	A	125	TYR
1	A	130	VAL
1	A	134	VAL
1	A	139	LEU
1	A	141	ARG
1	A	143	ARG
1	A	146	ARG
1	A	152	ASN
1	A	155	ILE
1	A	177	GLU
1	A	180	ILE
1	A	189	ASN
1	A	192	ARG
2	C	196	SER
2	C	197	ASN
2	C	200	ASP
2	C	202	LYS
2	C	203	THR
2	C	217	LYS
2	C	222	ILE
2	C	224	SER
2	C	229	ASP
2	C	230	ILE
2	C	231	ASP
2	C	233	HIS
2	C	235	ARG
2	C	236	ILE
2	C	238	ASP
2	C	239	GLU
2	C	240	LEU

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Mol	Chain	Res	Type
3	D	1	THR
3	D	3	GLN
3	D	6	THR
3	D	8	LEU
3	D	11	GLU
3	D	17	ILE
3	D	19	THR
3	D	21	ASN
3	D	26	SER
3	D	28	THR
3	D	31	LEU
3	D	34	LYS
3	D	37	MET
3	D	39	ILE
3	D	41	THR
3	D	51	GLU
3	D	52	VAL
3	D	58	ILE
3	D	59	ASP
3	D	62	LYS
3	D	65	ILE
3	D	73	ARG
3	D	74	ILE
3	D	81	LYS
3	D	84	LYS
3	D	92	THR
3	D	96	ILE
3	E	1	THR
3	E	8	LEU
3	E	16	GLN
3	E	17	ILE
3	E	19	THR
3	E	21	ASN
3	E	31	LEU
3	E	34	LYS
3	E	35	ARG
3	E	37	MET
3	E	39	ILE
3	E	40	ILE
3	E	51	GLU
3	E	52	VAL
3	E	58	ILE

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Mol	Chain	Res	Type
3	E	63	LYS
3	E	74	ILE
3	E	78	THR
3	E	81	LYS
3	E	82	VAL
3	E	89	ASN
3	E	99	ILE
3	E	100	SER
3	E	101	MET
3	E	103	ASN
3	F	6	THR
3	F	14	ASN
3	F	15	THR
3	F	17	ILE
3	F	19	THR
3	F	20	LEU
3	F	22	ASP
3	F	24	ILE
3	F	31	LEU
3	F	36	GLU
3	F	37	MET
3	F	40	ILE
3	F	41	THR
3	F	43	LYS
3	F	50	VAL
3	F	56	GLN
3	F	57	HIS
3	F	58	ILE
3	F	59	ASP
3	F	60	SER
3	F	72	LEU
3	F	73	ARG
3	F	74	ILE
3	F	77	LEU
3	F	78	THR
3	F	81	LYS
3	F	83	GLU
3	F	85	LEU
3	F	87	THR
3	F	99	ILE
3	G	8	LEU
3	G	11	GLU

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Mol	Chain	Res	Type
3	G	30	SER
3	G	31	LEU
3	G	34	LYS
3	G	37	MET
3	G	41	THR
3	G	43	LYS
3	G	47	ILE
3	G	49	GLN
3	G	52	VAL
3	G	54	SER
3	G	58	ILE
3	G	62	LYS
3	G	63	LYS
3	G	66	GLU
3	G	73	ARG
3	G	74	ILE
3	G	78	THR
3	G	79	GLU
3	G	90	ASN
3	G	99	ILE
3	G	103	ASN
3	H	1	THR
3	H	3	GLN
3	H	14	ASN
3	H	17	ILE
3	H	19	THR
3	H	20	LEU
3	H	23	LYS
3	H	28	THR
3	H	29	GLU
3	H	31	LEU
3	H	34	LYS
3	H	36	GLU
3	H	39	ILE
3	H	40	ILE
3	H	41	THR
3	H	47	ILE
3	H	52	VAL
3	H	54	SER
3	H	55	SER
3	H	56	GLN
3	H	58	ILE

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Mol	Chain	Res	Type
3	H	59	ASP
3	H	60	SER
3	H	61	GLN
3	H	65	ILE
3	H	66	GLU
3	H	68	MET
3	H	77	LEU
3	H	78	THR
3	H	82	VAL
3	H	83	GLU
3	H	84	LYS
3	H	89	ASN
3	H	90	ASN
3	H	91	LYS
3	H	99	ILE
3	H	101	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1	ASN
1	A	18	GLN
1	A	40	ASN
1	A	49	GLN
1	A	70	HIS
1	A	80	HIS
1	A	98	ASN
1	A	107	HIS
1	A	111	GLN
1	A	123	GLN
1	A	131	HIS
1	A	171	HIS
2	C	227	GLN
2	C	233	HIS
2	C	234	ASN
3	D	56	GLN
3	D	57	HIS
3	D	89	ASN
3	D	90	ASN
3	D	94	HIS
3	D	103	ASN
3	E	13	HIS

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Mol	Chain	Res	Type
3	E	14	ASN
3	E	16	GLN
3	E	44	ASN
3	E	89	ASN
3	E	103	ASN
3	F	3	GLN
3	F	14	ASN
3	F	44	ASN
3	F	57	HIS
3	F	61	GLN
3	F	103	ASN
3	G	3	GLN
3	G	57	HIS
3	G	89	ASN
3	H	4	ASN
3	H	13	HIS
3	H	14	ASN
3	H	49	GLN
3	H	56	GLN
3	H	57	HIS
3	H	61	GLN
3	H	94	HIS

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.