



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:16 AM UTC

PDB ID : 1FGB / pdb_00001fgb
Title : TOXIN
Authors : Zhang, R.-G.; Westbrook, E.
Deposited on : 1996-02-21
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

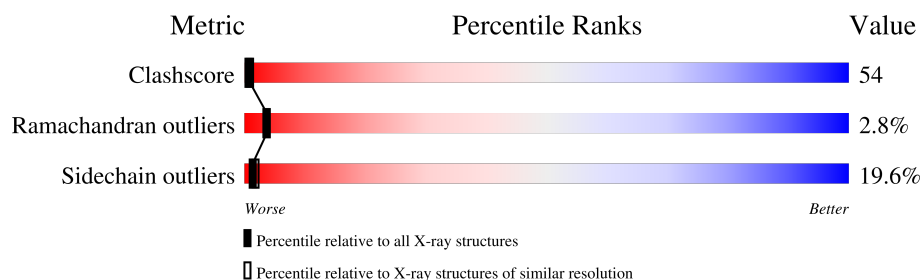
1 Overall quality at a glance

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	D	103	25% 31% 31% 13%
1	E	103	22% 45% 24% 9%
1	F	103	17% 44% 30% 10%
1	G	103	18% 46% 25% 11%
1	H	103	19% 41% 29% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4274 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 B SUBUNIT PENTAMER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	103	Total	C	N	O	S	0	0	0
			814	511	142	156	5			
1	E	103	Total	C	N	O	S	0	0	0
			814	511	142	156	5			
1	F	103	Total	C	N	O	S	0	0	0
			814	511	142	156	5			
1	G	103	Total	C	N	O	S	0	0	0
			814	511	142	156	5			
1	H	103	Total	C	N	O	S	0	0	0
			814	511	142	156	5			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	18	HIS	TYR	conflict	UNP P01556
D	47	THR	ILE	conflict	UNP P01556
E	18	HIS	TYR	conflict	UNP P01556
E	47	THR	ILE	conflict	UNP P01556
F	18	HIS	TYR	conflict	UNP P01556
F	47	THR	ILE	conflict	UNP P01556
G	18	HIS	TYR	conflict	UNP P01556
G	47	THR	ILE	conflict	UNP P01556
H	18	HIS	TYR	conflict	UNP P01556
H	47	THR	ILE	conflict	UNP P01556

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	52	Total	O	0	0
			52	52		
2	E	55	Total	O	0	0
			55	55		

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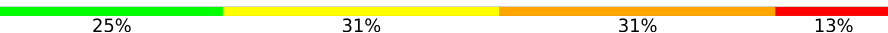
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	32	Total 32	O 32	0	0
2	G	35	Total 35	O 35	0	0
2	H	30	Total 30	O 30	0	0

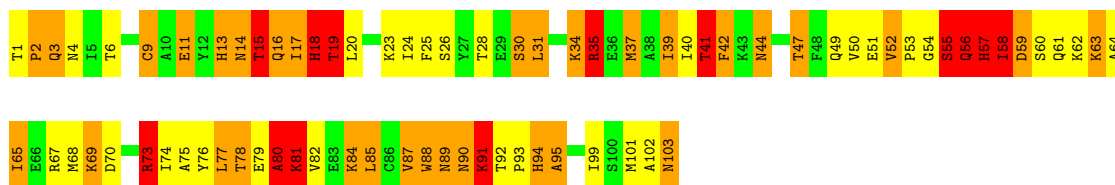
3 Residue-property plots

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.

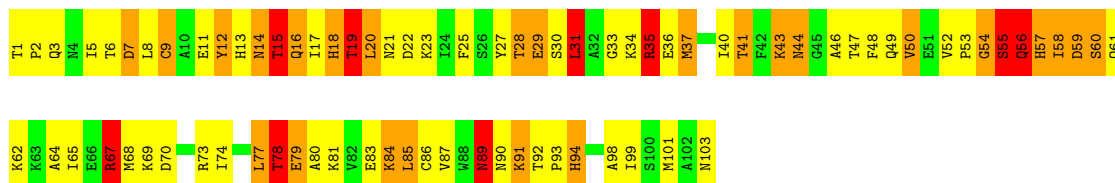
• Molecule 1: CHOLERA TOXIN B SUBUNIT PENTAMER

Chain D: 



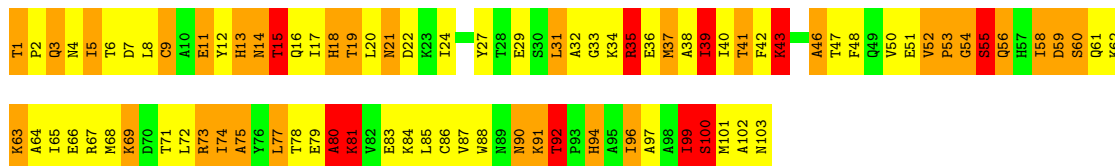
• Molecule 1: CHOLERA TOXIN B SUBUNIT PENTAMER

Chain E: 

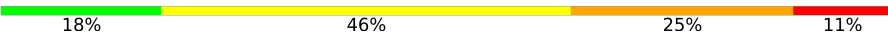


• Molecule 1: CHOLERA TOXIN B SUBUNIT PENTAMER

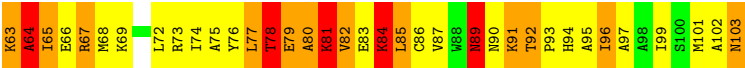
Chain F: 



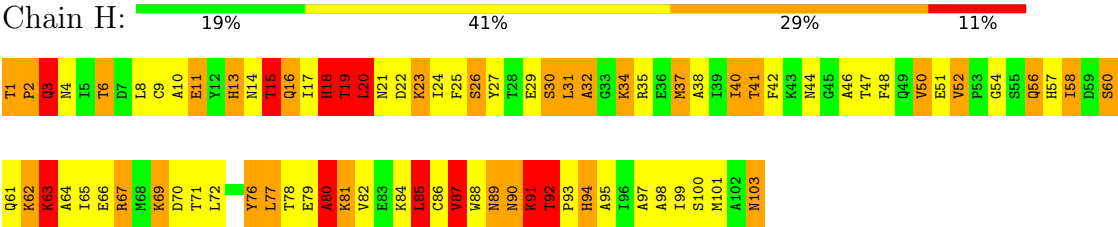
• Molecule 1: CHOLERA TOXIN B SUBUNIT PENTAMER

Chain G: 





● Molecule 1: CHOLERA TOXIN B SUBUNIT PENTAMER



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	39.10Å 94.50Å 67.60Å 90.00° 96.10° 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}	0.171 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4274	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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	D	1.73	8/828 (1.0%)	2.86	87/1118 (7.8%)
1	E	1.73	9/828 (1.1%)	2.99	76/1118 (6.8%)
1	F	2.09	18/828 (2.2%)	3.10	101/1118 (9.0%)
1	G	1.59	5/828 (0.6%)	2.64	69/1118 (6.2%)
1	H	1.77	9/828 (1.1%)	2.81	87/1118 (7.8%)
All	All	1.79	49/4140 (1.2%)	2.89	420/5590 (7.5%)

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	D	0	2
1	E	0	5
1	F	0	6
1	G	0	3
1	H	0	3
All	All	0	19

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	56	GLN	C-N	-22.30	1.01	1.33
1	F	54	GLY	C-N	20.19	1.62	1.33
1	E	54	GLY	C-N	17.32	1.57	1.33
1	F	55	SER	C-N	17.00	1.57	1.33
1	H	64	ALA	C-N	13.71	1.51	1.33
1	G	64	ALA	C-N	11.78	1.48	1.33
1	D	52	VAL	C-N	10.50	1.47	1.33
1	D	64	ALA	C-N	8.74	1.44	1.34
1	E	56	GLN	C-N	-8.39	1.20	1.33
1	H	51	GLU	C-N	8.37	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	13	HIS	C-O	7.71	1.34	1.24
1	F	96	ILE	CA-CB	7.13	1.62	1.54
1	D	13	HIS	C-O	6.86	1.32	1.24
1	F	80	ALA	CA-CB	6.70	1.64	1.53
1	H	38	ALA	CA-C	6.65	1.60	1.52
1	H	19	THR	N-CA	6.63	1.55	1.46
1	F	86	CYS	C-N	-6.42	1.25	1.33
1	E	15	THR	CA-CB	6.41	1.63	1.53
1	E	13	HIS	C-O	6.32	1.31	1.24
1	D	42	PHE	N-CA	6.31	1.53	1.45
1	H	80	ALA	N-CA	-6.30	1.38	1.46
1	F	52	VAL	CA-C	6.28	1.58	1.53
1	F	73	ARG	CD-NE	-6.21	1.37	1.46
1	F	91	LYS	N-CA	6.16	1.53	1.46
1	E	35	ARG	N-CA	6.16	1.52	1.46
1	H	52	VAL	C-N	6.10	1.40	1.33
1	E	18	HIS	C-N	-6.08	1.24	1.33
1	E	55	SER	N-CA	5.91	1.53	1.46
1	G	16	GLN	N-CA	5.80	1.53	1.45
1	H	63	LYS	N-CA	5.67	1.53	1.46
1	E	55	SER	C-N	-5.66	1.25	1.33
1	F	14	ASN	N-CA	5.66	1.55	1.46
1	E	58	ILE	N-CA	5.60	1.53	1.46
1	F	100	SER	N-CA	5.60	1.53	1.46
1	D	59	ASP	N-CA	5.59	1.53	1.46
1	H	80	ALA	CA-CB	5.50	1.62	1.53
1	D	73	ARG	CD-NE	-5.46	1.38	1.46
1	F	19	THR	N-CA	5.41	1.53	1.46
1	F	50	VAL	CA-C	5.36	1.59	1.52
1	F	58	ILE	C-N	-5.33	1.26	1.33
1	G	46	ALA	C-N	5.33	1.41	1.33
1	D	77	LEU	C-N	-5.25	1.26	1.33
1	F	58	ILE	C-O	5.25	1.30	1.24
1	F	15	THR	CA-CB	5.18	1.64	1.53
1	D	3	GLN	N-CA	5.16	1.52	1.46
1	G	60	SER	N-CA	5.15	1.52	1.46
1	F	12	TYR	N-CA	5.11	1.51	1.45
1	H	27	TYR	CA-C	5.07	1.58	1.52
1	G	50	VAL	CA-C	5.06	1.59	1.52

All (420) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	55	SER	O-C-N	-30.11	82.54	122.59
1	F	73	ARG	CD-NE-CZ	20.81	153.53	124.40
1	E	56	GLN	O-C-N	-18.07	98.55	122.59
1	E	55	SER	CA-C-N	16.93	153.88	121.54
1	E	55	SER	C-N-CA	16.93	153.88	121.54
1	D	64	ALA	O-C-N	-16.83	104.28	122.12
1	F	54	GLY	O-C-N	-16.12	101.75	122.70
1	D	73	ARG	CD-NE-CZ	15.15	145.61	124.40
1	H	79	GLU	CA-C-N	14.90	149.99	121.54
1	H	79	GLU	C-N-CA	14.90	149.99	121.54
1	E	13	HIS	CA-CB-CG	14.82	128.62	113.80
1	F	16	GLN	OE1-CD-NE2	-14.49	108.11	122.60
1	H	19	THR	CB-CA-C	14.02	135.34	111.22
1	F	54	GLY	CA-C-N	-13.74	99.58	122.11
1	F	54	GLY	C-N-CA	-13.74	99.58	122.11
1	E	12	TYR	CA-C-N	13.55	139.63	120.79
1	E	12	TYR	C-N-CA	13.55	139.63	120.79
1	F	55	SER	CA-C-N	12.99	146.35	121.54
1	F	55	SER	C-N-CA	12.99	146.35	121.54
1	G	22	ASP	CA-CB-CG	12.91	125.51	112.60
1	F	16	GLN	CB-CG-CD	12.53	133.90	112.60
1	F	94	HIS	CA-CB-CG	-12.20	101.60	113.80
1	G	64	ALA	O-C-N	-11.78	108.44	122.22
1	G	102	ALA	CA-C-N	11.77	142.88	121.70
1	G	102	ALA	C-N-CA	11.77	142.88	121.70
1	F	19	THR	CB-CA-C	11.57	129.29	110.78
1	E	103	ASN	CA-CB-CG	-11.37	101.23	112.60
1	G	50	VAL	N-CA-CB	11.22	125.60	111.46
1	F	9	CYS	CA-C-N	11.19	138.50	120.60
1	F	9	CYS	C-N-CA	11.19	138.50	120.60
1	F	39	ILE	O-C-N	11.04	135.13	123.20
1	D	14	ASN	CA-CB-CG	-10.74	101.86	112.60
1	G	65	ILE	O-C-N	10.61	132.16	121.87
1	H	70	ASP	CA-CB-CG	10.60	123.20	112.60
1	D	81	LYS	N-CA-CB	10.58	128.36	110.49
1	H	18	HIS	CA-C-N	-10.52	107.57	123.14
1	H	18	HIS	C-N-CA	-10.52	107.57	123.14
1	E	40	ILE	CA-C-N	10.26	138.54	122.74
1	E	40	ILE	C-N-CA	10.26	138.54	122.74
1	D	95	ALA	CA-C-O	10.20	132.12	120.60
1	H	64	ALA	CA-C-N	10.12	133.51	120.56
1	H	64	ALA	C-N-CA	10.12	133.51	120.56
1	F	52	VAL	N-CA-C	-10.02	100.02	108.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	79	GLU	CA-C-N	10.00	140.64	121.54
1	F	79	GLU	C-N-CA	10.00	140.64	121.54
1	F	55	SER	O-C-N	-10.00	110.38	122.48
1	F	52	VAL	O-C-N	9.87	132.92	121.57
1	D	70	ASP	O-C-N	9.77	133.29	122.15
1	D	19	THR	CB-CA-C	9.56	126.13	110.74
1	D	18	HIS	O-C-N	9.56	134.67	123.30
1	F	15	THR	N-CA-CB	-9.49	95.83	111.20
1	D	3	GLN	OE1-CD-NE2	9.41	132.01	122.60
1	H	94	HIS	CA-CB-CG	-9.41	104.39	113.80
1	D	78	THR	N-CA-CB	-9.35	96.91	110.47
1	E	54	GLY	CA-C-N	-9.25	103.86	121.54
1	E	54	GLY	C-N-CA	-9.25	103.86	121.54
1	G	79	GLU	CA-C-O	9.21	132.23	120.81
1	G	52	VAL	N-CA-C	-9.05	100.85	108.63
1	E	22	ASP	CA-CB-CG	9.04	121.64	112.60
1	F	58	ILE	O-C-N	-9.04	113.16	122.20
1	H	99	ILE	CA-C-N	9.02	135.48	122.77
1	H	99	ILE	C-N-CA	9.02	135.48	122.77
1	H	51	GLU	N-CA-C	8.92	123.16	110.23
1	H	90	ASN	CA-C-N	8.85	136.90	122.29
1	H	90	ASN	C-N-CA	8.85	136.90	122.29
1	E	77	LEU	CA-C-O	8.77	130.17	119.38
1	F	73	ARG	CA-C-N	8.71	131.53	120.56
1	F	73	ARG	C-N-CA	8.71	131.53	120.56
1	H	79	GLU	CA-CB-CG	8.66	131.43	114.10
1	D	11	GLU	CB-CG-CD	8.65	127.31	112.60
1	H	76	TYR	O-C-N	8.56	131.24	122.08
1	D	4	ASN	CA-C-O	-8.47	112.25	121.31
1	G	89	ASN	CA-C-O	-8.41	109.87	119.79
1	E	6	THR	CA-C-O	-8.40	112.00	120.82
1	F	15	THR	CA-C-O	8.40	131.28	121.46
1	G	6	THR	CA-C-N	8.38	131.33	120.44
1	G	6	THR	C-N-CA	8.38	131.33	120.44
1	F	15	THR	OG1-CB-CG2	8.34	125.98	109.30
1	F	60	SER	O-C-N	8.32	130.94	122.12
1	F	15	THR	N-CA-C	8.30	122.97	109.85
1	F	60	SER	N-CA-C	-8.26	102.27	111.28
1	E	41	THR	CA-C-O	8.25	129.48	120.32
1	D	47	THR	CA-C-N	8.19	136.46	122.37
1	D	47	THR	C-N-CA	8.19	136.46	122.37
1	D	13	HIS	N-CA-C	8.07	121.65	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	4	ASN	CA-CB-CG	8.04	120.64	112.60
1	G	12	TYR	CA-C-O	-8.02	112.05	121.11
1	D	34	LYS	CB-CG-CD	8.00	129.71	111.30
1	E	11	GLU	CB-CG-CD	7.97	126.15	112.60
1	D	64	ALA	CA-C-N	7.89	132.94	120.47
1	D	64	ALA	C-N-CA	7.89	132.94	120.47
1	D	84	LYS	N-CA-C	7.88	121.73	109.52
1	D	85	LEU	CA-CB-CG	7.83	143.70	116.30
1	F	80	ALA	CB-CA-C	-7.83	94.84	110.42
1	H	81	LYS	N-CA-CB	7.82	123.70	110.49
1	G	96	ILE	CA-C-O	7.81	129.95	121.36
1	E	89	ASN	CB-CA-C	7.77	124.20	110.37
1	H	103	ASN	CB-CA-C	7.75	124.83	110.10
1	F	7	ASP	CB-CA-C	7.74	123.64	110.79
1	F	50	VAL	N-CA-CB	7.74	121.21	111.46
1	H	90	ASN	CA-CB-CG	-7.72	104.88	112.60
1	D	58	ILE	O-C-N	-7.71	112.94	122.57
1	F	18	HIS	CA-C-N	-7.70	112.84	122.84
1	F	18	HIS	C-N-CA	-7.70	112.84	122.84
1	F	13	HIS	CA-C-O	-7.63	110.45	119.15
1	G	15	THR	CB-CA-C	7.63	124.87	109.38
1	E	44	ASN	CA-C-O	-7.62	110.62	119.61
1	E	14	ASN	OD1-CG-ND2	7.59	130.19	122.60
1	E	50	VAL	N-CA-CB	7.56	120.86	111.41
1	D	91	LYS	N-CA-CB	7.55	124.68	111.55
1	H	67	ARG	NE-CZ-NH2	-7.54	112.42	119.20
1	D	52	VAL	N-CA-C	-7.45	102.22	108.63
1	D	6	THR	CA-C-N	7.44	130.25	120.28
1	D	6	THR	C-N-CA	7.44	130.25	120.28
1	F	35	ARG	CA-C-O	7.42	130.09	121.78
1	G	18	HIS	CA-C-N	-7.42	112.76	123.00
1	G	18	HIS	C-N-CA	-7.42	112.76	123.00
1	E	68	MET	N-CA-CB	7.40	120.74	110.01
1	F	37	MET	CA-CB-CG	-7.39	99.31	114.10
1	D	16	GLN	OE1-CD-NE2	7.32	129.92	122.60
1	E	54	GLY	O-C-N	7.29	132.17	122.70
1	G	65	ILE	N-CA-C	-7.28	103.19	110.62
1	D	14	ASN	OD1-CG-ND2	7.27	129.87	122.60
1	G	60	SER	O-C-N	7.27	129.56	122.07
1	H	64	ALA	O-C-N	-7.26	112.95	122.39
1	D	50	VAL	N-CA-C	-7.24	97.42	107.99
1	F	91	LYS	CA-CB-CG	7.19	128.49	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	13	HIS	CA-CB-CG	-7.19	106.61	113.80
1	H	44	ASN	CA-CB-CG	-7.17	105.43	112.60
1	D	3	GLN	CA-CB-CG	7.16	128.43	114.10
1	E	7	ASP	CA-CB-CG	7.16	119.76	112.60
1	G	89	ASN	CA-CB-CG	7.15	119.75	112.60
1	D	35	ARG	CD-NE-CZ	-7.12	114.43	124.40
1	E	58	ILE	CB-CA-C	7.08	120.97	110.98
1	H	18	HIS	O-C-N	7.07	132.43	123.23
1	D	42	PHE	CA-C-O	-7.06	113.18	121.44
1	D	26	SER	CA-C-O	7.04	128.88	120.99
1	F	13	HIS	CA-CB-CG	7.02	120.82	113.80
1	E	70	ASP	N-CA-CB	6.97	120.17	110.07
1	H	42	PHE	CA-C-O	-6.95	113.33	121.46
1	D	51	GLU	N-CA-C	6.94	119.53	110.43
1	H	80	ALA	N-CA-C	6.92	125.55	110.80
1	G	4	ASN	O-C-N	6.91	130.20	123.29
1	E	68	MET	O-C-N	6.88	129.16	122.07
1	F	52	VAL	CA-C-N	6.88	128.44	119.84
1	F	52	VAL	C-N-CA	6.88	128.44	119.84
1	G	50	VAL	N-CA-C	-6.84	97.88	107.80
1	D	88	TRP	CA-C-O	6.83	128.21	120.84
1	F	35	ARG	CD-NE-CZ	-6.82	114.85	124.40
1	F	92	THR	N-CA-CB	6.82	123.10	110.27
1	H	80	ALA	CB-CA-C	-6.81	96.87	110.42
1	F	94	HIS	CB-CG-CD2	-6.81	122.35	131.20
1	H	86	CYS	N-CA-C	-6.81	99.13	109.95
1	D	85	LEU	CB-CA-C	6.79	120.16	110.24
1	E	21	ASN	N-CA-CB	6.77	121.72	111.70
1	F	50	VAL	N-CA-C	-6.76	98.00	107.80
1	E	35	ARG	CA-CB-CG	6.74	127.58	114.10
1	H	87	VAL	CA-C-N	6.71	133.76	123.23
1	H	87	VAL	C-N-CA	6.71	133.76	123.23
1	E	21	ASN	O-C-N	6.70	130.85	122.55
1	G	40	ILE	CA-C-N	6.70	133.58	122.73
1	G	40	ILE	C-N-CA	6.70	133.58	122.73
1	F	73	ARG	CG-CD-NE	6.67	126.67	112.00
1	D	69	LYS	CG-CD-CE	6.66	126.61	111.30
1	F	84	LYS	CA-C-N	6.65	132.95	121.64
1	F	84	LYS	C-N-CA	6.65	132.95	121.64
1	E	78	THR	N-CA-CB	-6.65	100.75	110.53
1	H	82	VAL	N-CA-C	-6.65	98.76	108.87
1	D	14	ASN	CB-CG-ND2	-6.64	106.45	116.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	58	ILE	CA-C-O	-6.63	112.17	119.20
1	E	78	THR	CB-CA-C	6.63	121.36	109.29
1	E	56	GLN	CA-C-N	6.62	133.46	122.73
1	E	56	GLN	C-N-CA	6.62	133.46	122.73
1	G	84	LYS	CA-C-O	6.62	128.85	121.11
1	F	13	HIS	CA-C-N	-6.61	113.35	122.87
1	F	13	HIS	C-N-CA	-6.61	113.35	122.87
1	F	51	GLU	N-CA-C	6.61	119.09	110.43
1	F	100	SER	CB-CA-C	6.60	121.64	109.70
1	H	32	ALA	CA-C-O	6.52	128.35	120.92
1	G	8	LEU	O-C-N	6.52	129.13	122.09
1	D	9	CYS	CA-C-N	6.52	131.03	120.60
1	D	9	CYS	C-N-CA	6.52	131.03	120.60
1	H	50	VAL	N-CA-CB	6.51	119.67	111.46
1	F	53	PRO	CA-C-N	6.49	134.13	121.41
1	F	53	PRO	C-N-CA	6.49	134.13	121.41
1	D	3	GLN	N-CA-CB	-6.49	100.28	110.98
1	F	80	ALA	N-CA-C	6.47	124.59	110.80
1	D	73	ARG	N-CA-CB	6.47	119.36	109.98
1	H	100	SER	CA-C-O	6.47	127.10	120.24
1	H	34	LYS	CA-C-O	-6.46	111.27	120.51
1	G	2	PRO	CB-CA-C	6.46	119.66	111.39
1	H	14	ASN	CA-CB-CG	-6.45	106.15	112.60
1	F	13	HIS	N-CA-CB	6.44	120.12	110.53
1	D	37	MET	N-CA-CB	-6.44	99.30	110.76
1	D	95	ALA	N-CA-C	6.43	118.63	108.67
1	H	2	PRO	N-CA-C	6.43	123.13	113.81
1	G	26	SER	CA-CB-OG	6.42	123.95	111.10
1	G	14	ASN	OD1-CG-ND2	6.41	129.01	122.60
1	G	23	LYS	CA-CB-CG	6.40	126.90	114.10
1	E	56	GLN	CB-CG-CD	6.38	123.45	112.60
1	F	21	ASN	N-CA-CB	6.38	121.14	111.70
1	F	43	LYS	N-CA-CB	6.36	119.60	110.06
1	G	86	CYS	CA-C-N	6.36	132.80	122.69
1	G	86	CYS	C-N-CA	6.36	132.80	122.69
1	D	79	GLU	N-CA-CB	6.35	121.56	111.91
1	G	44	ASN	N-CA-C	-6.35	105.52	113.20
1	H	89	ASN	OD1-CG-ND2	-6.34	116.26	122.60
1	E	67	ARG	N-CA-C	-6.33	104.45	111.36
1	H	103	ASN	CA-CB-CG	-6.33	106.27	112.60
1	E	78	THR	OG1-CB-CG2	6.31	121.93	109.30
1	F	79	GLU	CA-CB-CG	6.30	126.70	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	17	ILE	CA-C-O	6.28	127.80	120.71
1	E	19	THR	CA-C-O	-6.26	113.83	120.40
1	H	40	ILE	CA-C-N	6.25	132.38	122.62
1	H	40	ILE	C-N-CA	6.25	132.38	122.62
1	H	41	THR	CA-CB-OG1	-6.25	100.23	109.60
1	E	94	HIS	CA-CB-CG	-6.24	107.56	113.80
1	G	85	LEU	CA-C-N	6.23	131.78	123.05
1	G	85	LEU	C-N-CA	6.23	131.78	123.05
1	E	29	GLU	CB-CG-CD	6.23	123.19	112.60
1	G	81	LYS	N-CA-CB	6.21	120.98	110.49
1	D	78	THR	CA-CB-OG1	-6.20	100.31	109.60
1	H	21	ASN	OD1-CG-ND2	-6.19	116.41	122.60
1	G	103	ASN	CA-CB-CG	6.19	118.79	112.60
1	E	15	THR	N-CA-CB	-6.18	101.49	110.70
1	F	86	CYS	CA-C-N	6.17	131.94	122.25
1	F	86	CYS	C-N-CA	6.17	131.94	122.25
1	F	50	VAL	CA-CB-CG2	6.16	120.88	110.40
1	F	102	ALA	CA-C-N	6.16	132.79	121.70
1	F	102	ALA	C-N-CA	6.16	132.79	121.70
1	D	76	TYR	CA-C-N	6.15	131.14	120.68
1	D	76	TYR	C-N-CA	6.15	131.14	120.68
1	E	37	MET	N-CA-C	6.14	116.67	108.38
1	E	15	THR	N-CA-C	6.13	119.15	110.14
1	D	18	HIS	CA-C-N	-6.13	114.12	123.07
1	D	18	HIS	C-N-CA	-6.13	114.12	123.07
1	D	84	LYS	CA-C-O	6.13	128.61	121.44
1	F	63	LYS	N-CA-CB	6.12	119.22	110.16
1	E	73	ARG	CD-NE-CZ	6.08	132.91	124.40
1	H	89	ASN	CA-CB-CG	6.07	118.67	112.60
1	G	84	LYS	N-CA-C	6.05	119.06	109.50
1	F	39	ILE	CA-C-O	-6.03	113.97	120.36
1	F	75	ALA	CB-CA-C	6.03	121.10	110.85
1	H	94	HIS	CB-CG-CD2	-6.03	123.36	131.20
1	H	11	GLU	CA-CB-CG	6.02	126.14	114.10
1	F	60	SER	CA-C-N	6.01	128.34	120.28
1	F	60	SER	C-N-CA	6.01	128.34	120.28
1	H	79	GLU	N-CA-CB	6.01	120.64	110.49
1	H	15	THR	N-CA-CB	-6.00	101.15	110.46
1	D	102	ALA	CA-C-N	6.00	132.50	121.70
1	D	102	ALA	C-N-CA	6.00	132.50	121.70
1	H	62	LYS	CB-CA-C	-5.98	101.75	110.96
1	H	11	GLU	N-CA-C	5.97	120.30	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	52	VAL	N-CA-CB	5.97	116.61	110.23
1	H	60	SER	O-C-N	5.96	128.21	122.07
1	H	1	THR	CA-C-N	5.93	126.35	119.47
1	H	1	THR	C-N-CA	5.93	126.35	119.47
1	D	69	LYS	N-CA-CB	5.93	118.84	110.12
1	E	40	ILE	CA-C-O	5.93	128.93	121.40
1	D	35	ARG	N-CA-CB	-5.91	103.37	111.65
1	D	50	VAL	N-CA-CB	5.91	118.12	111.21
1	E	20	LEU	CA-C-N	5.91	130.75	122.36
1	E	20	LEU	C-N-CA	5.91	130.75	122.36
1	G	2	PRO	CA-C-O	5.88	128.02	121.43
1	F	36	GLU	CA-CB-CG	5.87	125.84	114.10
1	H	50	VAL	N-CA-C	-5.86	99.30	107.80
1	D	80	ALA	N-CA-C	5.84	123.25	110.80
1	D	15	THR	N-CA-C	5.84	119.08	109.85
1	G	15	THR	OG1-CB-CG2	5.83	120.97	109.30
1	D	4	ASN	CA-C-N	5.83	130.78	121.34
1	D	4	ASN	C-N-CA	5.83	130.78	121.34
1	G	51	GLU	CG-CD-OE2	-5.83	104.99	118.40
1	H	38	ALA	N-CA-CB	5.83	121.04	111.08
1	G	67	ARG	NH1-CZ-NH2	5.78	126.81	119.30
1	G	37	MET	CA-CB-CG	-5.77	102.56	114.10
1	H	37	MET	N-CA-CB	-5.76	102.28	111.62
1	F	56	GLN	OE1-CD-NE2	5.76	128.36	122.60
1	H	62	LYS	N-CA-C	5.76	117.25	110.97
1	H	15	THR	CA-CB-CG2	5.75	120.28	110.50
1	F	58	ILE	CB-CA-C	5.75	121.34	110.94
1	D	73	ARG	NE-CZ-NH1	5.74	127.24	121.50
1	H	11	GLU	CB-CG-CD	5.74	122.36	112.60
1	H	51	GLU	CG-CD-OE2	-5.74	105.21	118.40
1	H	85	LEU	CA-CB-CG	5.72	136.33	116.30
1	E	94	HIS	CB-CG-CD2	-5.71	123.77	131.20
1	H	69	LYS	N-CA-CB	5.70	119.12	110.28
1	G	89	ASN	CB-CG-ND2	5.69	124.94	116.40
1	F	58	ILE	CA-CB-CG1	5.69	120.07	110.40
1	E	28	THR	CA-CB-OG1	-5.67	101.09	109.60
1	E	27	TYR	CA-C-O	5.67	127.18	120.66
1	E	9	CYS	CA-C-O	5.67	126.56	120.55
1	G	15	THR	N-CA-CB	-5.67	100.99	111.13
1	H	3	GLN	CB-CG-CD	5.65	122.21	112.60
1	G	103	ASN	N-CA-CB	5.65	120.11	110.50
1	F	36	GLU	CB-CG-CD	5.65	122.20	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	15	THR	N-CA-C	5.65	118.82	110.46
1	E	50	VAL	N-CA-C	-5.64	99.11	107.51
1	D	76	TYR	CA-CB-CG	-5.63	103.76	113.90
1	F	100	SER	CA-CB-OG	5.63	122.36	111.10
1	F	64	ALA	O-C-N	-5.61	115.66	122.22
1	F	99	ILE	CA-C-N	-5.60	114.11	122.74
1	F	99	ILE	C-N-CA	-5.60	114.11	122.74
1	H	38	ALA	CA-C-O	-5.58	114.81	121.11
1	E	13	HIS	N-CA-C	5.57	117.81	111.02
1	E	79	GLU	CB-CA-C	-5.56	102.78	111.39
1	H	21	ASN	CA-CB-CG	5.56	118.16	112.60
1	E	60	SER	O-C-N	5.55	128.01	122.12
1	G	91	LYS	CA-CB-CG	5.55	125.21	114.10
1	H	26	SER	CA-C-N	5.55	131.66	122.33
1	H	26	SER	C-N-CA	5.55	131.66	122.33
1	D	81	LYS	CA-CB-CG	5.55	125.20	114.10
1	G	52	VAL	CA-C-O	-5.55	114.92	119.47
1	G	90	ASN	CA-CB-CG	-5.54	107.06	112.60
1	E	55	SER	CA-C-O	-5.53	112.61	120.51
1	H	6	THR	N-CA-CB	-5.51	102.01	110.01
1	G	89	ASN	OD1-CG-ND2	-5.50	117.10	122.60
1	F	48	PHE	CA-CB-CG	5.49	119.29	113.80
1	E	30	SER	CA-C-N	5.48	130.82	122.37
1	E	30	SER	C-N-CA	5.48	130.82	122.37
1	E	56	GLN	CA-CB-CG	5.48	125.07	114.10
1	E	41	THR	CA-CB-CG2	5.47	119.80	110.50
1	G	96	ILE	N-CA-C	5.46	117.49	109.63
1	H	38	ALA	N-CA-C	-5.43	101.03	109.72
1	F	74	ILE	CA-C-O	5.43	126.92	121.17
1	E	17	ILE	CA-C-O	5.43	126.84	120.71
1	D	16	GLN	CB-CG-CD	-5.41	103.40	112.60
1	F	8	LEU	O-C-N	5.41	128.32	122.15
1	D	3	GLN	O-C-N	5.41	128.73	122.19
1	G	41	THR	CA-C-O	5.40	126.87	120.66
1	F	12	TYR	CB-CA-C	5.40	118.71	109.80
1	F	46	ALA	CA-C-N	5.39	131.04	122.74
1	F	46	ALA	C-N-CA	5.39	131.04	122.74
1	G	43	LYS	CA-CB-CG	5.39	124.87	114.10
1	H	90	ASN	OD1-CG-ND2	5.38	127.98	122.60
1	H	56	GLN	N-CA-C	-5.37	106.72	113.28
1	D	1	THR	O-C-N	5.37	131.59	123.00
1	H	89	ASN	N-CA-C	-5.37	106.43	112.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	14	ASN	OD1-CG-ND2	5.36	127.96	122.60
1	E	6	THR	N-CA-C	5.34	116.78	111.07
1	F	78	THR	CA-C-N	5.34	130.53	122.68
1	F	78	THR	C-N-CA	5.34	130.53	122.68
1	D	9	CYS	CB-CA-C	5.33	119.25	110.88
1	F	69	LYS	CG-CD-CE	5.32	123.54	111.30
1	E	12	TYR	CA-C-O	5.32	126.35	120.71
1	G	91	LYS	O-C-N	5.31	129.31	123.25
1	H	87	VAL	O-C-N	-5.31	115.94	122.57
1	G	65	ILE	N-CA-CB	5.30	117.75	110.54
1	E	31	LEU	CA-C-O	5.30	125.73	119.48
1	F	90	ASN	OD1-CG-ND2	-5.30	117.30	122.60
1	D	41	THR	CA-CB-OG1	-5.29	101.67	109.60
1	G	95	ALA	N-CA-C	5.28	117.34	108.73
1	H	29	GLU	CA-CB-CG	5.28	124.66	114.10
1	H	38	ALA	O-C-N	5.26	130.03	123.19
1	H	71	THR	CA-CB-CG2	5.26	119.44	110.50
1	F	6	THR	N-CA-CB	5.26	117.63	110.01
1	G	86	CYS	N-CA-C	-5.24	99.98	108.52
1	D	2	PRO	CB-CA-C	5.24	118.09	111.39
1	D	78	THR	CA-CB-CG2	5.24	119.40	110.50
1	F	3	GLN	CB-CG-CD	-5.24	103.70	112.60
1	F	64	ALA	CA-C-N	5.24	127.85	120.42
1	F	64	ALA	C-N-CA	5.24	127.85	120.42
1	F	102	ALA	N-CA-CB	5.23	119.84	110.80
1	F	83	GLU	N-CA-CB	5.22	117.75	110.07
1	H	30	SER	CA-C-N	5.21	130.55	122.26
1	H	30	SER	C-N-CA	5.21	130.55	122.26
1	D	81	LYS	O-C-N	5.20	129.51	122.59
1	G	11	GLU	CA-CB-CG	5.20	124.51	114.10
1	F	15	THR	CA-CB-CG2	5.20	119.34	110.50
1	D	30	SER	N-CA-C	5.20	117.89	109.06
1	G	82	VAL	N-CA-CB	-5.20	103.39	110.56
1	E	28	THR	O-C-N	5.19	129.61	123.33
1	F	83	GLU	CG-CD-OE1	5.19	130.34	118.40
1	H	6	THR	CA-CB-CG2	5.19	119.32	110.50
1	G	4	ASN	CA-C-O	-5.18	115.74	121.28
1	G	92	THR	CA-CB-OG1	-5.18	101.83	109.60
1	G	42	PHE	O-C-N	5.15	129.65	123.16
1	D	79	GLU	CA-C-N	5.14	131.37	121.54
1	D	79	GLU	C-N-CA	5.14	131.37	121.54
1	G	91	LYS	N-CA-CB	5.14	120.25	111.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	90	ASN	CB-CA-C	5.14	119.70	110.81
1	H	10	ALA	CA-C-N	5.13	133.52	121.52
1	H	10	ALA	C-N-CA	5.13	133.52	121.52
1	H	92	THR	CB-CA-C	5.13	119.06	110.55
1	D	44	ASN	N-CA-C	-5.12	107.08	113.38
1	D	52	VAL	O-C-N	5.11	127.45	121.57
1	F	11	GLU	CB-CG-CD	5.11	121.28	112.60
1	G	60	SER	CA-C-N	5.11	127.12	120.28
1	G	60	SER	C-N-CA	5.11	127.12	120.28
1	G	42	PHE	CA-C-O	-5.09	115.40	121.16
1	H	91	LYS	CB-CA-C	-5.09	98.25	109.56
1	E	21	ASN	CA-C-O	-5.08	115.94	121.84
1	D	94	HIS	CA-CB-CG	-5.08	108.72	113.80
1	F	69	LYS	CA-C-N	5.08	127.50	120.29
1	F	69	LYS	C-N-CA	5.08	127.50	120.29
1	F	15	THR	O-C-N	-5.08	116.31	123.11
1	D	57	HIS	O-C-N	5.07	129.16	123.28
1	E	20	LEU	N-CA-C	5.06	119.48	112.45
1	E	36	GLU	CG-CD-OE1	-5.06	106.77	118.40
1	E	56	GLN	N-CA-CB	5.06	119.04	110.49
1	D	24	ILE	CA-CB-CG2	5.06	119.09	110.50
1	E	57	HIS	CA-C-N	-5.05	115.69	122.91
1	E	57	HIS	C-N-CA	-5.05	115.69	122.91
1	H	77	LEU	N-CA-C	5.04	118.53	112.38
1	G	78	THR	CA-CB-CG2	5.04	119.07	110.50
1	E	78	THR	CA-CB-OG1	-5.03	102.06	109.60
1	H	16	GLN	OE1-CD-NE2	5.03	127.63	122.60
1	D	26	SER	CA-C-N	5.03	129.85	122.77
1	D	26	SER	C-N-CA	5.03	129.85	122.77
1	E	13	HIS	CA-C-O	-5.03	115.54	121.07
1	D	85	LEU	CA-C-N	5.02	129.27	122.19
1	D	85	LEU	C-N-CA	5.02	129.27	122.19
1	D	67	ARG	NE-CZ-NH1	5.01	126.51	121.50
1	E	16	GLN	O-C-N	5.01	129.26	122.59
1	E	59	ASP	CA-C-N	5.01	127.25	120.38
1	E	59	ASP	C-N-CA	5.01	127.25	120.38
1	H	20	LEU	CA-CB-CG	5.01	133.84	116.30
1	D	65	ILE	CA-C-N	5.01	127.40	120.29
1	D	65	ILE	C-N-CA	5.01	127.40	120.29
1	G	59	ASP	CA-C-N	5.01	126.95	120.44
1	G	59	ASP	C-N-CA	5.01	126.95	120.44

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	18	HIS	Sidechain
1	D	87	VAL	Mainchain
1	E	18	HIS	Sidechain
1	E	50	VAL	Mainchain
1	E	55	SER	Mainchain
1	E	56	GLN	Mainchain
1	E	67	ARG	Sidechain
1	F	18	HIS	Sidechain
1	F	35	ARG	Sidechain
1	F	54	GLY	Mainchain
1	F	55	SER	Mainchain,Peptide
1	F	67	ARG	Sidechain
1	G	12	TYR	Mainchain
1	G	18	HIS	Sidechain
1	G	64	ALA	Mainchain
1	H	18	HIS	Sidechain
1	H	20	LEU	Mainchain
1	H	87	VAL	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	D	814	0	817	104	0
1	E	814	0	815	90	0
1	F	814	0	816	90	2
1	G	814	0	817	139	0
1	H	814	0	816	87	0
2	D	52	0	0	5	0
2	E	55	0	0	7	0
2	F	32	0	0	3	0
2	G	35	0	0	7	0
2	H	30	0	0	5	0
All	All	4274	0	4081	438	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 54.

All (438) 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:F:38:ALA:C	1:F:39:ILE:HD13	1.70	1.15
1:F:37:MET:HE2	1:F:39:ILE:CD1	1.78	1.12
1:E:23:LYS:HE2	1:F:103:ASN:HD21	1.10	1.10
1:D:23:LYS:HB2	1:D:80:ALA:HB3	1.35	1.08
1:G:75:ALA:HB1	1:G:80:ALA:CB	1.84	1.07
1:G:93:PRO:HB3	1:H:3:GLN:HE22	1.19	1.04
1:D:11:GLU:OE2	2:D:108:HOH:O	1.74	1.04
1:F:37:MET:CE	1:F:39:ILE:HD11	1.88	1.04
1:D:23:LYS:CB	1:D:80:ALA:HB3	1.89	1.03
1:F:58:ILE:O	1:F:59:ASP:HB2	1.56	1.03
1:E:80:ALA:HB1	1:E:101:MET:CE	1.89	1.02
1:H:87:VAL:CG1	1:H:94:HIS:HB3	1.88	1.02
1:D:58:ILE:HG13	1:D:61:GLN:CB	1.89	1.02
1:D:68:MET:HE1	1:D:99:ILE:HG22	1.43	1.00
1:D:58:ILE:HG13	1:D:61:GLN:HB2	1.04	1.00
1:G:56:GLN:H	1:G:56:GLN:NE2	1.57	1.00
1:D:54:GLY:O	1:D:57:HIS:HB2	1.62	1.00
1:D:58:ILE:CG1	1:D:61:GLN:HB2	1.91	0.99
1:F:37:MET:HE2	1:F:39:ILE:HD11	1.00	0.99
1:G:93:PRO:HD2	1:H:1:THR:HB	1.44	0.99
1:D:56:GLN:O	1:D:56:GLN:HG3	1.20	0.99
1:G:14:ASN:H	1:G:14:ASN:HD22	1.03	0.98
1:E:9:CYS:SG	1:E:15:THR:HG23	2.04	0.98
1:G:93:PRO:HB3	1:H:3:GLN:NE2	1.79	0.97
1:D:14:ASN:HB2	2:D:121:HOH:O	1.66	0.96
1:G:33:GLY:O	1:G:34:LYS:HG2	1.65	0.96
1:E:87:VAL:CG1	1:E:94:HIS:HB3	1.96	0.95
1:H:54:GLY:H	1:H:57:HIS:CD2	1.85	0.94
1:G:12:TYR:HB2	1:G:15:THR:HG21	1.50	0.94
1:G:56:GLN:H	1:G:56:GLN:HE21	1.05	0.94
1:F:38:ALA:O	1:F:39:ILE:HD13	1.68	0.93
1:F:58:ILE:O	1:F:59:ASP:CB	2.16	0.93
1:G:84:LYS:HE2	2:G:108:HOH:O	1.67	0.93
1:G:87:VAL:HG11	1:G:94:HIS:HB3	1.45	0.93
1:G:75:ALA:HB1	1:G:80:ALA:HB2	1.50	0.92
1:H:81:LYS:HB3	1:H:103:ASN:OD1	1.69	0.92
1:D:56:GLN:O	1:D:56:GLN:CG	2.10	0.92
1:D:60:SER:HA	1:D:63:LYS:HE3	1.50	0.92
1:E:65:ILE:HG22	1:E:69:LYS:HE2	1.49	0.91
1:D:55:SER:O	1:D:57:HIS:N	2.03	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:52:VAL:HG21	2:H:106:HOH:O	1.71	0.90
1:H:58:ILE:HG13	1:H:61:GLN:OE1	1.71	0.90
1:E:23:LYS:HE2	1:F:103:ASN:ND2	1.86	0.89
1:H:20:LEU:HD21	1:H:85:LEU:HD22	1.52	0.89
1:F:35:ARG:HH21	1:G:2:PRO:HD3	1.37	0.89
1:H:87:VAL:HG11	1:H:94:HIS:HB3	1.55	0.89
1:D:60:SER:HA	1:D:63:LYS:CE	2.03	0.88
1:E:58:ILE:H	1:E:61:GLN:HE21	1.15	0.88
1:G:12:TYR:HB2	1:G:15:THR:CG2	2.04	0.88
1:G:75:ALA:CA	1:G:80:ALA:HB2	2.04	0.87
1:H:54:GLY:H	1:H:57:HIS:HD2	0.93	0.87
1:G:56:GLN:HE21	1:G:56:GLN:N	1.72	0.87
1:H:9:CYS:O	1:H:15:THR:HG21	1.74	0.87
1:F:80:ALA:HB1	1:F:101:MET:HE1	1.57	0.86
1:G:58:ILE:HG13	1:G:61:GLN:OE1	1.75	0.86
1:F:39:ILE:HG12	2:G:121:HOH:O	1.75	0.85
1:E:87:VAL:HG13	1:E:94:HIS:HB3	1.57	0.85
1:G:93:PRO:CD	1:H:1:THR:HB	2.05	0.85
1:G:49:GLN:HB3	1:G:93:PRO:HG2	1.55	0.85
1:E:15:THR:HG22	2:E:140:HOH:O	1.77	0.85
1:E:23:LYS:CE	1:F:103:ASN:HD21	1.90	0.85
1:G:87:VAL:CG1	1:G:94:HIS:HB3	2.06	0.84
1:G:75:ALA:CB	1:G:80:ALA:HB2	2.06	0.84
1:H:87:VAL:HG13	1:H:94:HIS:HB3	1.58	0.84
1:D:103:ASN:HD22	1:D:103:ASN:H	1.25	0.83
1:G:33:GLY:O	1:G:34:LYS:CG	2.27	0.83
2:D:108:HOH:O	1:H:35:ARG:NH2	2.12	0.83
1:H:62:LYS:O	1:H:65:ILE:HB	1.77	0.83
1:G:19:THR:HA	1:G:84:LYS:HG3	1.59	0.83
1:D:53:PRO:HA	1:D:57:HIS:HD2	1.42	0.82
1:F:80:ALA:HB1	1:F:101:MET:CE	2.08	0.82
1:E:28:THR:OG1	2:E:116:HOH:O	1.97	0.82
1:G:91:LYS:HE2	2:G:127:HOH:O	1.78	0.82
1:E:9:CYS:SG	1:E:15:THR:CG2	2.69	0.81
1:E:80:ALA:CB	1:E:101:MET:CE	2.58	0.81
1:E:31:LEU:C	1:E:31:LEU:HD23	2.05	0.81
1:F:35:ARG:HE	1:G:2:PRO:CD	1.93	0.81
1:H:54:GLY:N	1:H:57:HIS:HD2	1.76	0.80
1:E:65:ILE:CG2	1:E:69:LYS:HE2	2.10	0.80
1:F:35:ARG:HE	1:G:2:PRO:CG	1.95	0.80
1:F:24:ILE:HG21	1:F:40:ILE:HB	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:75:ALA:HB1	1:G:80:ALA:HB1	1.64	0.79
1:D:37:MET:HE2	1:D:39:ILE:HG22	1.65	0.79
1:F:35:ARG:NH2	1:G:2:PRO:HD3	1.97	0.78
1:G:93:PRO:HD3	1:H:3:GLN:OE1	1.82	0.78
1:G:19:THR:HG22	1:G:84:LYS:CG	2.14	0.77
1:G:76:TYR:HD2	1:G:77:LEU:CD1	1.96	0.77
1:G:80:ALA:HB3	2:G:119:HOH:O	1.84	0.77
1:G:75:ALA:C	1:G:80:ALA:HB2	2.10	0.77
1:F:87:VAL:HG11	1:F:94:HIS:HB3	1.67	0.76
1:D:103:ASN:H	1:D:103:ASN:ND2	1.81	0.76
1:D:9:CYS:SG	1:D:15:THR:CG2	2.73	0.76
1:D:57:HIS:NE2	1:D:65:ILE:HD11	2.01	0.76
1:F:22:ASP:HA	1:F:81:LYS:HE3	1.68	0.75
1:E:87:VAL:HG11	1:E:94:HIS:HB3	1.69	0.75
1:D:68:MET:HE1	1:D:99:ILE:CG2	2.16	0.75
1:H:2:PRO:HG3	1:H:11:GLU:OE2	1.87	0.75
1:G:76:TYR:CD2	1:G:77:LEU:CD1	2.70	0.74
1:F:39:ILE:CG1	2:G:121:HOH:O	2.31	0.74
1:D:19:THR:HB	1:D:84:LYS:HE3	1.68	0.74
1:E:93:PRO:HD2	1:F:1:THR:HG22	1.67	0.74
1:G:14:ASN:H	1:G:14:ASN:ND2	1.85	0.74
1:E:31:LEU:HD22	1:F:97:ALA:O	1.88	0.74
1:G:80:ALA:HB1	1:G:101:MET:HE1	1.70	0.73
1:F:92:THR:O	1:G:1:THR:HG23	1.89	0.73
1:E:80:ALA:CB	1:E:101:MET:HE1	2.19	0.73
1:H:25:PHE:HB3	1:H:41:THR:HG22	1.70	0.73
1:D:58:ILE:CG1	1:D:61:GLN:OE1	2.37	0.72
1:D:9:CYS:SG	1:D:15:THR:HG23	2.28	0.72
1:F:31:LEU:CD2	1:G:97:ALA:HA	2.19	0.72
1:G:75:ALA:O	1:G:80:ALA:HB2	1.90	0.72
1:E:25:PHE:O	1:F:103:ASN:HB2	1.88	0.72
1:E:80:ALA:HB1	1:E:101:MET:HE2	1.69	0.71
1:F:9:CYS:O	1:F:15:THR:HG21	1.90	0.71
1:D:60:SER:CA	1:D:63:LYS:HE3	2.20	0.71
1:G:14:ASN:HD22	1:G:14:ASN:N	1.78	0.71
1:E:28:THR:CB	2:E:116:HOH:O	2.39	0.70
1:G:93:PRO:HD2	1:H:1:THR:CB	2.20	0.70
1:G:76:TYR:HD2	1:G:77:LEU:HD13	1.55	0.70
1:E:58:ILE:H	1:E:61:GLN:NE2	1.89	0.70
1:D:53:PRO:HA	1:D:57:HIS:CD2	2.25	0.70
1:F:3:GLN:HG2	2:F:113:HOH:O	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:LYS:HD3	1:D:95:ALA:CB	2.23	0.69
1:G:83:GLU:HG2	1:G:84:LYS:HD3	1.75	0.69
1:H:9:CYS:SG	1:H:15:THR:HG23	2.33	0.69
1:H:87:VAL:HA	1:H:95:ALA:O	1.93	0.68
1:G:93:PRO:CB	1:H:3:GLN:HE22	2.00	0.68
1:F:92:THR:O	1:G:1:THR:CG2	2.42	0.67
1:D:60:SER:HA	1:D:63:LYS:CD	2.24	0.67
1:H:62:LYS:HA	1:H:65:ILE:HD12	1.76	0.67
1:G:80:ALA:HB1	1:G:101:MET:CE	2.25	0.67
1:D:34:LYS:O	1:D:34:LYS:HG2	1.93	0.67
1:F:80:ALA:O	1:F:81:LYS:HB2	1.94	0.67
1:D:39:ILE:HD13	1:D:47:THR:HG23	1.77	0.67
1:H:19:THR:HB	1:H:84:LYS:HG2	1.75	0.67
1:F:31:LEU:HD22	1:G:97:ALA:HA	1.75	0.67
1:E:85:LEU:CD1	1:E:99:ILE:HG13	2.25	0.66
1:F:35:ARG:NE	1:G:2:PRO:CD	2.58	0.66
1:F:59:ASP:HA	1:F:62:LYS:HG3	1.77	0.66
1:D:23:LYS:CA	1:D:80:ALA:HB3	2.26	0.66
1:D:40:ILE:HD12	1:D:42:PHE:CE2	2.30	0.66
1:G:19:THR:HB	1:G:84:LYS:HD2	1.77	0.65
1:G:44:ASN:OD1	1:G:46:ALA:CB	2.45	0.65
1:E:2:PRO:HB3	1:E:8:LEU:HB2	1.79	0.65
1:E:52:VAL:O	2:E:156:HOH:O	2.15	0.65
1:H:91:LYS:O	1:H:94:HIS:HD2	1.78	0.65
1:E:93:PRO:CD	1:F:1:THR:HG22	2.26	0.65
1:E:1:THR:HG22	1:E:2:PRO:O	1.96	0.65
1:H:90:ASN:OD1	1:H:90:ASN:N	2.27	0.65
1:D:17:ILE:CG2	1:D:84:LYS:HD3	2.27	0.65
1:H:81:LYS:CB	1:H:103:ASN:OD1	2.42	0.65
1:G:76:TYR:CD2	1:G:77:LEU:HD12	2.31	0.65
1:F:73:ARG:HD3	1:G:74:ILE:HG21	1.78	0.65
1:F:77:LEU:HD21	1:G:74:ILE:HG23	1.77	0.65
1:F:87:VAL:CG1	1:F:94:HIS:HB3	2.27	0.65
1:F:39:ILE:HD13	1:F:39:ILE:N	2.06	0.64
1:E:35:ARG:HH11	1:F:11:GLU:CD	2.05	0.64
1:G:30:SER:HA	1:H:98:ALA:HB2	1.79	0.64
1:G:74:ILE:O	1:G:78:THR:HB	1.97	0.64
1:F:77:LEU:HD21	1:G:74:ILE:CG2	2.28	0.64
1:E:74:ILE:O	1:E:78:THR:HB	1.97	0.64
1:G:12:TYR:O	1:G:15:THR:HG22	1.98	0.64
1:F:80:ALA:CB	1:F:101:MET:HE1	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:49:GLN:HB3	1:G:93:PRO:CG	2.27	0.64
1:D:91:LYS:O	1:D:94:HIS:HD2	1.82	0.63
1:H:4:ASN:OD1	1:H:6:THR:HB	1.98	0.63
1:D:65:ILE:HA	1:H:31:LEU:HD12	1.79	0.63
1:D:103:ASN:ND2	1:H:25:PHE:O	2.31	0.63
1:E:1:THR:HG23	1:E:2:PRO:HD2	1.78	0.63
1:E:93:PRO:HD2	1:F:1:THR:CG2	2.28	0.63
1:D:49:GLN:HB3	1:D:93:PRO:HG2	1.81	0.63
1:G:14:ASN:HA	1:G:89:ASN:HD21	1.63	0.62
1:G:54:GLY:H	1:G:57:HIS:HD2	1.45	0.62
1:G:19:THR:HG22	1:G:84:LYS:HG2	1.82	0.62
1:H:13:HIS:ND1	1:H:13:HIS:N	2.47	0.62
1:D:39:ILE:HD13	1:D:47:THR:CG2	2.30	0.62
1:E:43:LYS:HG3	1:E:44:ASN:N	2.14	0.62
1:E:54:GLY:H	1:E:57:HIS:HD2	1.46	0.62
1:G:29:GLU:OE2	1:H:67:ARG:HG2	2.00	0.62
1:E:80:ALA:HB1	1:E:101:MET:HE1	1.72	0.62
1:G:49:GLN:CB	1:G:93:PRO:HG2	2.30	0.62
1:H:26:SER:OG	1:H:41:THR:HB	2.00	0.61
1:H:22:ASP:OD1	2:H:130:HOH:O	2.16	0.61
1:G:62:LYS:HA	1:G:65:ILE:HD12	1.82	0.61
1:E:8:LEU:C	1:E:8:LEU:HD23	2.25	0.61
1:F:24:ILE:CG2	1:F:40:ILE:HB	2.29	0.61
1:D:58:ILE:HG13	1:D:61:GLN:OE1	1.98	0.60
1:D:91:LYS:HD3	1:D:95:ALA:HB2	1.83	0.60
1:G:93:PRO:CD	1:H:3:GLN:OE1	2.49	0.60
1:E:31:LEU:HD23	1:E:31:LEU:O	2.00	0.60
1:F:87:VAL:HG11	1:F:94:HIS:CB	2.32	0.60
1:G:56:GLN:NE2	1:G:56:GLN:N	2.37	0.60
1:G:29:GLU:OE2	2:G:105:HOH:O	2.16	0.60
1:E:85:LEU:HD11	1:E:99:ILE:HG13	1.82	0.60
1:G:63:LYS:HE2	1:G:64:ALA:N	2.16	0.60
1:F:80:ALA:O	1:F:81:LYS:CB	2.49	0.60
1:G:54:GLY:H	1:G:57:HIS:CD2	2.18	0.60
1:D:18:HIS:HB3	1:D:20:LEU:CD2	2.32	0.59
1:E:25:PHE:CE1	1:F:103:ASN:HB3	2.37	0.59
1:G:19:THR:CA	1:G:84:LYS:HG3	2.32	0.59
1:G:35:ARG:HD2	1:G:37:MET:HE1	1.82	0.59
1:E:19:THR:HB	1:E:84:LYS:HG3	1.83	0.59
1:D:28:THR:HB	1:D:39:ILE:HG13	1.85	0.59
1:E:31:LEU:C	1:E:31:LEU:CD2	2.75	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:35:ARG:HD3	1:F:11:GLU:OE1	2.04	0.58
1:G:82:VAL:HG13	1:G:99:ILE:HD11	1.85	0.57
1:G:63:LYS:HE2	1:G:64:ALA:CA	2.34	0.57
1:E:55:SER:O	1:E:57:HIS:N	2.38	0.56
1:H:17:ILE:HA	1:H:85:LEU:O	2.04	0.56
1:D:65:ILE:O	1:D:69:LYS:HG3	2.05	0.56
1:D:82:VAL:HG13	1:D:99:ILE:CD1	2.36	0.56
1:E:43:LYS:HG2	2:E:142:HOH:O	2.05	0.56
1:F:38:ALA:O	1:F:39:ILE:CD1	2.48	0.56
1:G:44:ASN:OD1	1:G:46:ALA:HB2	2.06	0.56
1:D:37:MET:HE2	1:D:39:ILE:CG2	2.36	0.55
1:D:17:ILE:HG23	1:D:84:LYS:HD3	1.86	0.55
1:E:58:ILE:O	1:E:59:ASP:C	2.48	0.55
1:G:87:VAL:HG11	1:G:94:HIS:CB	2.30	0.55
1:F:17:ILE:HA	1:F:85:LEU:O	2.07	0.55
1:E:35:ARG:NH1	1:F:11:GLU:OE2	2.40	0.55
1:H:88:TRP:HB2	1:H:95:ALA:HB3	1.87	0.55
1:D:58:ILE:HB	1:D:61:GLN:H	1.69	0.55
1:E:28:THR:HB	2:E:116:HOH:O	2.03	0.55
1:D:55:SER:C	1:D:57:HIS:N	2.64	0.55
1:F:87:VAL:HG11	1:F:94:HIS:CG	2.42	0.55
1:H:2:PRO:CG	1:H:11:GLU:OE2	2.55	0.55
1:D:82:VAL:HG13	1:D:99:ILE:HD12	1.89	0.54
1:F:85:LEU:HD21	1:F:96:ILE:HD13	1.89	0.54
1:G:35:ARG:HH21	1:H:2:PRO:HD3	1.73	0.54
1:H:58:ILE:HG13	1:H:61:GLN:HB2	1.90	0.53
1:H:87:VAL:HG11	1:H:94:HIS:CB	2.36	0.53
1:F:41:THR:HA	1:F:46:ALA:O	2.09	0.53
1:G:18:HIS:N	1:G:85:LEU:O	2.31	0.53
1:D:89:ASN:HD22	1:D:90:ASN:N	2.05	0.53
1:F:5:ILE:HD12	1:F:100:SER:HB3	1.91	0.53
1:H:18:HIS:O	1:H:84:LYS:HA	2.08	0.53
1:D:31:LEU:C	1:D:31:LEU:CD2	2.82	0.53
1:E:59:ASP:O	1:E:62:LYS:HG3	2.09	0.53
1:E:78:THR:HG22	1:E:80:ALA:HB2	1.91	0.53
1:D:75:ALA:HB2	1:D:101:MET:HE1	1.90	0.53
1:E:53:PRO:HA	1:E:57:HIS:CD2	2.43	0.53
1:F:27:TYR:CE1	1:F:29:GLU:HB2	2.44	0.53
1:G:19:THR:HG21	1:G:84:LYS:HZ3	1.74	0.53
1:G:75:ALA:HA	1:G:80:ALA:HB2	1.88	0.53
1:G:93:PRO:CD	1:H:1:THR:CB	2.84	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:87:VAL:HG11	1:E:94:HIS:CB	2.38	0.52
1:F:77:LEU:HG	1:G:78:THR:HG21	1.91	0.52
1:D:101:MET:HB3	1:H:76:TYR:CE2	2.44	0.52
1:D:23:LYS:HA	1:D:80:ALA:HB3	1.91	0.52
1:G:44:ASN:OD1	1:G:46:ALA:N	2.39	0.52
1:G:68:MET:O	1:G:72:LEU:HG	2.10	0.52
1:D:17:ILE:HG21	1:D:84:LYS:HD3	1.90	0.52
1:H:91:LYS:O	1:H:94:HIS:CD2	2.61	0.52
1:D:56:GLN:O	1:D:57:HIS:ND1	2.44	0.51
1:D:91:LYS:HD3	1:D:95:ALA:HB3	1.91	0.51
1:F:88:TRP:HB3	1:F:90:ASN:OD1	2.09	0.51
1:F:14:ASN:O	1:F:88:TRP:HA	2.11	0.51
1:G:3:GLN:HG3	1:G:3:GLN:O	2.11	0.51
1:D:59:ASP:O	1:D:63:LYS:HG3	2.11	0.51
1:D:75:ALA:CB	1:D:101:MET:HE1	2.40	0.51
1:D:89:ASN:HD22	1:D:89:ASN:C	2.19	0.51
1:E:48:PHE:CD1	1:E:94:HIS:HB2	2.46	0.51
1:G:93:PRO:CD	1:H:1:THR:CG2	2.89	0.51
1:H:66:GLU:HA	1:H:69:LYS:HE3	1.92	0.51
1:D:31:LEU:O	1:E:61:GLN:HG3	2.10	0.51
1:D:35:ARG:HB2	1:E:12:TYR:OH	2.10	0.51
1:D:15:THR:CG2	1:D:16:GLN:N	2.73	0.51
1:D:59:ASP:O	1:D:62:LYS:HB2	2.11	0.51
1:G:35:ARG:HE	1:H:2:PRO:HG2	1.76	0.51
1:D:39:ILE:CD1	1:D:47:THR:HG23	2.41	0.50
1:G:15:THR:HA	1:G:87:VAL:O	2.12	0.50
1:E:20:LEU:N	1:E:20:LEU:HD22	2.26	0.50
1:D:15:THR:HG23	1:D:16:GLN:N	2.26	0.50
1:D:23:LYS:HA	1:D:80:ALA:CB	2.41	0.50
1:G:93:PRO:HD3	1:H:1:THR:HB	1.90	0.50
1:D:9:CYS:SG	1:D:15:THR:HG21	2.52	0.50
1:E:84:LYS:O	1:E:85:LEU:CD1	2.60	0.50
1:F:31:LEU:HD21	1:G:97:ALA:HA	1.93	0.50
1:G:26:SER:HB2	1:H:101:MET:O	2.11	0.50
1:G:31:LEU:HD12	1:H:97:ALA:O	2.11	0.50
1:F:5:ILE:N	2:F:125:HOH:O	2.42	0.50
1:H:46:ALA:HB1	1:H:48:PHE:CZ	2.46	0.50
1:H:20:LEU:CD2	1:H:85:LEU:HD22	2.34	0.49
1:H:78:THR:HG21	2:H:107:HOH:O	2.12	0.49
1:E:58:ILE:O	1:E:61:GLN:N	2.45	0.49
1:H:32:ALA:O	1:H:35:ARG:N	2.36	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:83:GLU:HG2	1:G:84:LYS:N	2.27	0.49
1:H:54:GLY:O	1:H:57:HIS:HB2	2.12	0.49
1:E:46:ALA:HB1	1:E:48:PHE:CE2	2.48	0.49
1:F:31:LEU:HD21	1:G:96:ILE:O	2.13	0.49
1:D:93:PRO:HD2	1:E:1:THR:HB	1.95	0.49
1:G:54:GLY:N	1:G:57:HIS:HD2	2.10	0.49
1:G:31:LEU:HD23	1:H:65:ILE:HA	1.95	0.49
1:F:37:MET:CE	1:F:39:ILE:CD1	2.68	0.48
1:G:19:THR:CG2	1:G:84:LYS:NZ	2.75	0.48
1:H:4:ASN:O	1:H:8:LEU:HB2	2.12	0.48
1:E:49:GLN:HB3	1:E:93:PRO:HG2	1.95	0.48
1:G:75:ALA:O	1:G:80:ALA:CB	2.61	0.48
1:D:58:ILE:O	1:D:62:LYS:HG3	2.14	0.48
1:E:92:THR:HA	1:E:93:PRO:C	2.37	0.48
1:G:16:GLN:HE22	1:G:18:HIS:CE1	2.31	0.48
1:G:58:ILE:O	1:G:61:GLN:HB2	2.14	0.48
1:F:33:GLY:O	1:F:34:LYS:HB2	2.14	0.48
1:G:35:ARG:NH2	1:H:2:PRO:HD3	2.28	0.48
1:H:19:THR:HB	1:H:84:LYS:CG	2.42	0.48
1:E:86:CYS:HB3	1:E:98:ALA:HB3	1.95	0.48
1:G:80:ALA:O	1:G:81:LYS:HB3	2.14	0.48
1:E:83:GLU:CD	1:E:84:LYS:HD3	2.38	0.48
1:G:81:LYS:HD2	2:G:109:HOH:O	2.13	0.48
1:G:79:GLU:O	1:G:80:ALA:C	2.57	0.48
1:E:54:GLY:O	1:E:55:SER:C	2.57	0.48
1:D:58:ILE:CG1	1:D:61:GLN:CB	2.70	0.48
1:E:85:LEU:HD12	1:E:99:ILE:HG13	1.95	0.47
1:G:19:THR:HG21	1:G:84:LYS:NZ	2.28	0.47
1:D:58:ILE:O	1:D:59:ASP:C	2.57	0.47
1:D:101:MET:O	1:H:26:SER:HA	2.14	0.47
1:F:31:LEU:HD22	1:G:97:ALA:O	2.14	0.47
1:F:35:ARG:NH2	1:G:2:PRO:CD	2.75	0.47
1:F:35:ARG:CZ	1:G:2:PRO:CD	2.93	0.47
1:D:73:ARG:O	1:D:73:ARG:HG2	2.15	0.47
1:F:35:ARG:NE	1:G:2:PRO:HD2	2.29	0.47
1:H:15:THR:HA	1:H:87:VAL:O	2.13	0.47
1:F:27:TYR:CD1	1:F:27:TYR:C	2.92	0.47
1:F:31:LEU:O	1:G:61:GLN:HG2	2.14	0.47
1:H:34:LYS:HA	2:H:117:HOH:O	2.14	0.47
1:F:52:VAL:HA	1:F:53:PRO:HD2	1.40	0.47
1:G:34:LYS:O	1:G:35:ARG:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1:THR:O	1:E:2:PRO:C	2.57	0.46
1:H:52:VAL:CG2	2:H:106:HOH:O	2.44	0.46
1:D:3:GLN:HG3	1:H:47:THR:HG21	1.97	0.46
1:G:7:ASP:O	1:G:10:ALA:HB3	2.16	0.46
1:G:18:HIS:O	1:G:85:LEU:N	2.43	0.46
1:G:53:PRO:HA	1:G:57:HIS:HD2	1.80	0.46
1:D:37:MET:HB3	1:D:52:VAL:HG22	1.97	0.46
1:D:69:LYS:HB2	1:E:67:ARG:CZ	2.46	0.46
1:D:92:THR:HA	1:D:93:PRO:C	2.40	0.46
1:E:2:PRO:HG2	1:E:8:LEU:HG	1.98	0.46
1:H:65:ILE:O	1:H:69:LYS:HG3	2.15	0.46
1:G:30:SER:HA	1:H:98:ALA:CB	2.45	0.46
1:H:23:LYS:HB3	1:H:81:LYS:H	1.80	0.46
1:D:58:ILE:HG12	1:D:61:GLN:OE1	2.15	0.46
1:E:29:GLU:HB3	1:F:99:ILE:HG22	1.98	0.46
1:D:40:ILE:HG13	1:D:40:ILE:O	2.13	0.46
1:F:68:MET:O	1:F:72:LEU:HG	2.15	0.46
1:G:31:LEU:CD1	1:H:97:ALA:HA	2.46	0.46
1:G:19:THR:HG22	1:G:84:LYS:CD	2.46	0.46
1:G:87:VAL:HG13	1:G:94:HIS:HB3	1.94	0.46
1:D:74:ILE:HG23	1:H:77:LEU:HD11	1.98	0.45
1:G:14:ASN:ND2	1:G:14:ASN:N	2.52	0.45
1:E:90:ASN:OD1	1:E:91:LYS:HD2	2.16	0.45
1:F:35:ARG:CZ	1:G:2:PRO:HD3	2.45	0.45
1:G:66:GLU:HG3	1:H:63:LYS:NZ	2.32	0.45
1:G:75:ALA:CB	1:G:80:ALA:CB	2.66	0.45
1:G:19:THR:CB	1:G:84:LYS:HG3	2.47	0.45
1:D:60:SER:HA	1:D:63:LYS:HD2	1.97	0.45
1:E:65:ILE:CG2	1:E:69:LYS:CE	2.90	0.45
1:G:83:GLU:CG	1:G:84:LYS:HD3	2.43	0.45
1:H:92:THR:HA	1:H:93:PRO:HA	1.85	0.45
1:E:43:LYS:CG	2:E:142:HOH:O	2.63	0.45
1:E:49:GLN:O	1:E:49:GLN:HG3	2.17	0.45
1:H:41:THR:HA	1:H:46:ALA:O	2.17	0.45
1:E:47:THR:HG21	1:F:3:GLN:HB2	1.98	0.44
1:G:49:GLN:CG	1:G:93:PRO:HG2	2.47	0.44
1:D:91:LYS:O	1:D:94:HIS:CD2	2.68	0.44
1:H:23:LYS:HB3	1:H:80:ALA:HB3	1.98	0.44
1:D:74:ILE:O	1:D:78:THR:HB	2.17	0.44
1:F:35:ARG:HE	1:G:2:PRO:HG3	1.75	0.44
1:H:15:THR:O	1:H:16:GLN:CB	2.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:84:LYS:O	1:E:85:LEU:HD12	2.18	0.44
1:G:53:PRO:HA	1:G:57:HIS:CD2	2.52	0.44
1:F:32:ALA:HB3	1:F:35:ARG:HB3	1.99	0.44
1:F:42:PHE:CD1	1:F:42:PHE:N	2.85	0.44
1:D:14:ASN:O	1:D:88:TRP:HA	2.17	0.43
1:E:9:CYS:O	1:E:15:THR:HG21	2.18	0.43
1:E:33:GLY:O	1:E:34:LYS:HB2	2.18	0.43
1:F:91:LYS:HE2	1:F:91:LYS:HB2	1.88	0.43
1:F:99:ILE:HG12	1:F:100:SER:N	2.34	0.43
1:F:29:GLU:OE2	1:G:67:ARG:HG2	2.19	0.43
1:F:66:GLU:OE2	1:F:69:LYS:HE2	2.18	0.43
1:H:23:LYS:CB	1:H:80:ALA:HB3	2.48	0.43
1:D:13:HIS:HD2	2:D:125:HOH:O	2.00	0.43
1:D:39:ILE:HG13	1:D:39:ILE:O	2.19	0.43
1:D:87:VAL:HA	1:D:95:ALA:O	2.18	0.43
1:E:20:LEU:N	1:E:20:LEU:CD2	2.81	0.43
1:D:18:HIS:HB3	1:D:20:LEU:HD21	2.00	0.42
1:G:14:ASN:CA	1:G:89:ASN:HD21	2.31	0.42
1:E:8:LEU:HD23	1:E:8:LEU:O	2.19	0.42
1:E:61:GLN:O	1:E:64:ALA:HB3	2.19	0.42
1:F:80:ALA:HB3	1:F:81:LYS:H	1.46	0.42
1:G:16:GLN:NE2	1:G:18:HIS:NE2	2.67	0.42
1:D:57:HIS:HB3	1:D:62:LYS:HG2	2.02	0.42
1:F:39:ILE:CG2	1:F:47:THR:HG23	2.50	0.42
1:F:75:ALA:HB1	1:F:80:ALA:HB2	2.02	0.42
1:G:35:ARG:HE	1:H:2:PRO:CG	2.32	0.42
1:D:25:PHE:CD1	1:D:25:PHE:C	2.98	0.42
1:D:31:LEU:C	1:D:31:LEU:HD22	2.45	0.42
1:D:74:ILE:HD12	1:D:74:ILE:HA	1.81	0.42
1:E:35:ARG:O	1:E:37:MET:HG2	2.20	0.42
1:D:40:ILE:HD12	1:D:42:PHE:HE2	1.82	0.41
1:E:15:THR:CG2	1:E:16:GLN:N	2.83	0.41
1:E:58:ILE:O	1:E:60:SER:N	2.52	0.41
1:H:50:VAL:HG21	1:H:72:LEU:HD12	2.02	0.41
1:F:71:THR:O	1:F:74:ILE:HG22	2.20	0.41
1:H:37:MET:HE3	1:H:37:MET:HB2	1.55	0.41
1:E:84:LYS:O	1:E:85:LEU:HD13	2.20	0.41
1:E:9:CYS:C	1:E:15:THR:HG21	2.46	0.41
1:F:81:LYS:HD2	2:F:131:HOH:O	2.19	0.41
1:H:30:SER:HB3	1:H:35:ARG:O	2.21	0.41
1:E:15:THR:HG23	1:E:16:GLN:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:58:ILE:HG21	1:G:58:ILE:HD13	1.78	0.41
1:G:25:PHE:HD1	1:G:41:THR:HG22	1.85	0.41
1:G:96:ILE:H	1:G:96:ILE:HG13	1.74	0.41
1:H:40:ILE:HD12	1:H:48:PHE:HD2	1.85	0.41
1:D:2:PRO:HD3	1:H:35:ARG:NH2	2.36	0.41
1:D:25:PHE:HB3	1:D:41:THR:HG22	2.03	0.41
1:D:91:LYS:CD	1:D:95:ALA:HB3	2.51	0.41
1:F:9:CYS:SG	1:F:15:THR:HG23	2.60	0.41
1:F:61:GLN:O	1:F:65:ILE:HG13	2.21	0.41
1:G:51:GLU:OE1	1:G:57:HIS:HE1	2.03	0.41
1:D:23:LYS:HA	1:D:81:LYS:H	1.85	0.41
1:D:63:LYS:HG3	1:D:63:LYS:H	1.48	0.40
1:E:9:CYS:SG	1:E:15:THR:HG21	2.58	0.40
1:E:89:ASN:C	1:E:89:ASN:HD22	2.30	0.40
1:G:41:THR:HA	1:G:46:ALA:O	2.21	0.40
1:H:24:ILE:CG2	1:H:26:SER:O	2.68	0.40
1:D:35:ARG:HD3	1:D:35:ARG:HA	1.92	0.40
1:D:58:ILE:HG12	1:D:58:ILE:H	1.23	0.40
1:D:69:LYS:HD2	1:E:67:ARG:NE	2.35	0.40
1:E:14:ASN:O	1:E:89:ASN:N	2.40	0.40
1:G:28:THR:O	1:G:38:ALA:HA	2.22	0.40
1:G:81:LYS:HB3	1:G:103:ASN:HD21	1.87	0.40
1:H:97:ALA:O	1:H:98:ALA:HB2	2.21	0.40
1:D:15:THR:HA	1:D:87:VAL:O	2.21	0.40
1:D:44:ASN:ND2	2:D:115:HOH:O	2.54	0.40
1:F:1:THR:HG23	1:F:2:PRO:N	2.37	0.40
1:F:101:MET:HE2	1:F:101:MET:HB3	1.92	0.40
1:G:25:PHE:CD1	1:G:25:PHE:C	2.99	0.40
1:G:65:ILE:HG22	1:G:69:LYS:HE2	2.04	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:F:43:LYS:NZ	1:F:55:SER:O[1_455]	1.81	0.39
1:F:43:LYS:CE	1:F:55:SER:O[1_455]	2.10	0.10

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	D	101/103 (98%)	91 (90%)	6 (6%)	4 (4%)	2	2
1	E	101/103 (98%)	92 (91%)	7 (7%)	2 (2%)	6	7
1	F	101/103 (98%)	91 (90%)	6 (6%)	4 (4%)	2	2
1	G	101/103 (98%)	94 (93%)	4 (4%)	3 (3%)	3	3
1	H	101/103 (98%)	89 (88%)	11 (11%)	1 (1%)	12	20
All	All	505/515 (98%)	457 (90%)	34 (7%)	14 (3%)	4	3

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	56	GLN
1	E	55	SER
1	E	56	GLN
1	F	59	ASP
1	H	80	ALA
1	D	80	ALA
1	D	81	LYS
1	F	80	ALA
1	F	81	LYS
1	G	80	ALA
1	D	55	SER
1	F	56	GLN
1	G	81	LYS
1	G	53	PRO

5.3.2 Protein sidechains [i](#)

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	D	89/89 (100%)	70 (79%)	19 (21%)	1	1
1	E	89/89 (100%)	71 (80%)	18 (20%)	1	1
1	F	89/89 (100%)	71 (80%)	18 (20%)	1	1
1	G	89/89 (100%)	71 (80%)	18 (20%)	1	1
1	H	89/89 (100%)	75 (84%)	14 (16%)	2	3
All	All	445/445 (100%)	358 (80%)	87 (20%)	1	2

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	15	THR
1	D	19	THR
1	D	30	SER
1	D	31	LEU
1	D	35	ARG
1	D	39	ILE
1	D	41	THR
1	D	55	SER
1	D	56	GLN
1	D	57	HIS
1	D	58	ILE
1	D	63	LYS
1	D	73	ARG
1	D	77	LEU
1	D	81	LYS
1	D	85	LEU
1	D	89	ASN
1	D	91	LYS
1	D	103	ASN
1	E	3	GLN
1	E	5	ILE
1	E	7	ASP
1	E	15	THR
1	E	19	THR
1	E	31	LEU
1	E	35	ARG
1	E	41	THR
1	E	43	LYS

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Mol	Chain	Res	Type
1	E	56	GLN
1	E	77	LEU
1	E	78	THR
1	E	79	GLU
1	E	81	LYS
1	E	84	LYS
1	E	85	LEU
1	E	89	ASN
1	E	91	LYS
1	F	1	THR
1	F	5	ILE
1	F	13	HIS
1	F	15	THR
1	F	19	THR
1	F	20	LEU
1	F	21	ASN
1	F	31	LEU
1	F	39	ILE
1	F	41	THR
1	F	43	LYS
1	F	60	SER
1	F	63	LYS
1	F	77	LEU
1	F	81	LYS
1	F	92	THR
1	F	99	ILE
1	F	100	SER
1	G	1	THR
1	G	14	ASN
1	G	15	THR
1	G	19	THR
1	G	23	LYS
1	G	31	LEU
1	G	37	MET
1	G	41	THR
1	G	43	LYS
1	G	56	GLN
1	G	59	ASP
1	G	63	LYS
1	G	73	ARG
1	G	77	LEU
1	G	78	THR

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Mol	Chain	Res	Type
1	G	84	LYS
1	G	89	ASN
1	G	92	THR
1	H	3	GLN
1	H	13	HIS
1	H	15	THR
1	H	19	THR
1	H	23	LYS
1	H	31	LEU
1	H	56	GLN
1	H	58	ILE
1	H	60	SER
1	H	63	LYS
1	H	85	LEU
1	H	89	ASN
1	H	91	LYS
1	H	92	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	13	HIS
1	D	21	ASN
1	D	57	HIS
1	D	89	ASN
1	D	94	HIS
1	D	103	ASN
1	E	16	GLN
1	E	18	HIS
1	E	49	GLN
1	E	57	HIS
1	E	61	GLN
1	E	89	ASN
1	E	94	HIS
1	F	44	ASN
1	F	49	GLN
1	F	103	ASN
1	G	13	HIS
1	G	14	ASN
1	G	16	GLN
1	G	21	ASN
1	G	49	GLN

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Mol	Chain	Res	Type
1	G	56	GLN
1	G	57	HIS
1	G	89	ASN
1	G	94	HIS
1	G	103	ASN
1	H	14	ASN
1	H	57	HIS
1	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	54:GLY	C	55:SER	N	1.62
1	F	56:GLN	C	57:HIS	N	1.01

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.