



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:15 PM UTC

PDB ID : 1CLX / pdb_00001clx
Title : CATALYTIC CORE OF XYLANASE A
Authors : Harris, G.W.; Jenkins, J.A.; Connerton, I.; Pickersgill, R.W.
Deposited on : 1995-08-31
Resolution : 1.80 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

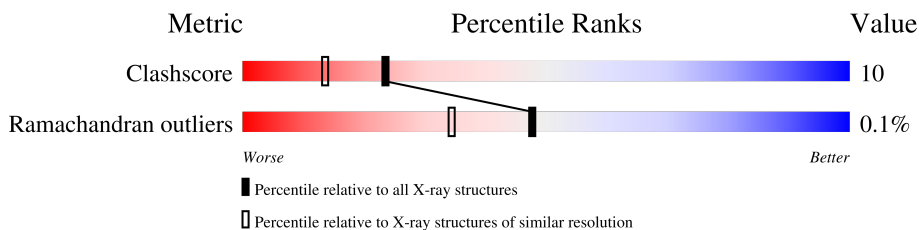
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)

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	347	68% 27% 5% ..
1	B	347	69% 25% 5% .
1	C	347	67% 25% 7% .
1	D	347	71% 24% . ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11908 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 XYLANASE A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	0	0
			2699	1693	479	519	8			
1	B	345	Total	C	N	O	S	0	0	0
			2699	1693	479	519	8			
1	C	345	Total	C	N	O	S	0	0	0
			2699	1693	479	519	8			
1	D	345	Total	C	N	O	S	0	0	0
			2699	1693	479	519	8			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		

- Molecule 3 is water.

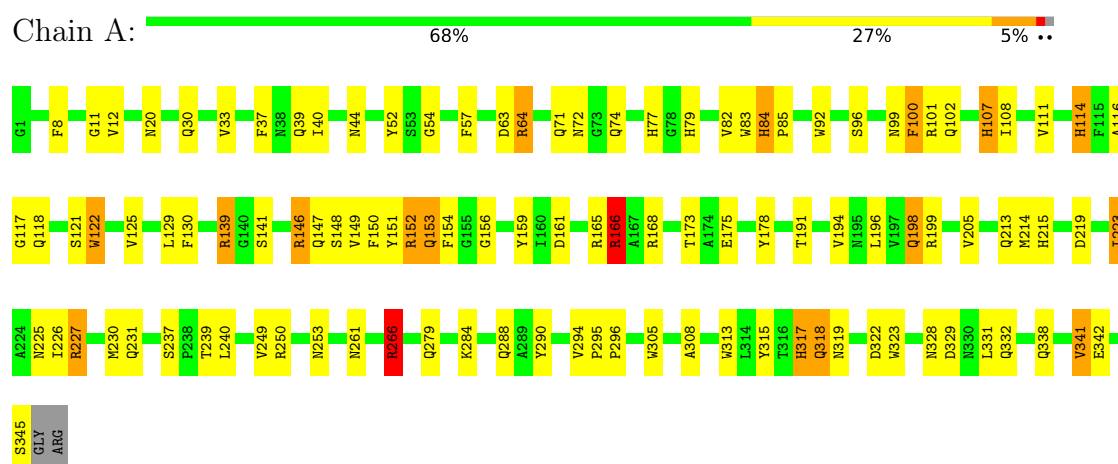
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	272	Total	O	0	0
			272	272		
3	B	278	Total	O	0	0
			278	278		
3	C	276	Total	O	0	0
			276	276		
3	D	282	Total	O	0	0
			282	282		

3 Residue-property plots

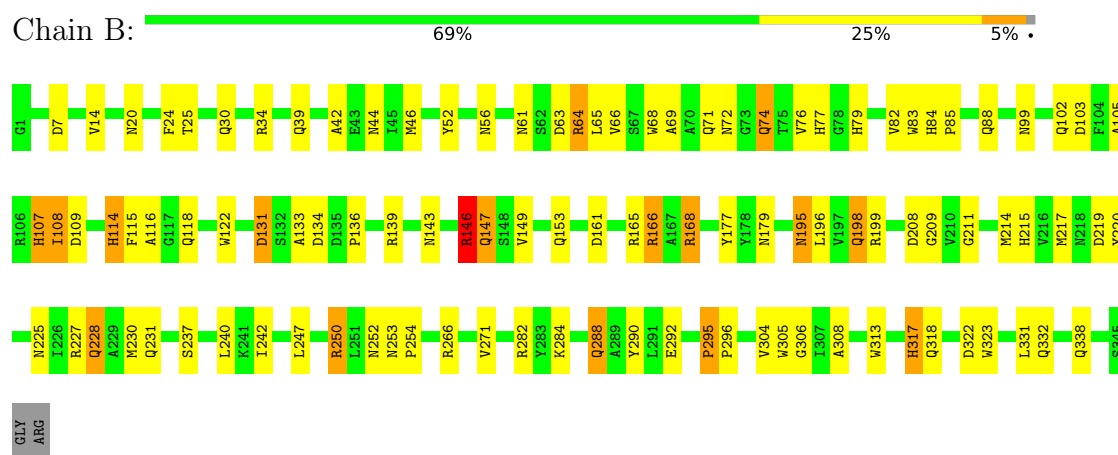
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

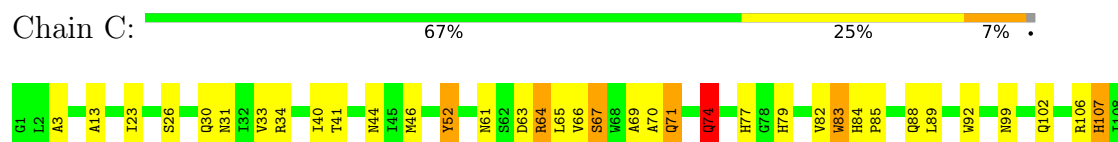
• Molecule 1: XYLANASE A

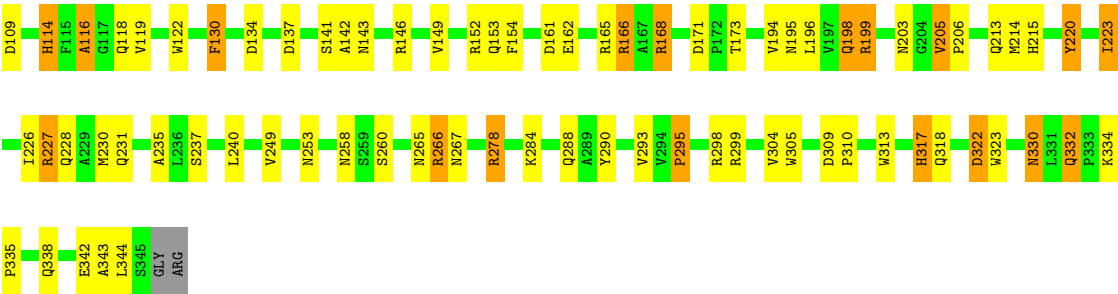


• Molecule 1: XYLANASE A

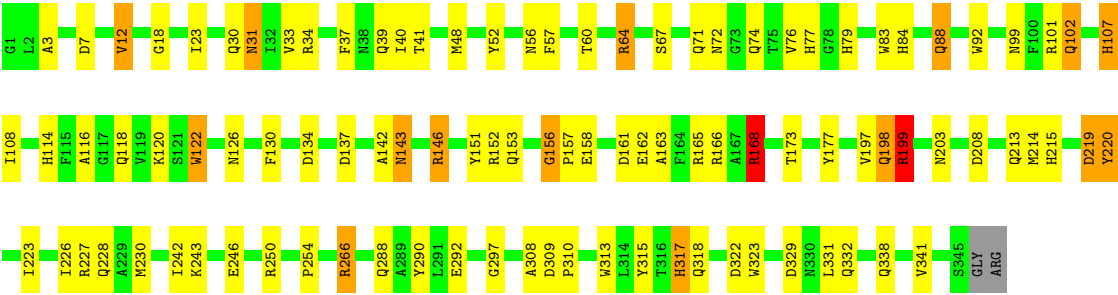


• Molecule 1: XYLANASE A





● Molecule 1: XYLANASE A



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.11Å 97.32Å 151.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.80	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-1.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	RESTRAIN	Depositor
R, R_{free}	0.166 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11908	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section:
CA

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	1.19	33/2766 (1.2%)	1.80	48/3769 (1.3%)
1	B	1.20	33/2766 (1.2%)	1.84	59/3769 (1.6%)
1	C	1.21	35/2766 (1.3%)	1.79	43/3769 (1.1%)
1	D	1.20	36/2766 (1.3%)	1.81	43/3769 (1.1%)
All	All	1.20	137/11064 (1.2%)	1.81	193/15076 (1.3%)

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	8
1	B	0	7
1	C	0	12
1	D	0	8
All	All	0	35

All (137) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	77	HIS	CE1-NE2	8.22	1.40	1.32
1	A	317	HIS	ND1-CE1	8.03	1.40	1.32
1	A	84	HIS	CE1-NE2	7.83	1.40	1.32
1	C	77	HIS	CE1-NE2	7.74	1.40	1.32
1	B	317	HIS	CE1-NE2	7.68	1.40	1.32
1	A	317	HIS	CE1-NE2	7.43	1.40	1.32
1	C	317	HIS	ND1-CE1	7.37	1.40	1.32
1	C	84	HIS	CE1-NE2	7.37	1.40	1.32
1	D	79	HIS	CE1-NE2	7.37	1.40	1.32
1	D	107	HIS	ND1-CE1	7.32	1.39	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	84	HIS	ND1-CE1	7.31	1.39	1.32
1	D	79	HIS	ND1-CE1	7.29	1.39	1.32
1	D	84	HIS	ND1-CE1	7.25	1.39	1.32
1	C	317	HIS	CE1-NE2	7.16	1.39	1.32
1	C	107	HIS	CE1-NE2	7.15	1.39	1.32
1	B	114	HIS	ND1-CE1	7.12	1.39	1.32
1	C	215	HIS	CE1-NE2	7.12	1.39	1.32
1	B	79	HIS	CE1-NE2	7.08	1.39	1.32
1	D	215	HIS	CE1-NE2	7.07	1.39	1.32
1	B	107	HIS	ND1-CE1	7.01	1.39	1.32
1	D	114	HIS	CE1-NE2	7.01	1.39	1.32
1	B	84	HIS	ND1-CE1	7.00	1.39	1.32
1	A	107	HIS	ND1-CE1	6.92	1.39	1.32
1	D	114	HIS	ND1-CE1	6.92	1.39	1.32
1	C	77	HIS	ND1-CE1	6.91	1.39	1.32
1	D	317	HIS	ND1-CE1	6.90	1.39	1.32
1	D	215	HIS	ND1-CE1	6.86	1.39	1.32
1	D	77	HIS	CE1-NE2	6.85	1.39	1.32
1	D	84	HIS	CE1-NE2	6.84	1.39	1.32
1	B	215	HIS	CE1-NE2	6.83	1.39	1.32
1	B	84	HIS	CE1-NE2	6.81	1.39	1.32
1	B	107	HIS	CE1-NE2	6.73	1.39	1.32
1	B	79	HIS	ND1-CE1	6.62	1.39	1.32
1	C	79	HIS	ND1-CE1	6.59	1.39	1.32
1	A	114	HIS	ND1-CE1	6.58	1.39	1.32
1	B	317	HIS	ND1-CE1	6.57	1.39	1.32
1	C	114	HIS	CE1-NE2	6.55	1.39	1.32
1	A	114	HIS	CE1-NE2	6.49	1.39	1.32
1	B	114	HIS	CE1-NE2	6.46	1.39	1.32
1	C	114	HIS	ND1-CE1	6.45	1.39	1.32
1	A	79	HIS	ND1-CE1	6.41	1.39	1.32
1	C	215	HIS	ND1-CE1	6.40	1.39	1.32
1	A	215	HIS	ND1-CE1	6.32	1.38	1.32
1	D	107	HIS	CE1-NE2	6.32	1.38	1.32
1	A	77	HIS	ND1-CE1	6.25	1.38	1.32
1	D	317	HIS	CE1-NE2	6.22	1.38	1.32
1	A	79	HIS	CE1-NE2	6.15	1.38	1.32
1	B	215	HIS	ND1-CE1	6.10	1.38	1.32
1	A	107	HIS	CE1-NE2	6.07	1.38	1.32
1	B	71	GLN	CD-OE1	5.94	1.34	1.23
1	A	84	HIS	ND1-CE1	5.92	1.38	1.32
1	C	313	TRP	NE1-CE2	-5.91	1.30	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	338	GLN	CD-OE1	5.85	1.34	1.23
1	C	107	HIS	ND1-CE1	5.83	1.38	1.32
1	B	332	GLN	CD-OE1	5.82	1.34	1.23
1	A	77	HIS	CE1-NE2	5.81	1.38	1.32
1	D	102	GLN	CD-OE1	5.79	1.34	1.23
1	D	313	TRP	NE1-CE2	-5.78	1.31	1.37
1	C	71	GLN	CD-OE1	5.78	1.34	1.23
1	D	77	HIS	ND1-CE1	5.76	1.38	1.32
1	C	79	HIS	CE1-NE2	5.76	1.38	1.32
1	A	92	TRP	NE1-CE2	-5.76	1.31	1.37
1	B	102	GLN	CD-OE1	5.73	1.34	1.23
1	C	228	GLN	CD-OE1	5.70	1.34	1.23
1	C	102	GLN	CD-OE1	5.64	1.34	1.23
1	D	88	GLN	CD-OE1	5.63	1.34	1.23
1	B	313	TRP	NE1-CE2	-5.61	1.31	1.37
1	B	198	GLN	CD-OE1	5.59	1.34	1.23
1	A	318	GLN	CD-OE1	5.59	1.34	1.23
1	D	318	GLN	CD-OE1	5.59	1.34	1.23
1	C	153	GLN	CD-OE1	5.58	1.34	1.23
1	A	198	GLN	CD-OE1	5.58	1.34	1.23
1	A	71	GLN	CD-OE1	5.54	1.34	1.23
1	C	92	TRP	NE1-CE2	-5.54	1.31	1.37
1	D	198	GLN	CD-OE1	5.53	1.34	1.23
1	A	102	GLN	CD-OE1	5.51	1.34	1.23
1	D	83	TRP	NE1-CE2	-5.51	1.31	1.37
1	D	153	GLN	CD-OE1	5.46	1.33	1.23
1	C	332	GLN	CD-OE1	5.40	1.33	1.23
1	D	332	GLN	CD-OE1	5.40	1.33	1.23
1	B	88	GLN	CD-OE1	5.39	1.33	1.23
1	C	318	GLN	CD-OE1	5.38	1.33	1.23
1	A	338	GLN	CD-OE1	5.38	1.33	1.23
1	B	318	GLN	CD-OE1	5.37	1.33	1.23
1	D	338	GLN	CD-OE1	5.37	1.33	1.23
1	D	71	GLN	CD-OE1	5.36	1.33	1.23
1	C	88	GLN	CD-OE1	5.36	1.33	1.23
1	D	118	GLN	CD-OE1	5.36	1.33	1.23
1	C	198	GLN	CD-OE1	5.35	1.33	1.23
1	C	118	GLN	CD-OE1	5.34	1.33	1.23
1	A	332	GLN	CD-OE1	5.34	1.33	1.23
1	A	215	HIS	CE1-NE2	5.34	1.37	1.32
1	D	228	GLN	CD-OE1	5.34	1.33	1.23
1	B	118	GLN	CD-OE1	5.33	1.33	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	323	TRP	NE1-CE2	-5.32	1.31	1.37
1	A	305	TRP	NE1-CE2	-5.31	1.31	1.37
1	C	338	GLN	CD-OE1	5.30	1.33	1.23
1	B	228	GLN	CD-OE1	5.30	1.33	1.23
1	B	39	GLN	CD-OE1	5.30	1.33	1.23
1	B	288	GLN	CD-OE1	5.29	1.33	1.23
1	A	118	GLN	CD-OE1	5.29	1.33	1.23
1	B	153	GLN	CD-OE1	5.26	1.33	1.23
1	D	122	TRP	NE1-CE2	-5.26	1.31	1.37
1	C	288	GLN	CD-OE1	5.25	1.33	1.23
1	A	288	GLN	CD-OE1	5.20	1.33	1.23
1	B	305	TRP	NE1-CE2	-5.20	1.31	1.37
1	C	267	ASN	CG-OD1	5.20	1.33	1.23
1	D	288	GLN	CD-OE1	5.20	1.33	1.23
1	C	231	GLN	CD-OE1	5.17	1.33	1.23
1	A	83	TRP	NE1-CE2	-5.17	1.31	1.37
1	D	223	ILE	CA-CB	-5.16	1.47	1.54
1	B	30	GLN	CD-OE1	5.16	1.33	1.23
1	B	147	GLN	CD-OE1	5.16	1.33	1.23
1	A	153	GLN	CD-OE1	5.16	1.33	1.23
1	B	231	GLN	CD-OE1	5.16	1.33	1.23
1	D	39	GLN	CD-OE1	5.16	1.33	1.23
1	D	213	GLN	CD-OE1	5.15	1.33	1.23
1	C	83	TRP	NE1-CE2	-5.15	1.31	1.37
1	C	265	ASN	CG-OD1	5.14	1.33	1.23
1	A	313	TRP	NE1-CE2	-5.14	1.31	1.37
1	B	77	HIS	ND1-CE1	5.14	1.37	1.32
1	B	68	TRP	NE1-CE2	-5.11	1.31	1.37
1	D	30	GLN	CD-OE1	5.10	1.33	1.23
1	A	122	TRP	NE1-CE2	-5.07	1.31	1.37
1	A	213	GLN	CD-OE1	5.07	1.33	1.23
1	A	279	GLN	CD-OE1	5.07	1.33	1.23
1	C	30	GLN	CD-OE1	5.06	1.33	1.23
1	D	92	TRP	NE1-CE2	-5.06	1.31	1.37
1	C	74	GLN	CD-OE1	5.05	1.33	1.23
1	B	323	TRP	NE1-CE2	-5.05	1.31	1.37
1	C	323	TRP	NE1-CE2	-5.04	1.31	1.37
1	A	117	GLY	N-CA	5.03	1.52	1.45
1	C	195	ASN	CG-OD1	5.03	1.33	1.23
1	D	56	ASN	CG-OD1	5.03	1.33	1.23
1	D	143	ASN	CG-OD1	5.03	1.33	1.23
1	A	323	TRP	NE1-CE2	-5.03	1.31	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	30	GLN	CD-OE1	5.01	1.33	1.23

All (193) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	266	ARG	CD-NE-CZ	13.71	143.59	124.40
1	A	116	ALA	CA-C-N	-9.33	103.12	121.41
1	A	116	ALA	C-N-CA	-9.33	103.12	121.41
1	B	44	ASN	CA-CB-CG	-8.35	104.25	112.60
1	D	130	PHE	CA-CB-CG	-8.11	105.69	113.80
1	A	20	ASN	CA-C-O	-8.10	110.66	119.97
1	C	154	PHE	CA-CB-CG	-8.06	105.74	113.80
1	B	56	ASN	CA-CB-CG	-7.96	104.64	112.60
1	A	20	ASN	CA-CB-CG	-7.94	104.66	112.60
1	B	99	ASN	CA-CB-CG	-7.76	104.84	112.60
1	A	44	ASN	CA-CB-CG	-7.53	105.07	112.60
1	B	195	ASN	CA-CB-CG	-7.46	105.14	112.60
1	B	116	ALA	CA-C-N	-7.45	106.80	121.41
1	B	116	ALA	C-N-CA	-7.45	106.80	121.41
1	A	84	HIS	CA-CB-CG	-7.38	106.42	113.80
1	B	79	HIS	CA-C-N	7.28	134.80	121.70
1	B	79	HIS	C-N-CA	7.28	134.80	121.70
1	B	115	PHE	CA-CB-CG	-7.27	106.53	113.80
1	A	168	ARG	NE-CZ-NH1	7.24	128.74	121.50
1	B	74	GLN	OE1-CD-NE2	-7.22	115.38	122.60
1	C	137	ASP	CA-CB-CG	-7.11	105.49	112.60
1	B	295	PRO	N-CA-CB	-7.04	99.25	103.19
1	B	254	PRO	N-CA-C	-6.97	106.62	114.92
1	A	20	ASN	O-C-N	6.96	130.83	122.27
1	A	72	ASN	CA-CB-CG	-6.87	105.73	112.60
1	B	82	VAL	CA-CB-CG2	6.82	122.00	110.40
1	D	116	ALA	O-C-N	-6.78	113.58	122.59
1	D	12	VAL	CA-CB-CG2	6.77	121.91	110.40
1	A	168	ARG	O-C-N	-6.73	114.99	122.12
1	C	99	ASN	CA-CB-CG	-6.73	105.87	112.60
1	D	266	ARG	NE-CZ-NH2	-6.69	113.18	119.20
1	C	149	VAL	CA-CB-CG1	6.68	121.76	110.40
1	D	146	ARG	CD-NE-CZ	6.67	133.73	124.40
1	A	261	ASN	OD1-CG-ND2	-6.67	115.94	122.60
1	A	116	ALA	N-CA-CB	6.66	121.75	110.49
1	D	23	ILE	CA-C-N	6.65	129.85	120.28
1	D	23	ILE	C-N-CA	6.65	129.85	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	146	ARG	NE-CZ-NH1	6.60	128.10	121.50
1	D	114	HIS	CA-CB-CG	-6.59	107.21	113.80
1	C	295	PRO	N-CA-CB	-6.54	99.82	103.22
1	D	37	PHE	CA-CB-CG	-6.44	107.36	113.80
1	B	227	ARG	CD-NE-CZ	-6.42	115.41	124.40
1	B	24	PHE	CA-C-N	6.40	132.29	122.24
1	B	24	PHE	C-N-CA	6.40	132.29	122.24
1	D	126	ASN	OD1-CG-ND2	-6.38	116.22	122.60
1	D	156	GLY	O-C-N	6.35	128.12	121.77
1	B	306	GLY	CA-C-O	-6.32	117.22	122.33
1	A	139	ARG	CD-NE-CZ	-6.31	115.56	124.40
1	C	205	VAL	CA-CB-CG2	6.30	121.10	110.40
1	D	3	ALA	CA-C-N	6.29	130.66	120.60
1	D	3	ALA	C-N-CA	6.29	130.66	120.60
1	C	266	ARG	CD-NE-CZ	6.28	133.20	124.40
1	B	84	HIS	CB-CG-CD2	-6.27	123.05	131.20
1	C	299	ARG	CD-NE-CZ	-6.27	115.62	124.40
1	B	253	ASN	CA-C-N	-6.24	113.77	121.00
1	B	253	ASN	C-N-CA	-6.24	113.77	121.00
1	D	223	ILE	CA-CB-CG2	6.21	121.06	110.50
1	A	319	ASN	CA-CB-CG	-6.20	106.40	112.60
1	A	96	SER	N-CA-C	-6.20	105.54	113.23
1	B	108	ILE	N-CA-CB	6.17	117.77	110.55
1	A	37	PHE	CA-CB-CG	-6.15	107.65	113.80
1	C	116	ALA	CA-C-N	-6.15	109.36	121.41
1	C	116	ALA	C-N-CA	-6.15	109.36	121.41
1	D	74	GLN	OE1-CD-NE2	-6.13	116.47	122.60
1	C	267	ASN	CA-CB-CG	6.12	118.72	112.60
1	D	266	ARG	NE-CZ-NH1	6.10	127.60	121.50
1	D	246	GLU	CA-C-O	-6.09	116.00	121.67
1	B	147	GLN	CA-C-N	6.08	131.77	120.95
1	B	147	GLN	C-N-CA	6.08	131.77	120.95
1	C	44	ASN	CA-CB-CG	-6.05	106.55	112.60
1	B	304	VAL	N-CA-CB	-6.05	104.13	110.72
1	D	116	ALA	CA-C-N	-6.04	109.56	121.41
1	D	116	ALA	C-N-CA	-6.04	109.56	121.41
1	A	253	ASN	OD1-CG-ND2	-6.04	116.56	122.60
1	C	26	SER	O-C-N	-6.03	115.60	122.84
1	B	271	VAL	CA-CB-CG2	6.02	120.63	110.40
1	A	100	PHE	O-C-N	-5.99	115.86	122.09
1	D	197	VAL	CA-CB-CG2	5.98	120.56	110.40
1	D	31	ASN	CA-CB-CG	-5.96	106.64	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	76	VAL	CA-CB-CG2	5.94	120.50	110.40
1	B	146	ARG	CB-CA-C	5.94	119.17	110.26
1	C	220	TYR	CA-CB-CG	-5.91	103.27	113.90
1	A	146	ARG	CD-NE-CZ	5.88	132.64	124.40
1	D	219	ASP	CA-CB-CG	-5.88	106.72	112.60
1	A	57	PHE	CA-CB-CG	-5.88	107.92	113.80
1	B	116	ALA	N-CA-CB	5.86	118.68	109.94
1	A	150	PHE	CA-CB-CG	-5.86	107.94	113.80
1	D	137	ASP	CA-CB-CG	-5.84	106.76	112.60
1	A	266	ARG	NE-CZ-NH2	-5.83	113.95	119.20
1	C	119	VAL	CA-CB-CG2	5.83	120.31	110.40
1	A	194	VAL	CA-CB-CG2	5.81	120.28	110.40
1	C	304	VAL	CA-CB-CG2	5.81	120.28	110.40
1	D	203	ASN	CA-CB-CG	-5.80	106.80	112.60
1	D	84	HIS	CA-CB-CG	-5.79	108.01	113.80
1	C	194	VAL	CA-CB-CG2	5.78	120.22	110.40
1	A	74	GLN	OE1-CD-NE2	-5.76	116.84	122.60
1	D	199	ARG	CD-NE-CZ	-5.72	116.39	124.40
1	B	25	THR	CB-CA-C	5.72	118.63	109.02
1	C	253	ASN	CB-CA-C	5.72	116.17	110.33
1	C	70	ALA	CA-C-O	5.71	126.54	119.97
1	D	220	TYR	CA-CB-CG	-5.70	103.65	113.90
1	D	297	GLY	N-CA-C	-5.67	107.55	114.92
1	C	23	ILE	O-C-N	-5.65	116.16	121.87
1	A	231	GLN	O-C-N	5.65	127.89	122.07
1	D	168	ARG	CA-CB-CG	-5.64	102.81	114.10
1	A	205	VAL	CA-CB-CG2	5.64	119.98	110.40
1	A	99	ASN	CA-CB-CG	-5.63	106.97	112.60
1	B	14	VAL	CA-CB-CG2	5.63	119.97	110.40
1	B	88	GLN	OE1-CD-NE2	-5.62	116.98	122.60
1	C	67	SER	CA-C-N	5.62	128.12	120.54
1	C	67	SER	C-N-CA	5.62	128.12	120.54
1	A	12	VAL	CA-CB-CG2	5.60	119.93	110.40
1	A	223	ILE	N-CA-CB	5.59	120.88	110.77
1	C	66	VAL	CA-CB-CG2	5.57	119.87	110.40
1	C	130	PHE	CA-CB-CG	-5.55	108.25	113.80
1	C	235	ALA	CA-C-N	5.51	128.11	120.29
1	C	235	ALA	C-N-CA	5.51	128.11	120.29
1	A	178	TYR	CA-CB-CG	-5.50	103.99	113.90
1	B	295	PRO	O-C-N	-5.46	118.80	121.31
1	A	168	ARG	CA-C-O	5.45	126.33	120.55
1	A	8	PHE	CA-C-O	-5.45	115.44	120.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	20	ASN	CA-CB-CG	-5.42	107.18	112.60
1	A	166	ARG	N-CA-CB	-5.41	102.22	110.07
1	B	114	HIS	CB-CG-CD2	-5.41	124.17	131.20
1	C	344	LEU	CA-C-O	-5.41	113.99	120.10
1	A	149	VAL	CA-CB-CG1	5.40	119.58	110.40
1	A	225	ASN	CA-CB-CG	-5.38	107.22	112.60
1	A	223	ILE	CA-C-O	-5.36	114.68	120.47
1	B	149	VAL	CA-CB-CG1	5.35	119.49	110.40
1	D	76	VAL	CA-CB-CG2	5.32	119.44	110.40
1	B	247	LEU	CA-C-N	5.31	131.82	121.63
1	B	247	LEU	C-N-CA	5.31	131.82	121.63
1	A	101	ARG	NE-CZ-NH1	-5.30	116.20	121.50
1	B	225	ASN	CA-CB-CG	-5.30	107.30	112.60
1	A	101	ARG	CD-NE-CZ	-5.29	116.99	124.40
1	D	126	ASN	CA-C-O	-5.28	114.66	120.36
1	A	116	ALA	O-C-N	-5.26	115.59	122.59
1	B	84	HIS	CA-CB-CG	-5.26	108.54	113.80
1	A	82	VAL	CA-CB-CG2	5.26	119.34	110.40
1	B	105	ALA	CA-C-N	5.26	127.33	120.28
1	B	105	ALA	C-N-CA	5.26	127.33	120.28
1	C	322	ASP	CA-C-N	-5.25	117.08	122.85
1	C	322	ASP	C-N-CA	-5.25	117.08	122.85
1	A	191	THR	CA-C-N	5.24	127.73	120.29
1	A	191	THR	C-N-CA	5.24	127.73	120.29
1	A	328	ASN	OD1-CG-ND2	-5.24	117.36	122.60
1	D	292	GLU	CA-CB-CG	-5.22	103.66	114.10
1	C	253	ASN	OD1-CG-ND2	-5.21	117.39	122.60
1	B	66	VAL	CA-C-N	5.21	127.52	120.65
1	B	66	VAL	C-N-CA	5.21	127.52	120.65
1	C	330	ASN	CA-C-N	5.19	129.50	122.19
1	C	330	ASN	C-N-CA	5.19	129.50	122.19
1	A	111	VAL	CA-CB-CG1	5.19	119.22	110.40
1	C	299	ARG	NE-CZ-NH1	-5.18	116.32	121.50
1	B	114	HIS	CA-CB-CG	-5.18	108.62	113.80
1	B	211	GLY	CA-C-N	5.18	129.58	122.84
1	B	211	GLY	C-N-CA	5.18	129.58	122.84
1	C	203	ASN	CB-CG-ND2	5.18	124.17	116.40
1	A	341	VAL	CA-CB-CG2	5.18	119.20	110.40
1	A	8	PHE	O-C-N	5.17	125.72	121.32
1	A	249	VAL	CA-CB-CG2	5.17	119.18	110.40
1	B	179	ASN	O-C-N	-5.16	116.97	123.27
1	C	344	LEU	CA-C-N	5.16	130.99	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	344	LEU	C-N-CA	5.16	130.99	121.70
1	B	214	MET	CB-CA-C	-5.16	104.95	111.86
1	B	118	GLN	OE1-CD-NE2	-5.15	117.45	122.60
1	C	253	ASN	CA-C-N	-5.15	115.03	121.00
1	C	253	ASN	C-N-CA	-5.15	115.03	121.00
1	A	125	VAL	O-C-N	5.15	128.76	123.20
1	B	25	THR	O-C-N	-5.14	116.69	122.34
1	C	3	ALA	N-CA-C	-5.13	106.28	112.54
1	D	152	ARG	CA-C-N	5.13	127.66	120.28
1	D	152	ARG	C-N-CA	5.13	127.66	120.28
1	D	41	THR	CA-C-O	-5.12	115.28	120.71
1	B	103	ASP	CA-CB-CG	-5.12	107.48	112.60
1	D	67	SER	CB-CA-C	5.11	119.54	110.85
1	B	252	ASN	CB-CG-ND2	5.11	124.07	116.40
1	C	82	VAL	CA-CB-CG2	5.11	119.09	110.40
1	B	131	ASP	CA-C-N	5.11	127.64	120.28
1	B	131	ASP	C-N-CA	5.11	127.64	120.28
1	B	208	ASP	CA-CB-CG	-5.08	107.52	112.60
1	B	292	GLU	CA-CB-CG	-5.08	103.94	114.10
1	C	249	VAL	CA-CB-CG2	5.06	119.01	110.40
1	D	57	PHE	CA-CB-CG	-5.06	108.74	113.80
1	B	228	GLN	CB-CG-CD	-5.05	104.02	112.60
1	D	146	ARG	NE-CZ-NH1	5.05	126.55	121.50
1	D	341	VAL	CA-CB-CG2	5.04	118.97	110.40
1	B	77	HIS	CB-CG-CD2	-5.04	124.64	131.20
1	C	227	ARG	CD-NE-CZ	-5.02	117.37	124.40
1	D	223	ILE	N-CA-CB	5.02	119.23	110.65
1	D	18	GLY	CA-C-N	-5.01	113.20	121.57
1	D	18	GLY	C-N-CA	-5.01	113.20	121.57
1	C	223	ILE	CA-CB-CG2	5.01	119.01	110.50

There are no chirality outliers.

All (35) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	122	TRP	Peptide
1	A	146	ARG	Sidechain
1	A	152	ARG	Sidechain
1	A	166	ARG	Sidechain
1	A	227	ARG	Sidechain
1	A	250	ARG	Sidechain
1	A	266	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	64	ARG	Sidechain
1	B	122	TRP	Peptide
1	B	146	ARG	Sidechain
1	B	166	ARG	Sidechain
1	B	168	ARG	Sidechain
1	B	250	ARG	Sidechain
1	B	282	ARG	Sidechain
1	B	64	ARG	Sidechain
1	C	106	ARG	Sidechain
1	C	122	TRP	Peptide
1	C	152	ARG	Sidechain
1	C	165	ARG	Sidechain
1	C	166	ARG	Sidechain
1	C	168	ARG	Sidechain
1	C	199	ARG	Sidechain
1	C	278	ARG	Sidechain
1	C	298	ARG	Sidechain
1	C	52	TYR	Peptide
1	C	64	ARG	Sidechain
1	C	74	GLN	Peptide
1	D	101	ARG	Sidechain
1	D	122	TRP	Peptide
1	D	165	ARG	Sidechain
1	D	168	ARG	Sidechain
1	D	199	ARG	Sidechain
1	D	227	ARG	Sidechain
1	D	250	ARG	Sidechain
1	D	64	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	2699	0	2560	53	6
1	B	2699	0	2560	50	2
1	C	2699	0	2560	61	1
1	D	2699	0	2560	51	4
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	272	0	0	13	9
3	B	278	0	0	10	3
3	C	276	0	0	16	3
3	D	282	0	0	17	10
All	All	11908	0	10240	215	20

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 10.

All (215) 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:C:143:ASN:CG	3:C:1031:HOH:O	1.77	1.23
1:C:198:GLN:CG	3:C:1123:HOH:O	1.99	1.09
1:C:198:GLN:HG3	3:C:1123:HOH:O	1.53	1.08
1:A:230:MET:HE1	1:A:290:TYR:HD1	1.18	1.03
1:C:161:ASP:OD1	1:C:199:ARG:NH2	1.92	1.00
1:C:61:ASN:HD22	1:C:64:ARG:HH12	1.08	0.99
1:B:198:GLN:CG	3:B:846:HOH:O	2.10	0.98
1:C:230:MET:HE1	1:C:290:TYR:HD1	1.26	0.97
1:C:61:ASN:ND2	1:C:64:ARG:HH12	1.63	0.95
1:D:230:MET:HE1	1:D:290:TYR:HD1	1.31	0.94
1:B:198:GLN:HG2	3:B:846:HOH:O	1.68	0.92
1:A:198:GLN:HG2	3:A:569:HOH:O	1.70	0.92
1:C:61:ASN:HD22	1:C:64:ARG:NH1	1.69	0.91
1:B:7:ASP:OD1	3:B:711:HOH:O	1.88	0.90
1:B:317:HIS:HD2	3:B:655:HOH:O	1.56	0.88
1:A:230:MET:HE1	1:A:290:TYR:CD1	2.08	0.88
1:C:40:ILE:HG22	3:C:1102:HOH:O	1.76	0.85
1:D:308:ALA:HB2	1:D:331:LEU:CD1	2.07	0.84
1:B:198:GLN:HG3	3:B:846:HOH:O	1.74	0.84
1:C:230:MET:HE1	1:C:290:TYR:CD1	2.13	0.83
1:D:52:TYR:OH	1:D:107:HIS:HD2	1.61	0.82
1:B:230:MET:HE1	1:B:290:TYR:HD1	1.42	0.82
1:D:161:ASP:OD1	1:D:199:ARG:NH2	2.13	0.82
1:D:230:MET:HE1	1:D:290:TYR:CD1	2.14	0.82
1:D:120:LYS:NZ	3:D:1367:HOH:O	2.13	0.81
1:B:52:TYR:OH	1:B:107:HIS:HD2	1.65	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:HIS:HD2	3:A:378:HOH:O	1.65	0.79
1:D:198:GLN:CG	3:D:1400:HOH:O	2.31	0.79
1:A:219:ASP:HB2	3:A:394:HOH:O	1.83	0.78
1:D:219:ASP:HB2	3:D:1225:HOH:O	1.83	0.78
1:B:61:ASN:HD22	1:B:64:ARG:HH12	1.31	0.77
1:D:40:ILE:HG22	3:D:1379:HOH:O	1.83	0.77
1:C:109:ASP:OD1	1:C:166:ARG:HG2	1.85	0.77
1:D:198:GLN:HG2	3:D:1400:HOH:O	1.83	0.77
1:B:134:ASP:O	1:B:146:ARG:NH2	2.19	0.76
1:C:258:ASN:OD1	1:C:260:SER:HB2	1.85	0.74
1:C:198:GLN:HG2	3:C:1123:HOH:O	1.70	0.74
1:D:134:ASP:O	1:D:146:ARG:NH2	2.19	0.74
1:C:214:MET:HE1	1:C:226:ILE:HG23	1.68	0.73
1:C:134:ASP:CG	1:C:146:ARG:HH22	1.95	0.73
1:B:219:ASP:HB2	3:B:671:HOH:O	1.89	0.73
1:B:230:MET:HE1	1:B:290:TYR:CD1	2.23	0.73
1:B:230:MET:CE	1:B:242:ILE:HG21	2.19	0.73
1:A:40:ILE:HG22	3:A:548:HOH:O	1.87	0.73
1:D:33:VAL:HG13	3:D:1379:HOH:O	1.89	0.72
1:C:52:TYR:OH	1:C:107:HIS:HD2	1.71	0.72
1:A:63:ASP:OD1	1:A:114:HIS:HE1	1.73	0.72
1:C:142:ALA:CB	3:C:1151:HOH:O	2.36	0.72
1:C:266:ARG:HD2	3:C:1245:HOH:O	1.88	0.71
1:A:100:PHE:CB	1:A:153:GLN:HE21	2.03	0.71
1:B:63:ASP:OD1	1:B:114:HIS:HE1	1.73	0.71
1:A:227:ARG:HG3	1:A:227:ARG:NH1	2.06	0.71
1:B:168:ARG:HG3	1:B:168:ARG:O	1.94	0.68
1:D:230:MET:CE	1:D:242:ILE:HG21	2.23	0.68
1:C:134:ASP:OD2	1:C:146:ARG:NH2	2.24	0.68
1:C:142:ALA:HB2	3:C:1151:HOH:O	1.92	0.68
1:C:46:MET:HE3	1:C:65:LEU:HD23	1.76	0.68
1:B:230:MET:HE3	1:B:242:ILE:HG21	1.76	0.67
1:C:63:ASP:OD1	1:C:114:HIS:HE1	1.78	0.67
1:A:296:PRO:O	3:A:401:HOH:O	2.13	0.66
1:A:161:ASP:O	1:A:165:ARG:HG3	1.96	0.66
1:D:162:GLU:O	1:D:166:ARG:HB2	1.96	0.66
1:C:40:ILE:CG2	3:C:1102:HOH:O	2.39	0.65
1:A:40:ILE:CG2	3:A:548:HOH:O	2.44	0.64
1:B:61:ASN:ND2	1:B:64:ARG:HH12	1.96	0.64
1:C:61:ASN:ND2	1:C:64:ARG:NH1	2.36	0.63
1:A:230:MET:CE	1:A:290:TYR:HD1	2.02	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:VAL:O	1:A:345:SER:OG	2.10	0.63
1:A:317:HIS:HE1	1:A:322:ASP:OD2	1.82	0.63
1:B:109:ASP:OD1	1:B:166:ARG:HG2	1.98	0.62
1:C:161:ASP:CG	1:C:199:ARG:HH22	2.00	0.62
1:A:129:LEU:HD21	1:A:196:LEU:HD12	1.81	0.62
1:D:52:TYR:OH	1:D:107:HIS:CD2	2.50	0.62
1:D:60:THR:HG21	3:D:1281:HOH:O	2.00	0.62
1:D:230:MET:HE3	1:D:242:ILE:HG21	1.81	0.62
1:C:309:ASP:N	1:C:310:PRO:HD2	2.15	0.62
1:C:227:ARG:NH1	3:C:949:HOH:O	2.31	0.62
1:A:308:ALA:HB2	1:A:331:LEU:CD1	2.30	0.61
1:B:34:ARG:NH1	1:B:72:ASN:OD1	2.28	0.61
1:C:317:HIS:HE1	1:C:322:ASP:OD2	1.83	0.61
1:D:108:ILE:HG21	1:D:166:ARG:HB3	1.82	0.60
1:D:33:VAL:CG1	3:D:1379:HOH:O	2.46	0.60
1:D:108:ILE:HD12	1:D:163:ALA:HA	1.84	0.60
1:D:266:ARG:HD2	3:D:968:HOH:O	2.03	0.58
1:A:129:LEU:CD2	1:A:196:LEU:HD12	2.33	0.58
1:D:308:ALA:HB2	1:D:331:LEU:HD11	1.85	0.58
1:C:143:ASN:CB	3:C:1031:HOH:O	2.35	0.57
1:D:317:HIS:HE1	1:D:322:ASP:OD2	1.87	0.57
1:B:52:TYR:OH	1:B:107:HIS:CD2	2.54	0.57
1:A:52:TYR:OH	1:A:107:HIS:HD2	1.88	0.57
1:D:317:HIS:HD2	3:D:1209:HOH:O	1.87	0.56
1:B:161:ASP:OD1	1:B:199:ARG:NH2	2.38	0.56
1:D:34:ARG:NH1	1:D:72:ASN:OD1	2.38	0.56
1:D:317:HIS:CD2	3:D:1209:HOH:O	2.58	0.55
1:B:131:ASP:OD1	1:B:133:ALA:HB3	2.07	0.55
1:B:230:MET:HE2	1:B:242:ILE:HG21	1.88	0.55
1:A:100:PHE:HB2	1:A:153:GLN:HE21	1.72	0.55
1:A:108:ILE:HG21	1:A:166:ARG:HB3	1.89	0.54
1:A:317:HIS:CD2	3:A:378:HOH:O	2.48	0.54
1:B:108:ILE:HG21	1:B:166:ARG:HB3	1.90	0.54
1:D:162:GLU:O	1:D:162:GLU:HG3	2.08	0.54
1:C:130:PHE:CD2	1:C:141:SER:HB2	2.43	0.54
1:B:136:PRO:HD2	3:B:753:HOH:O	2.09	0.53
1:C:52:TYR:OH	1:C:107:HIS:CD2	2.59	0.53
1:C:116:ALA:O	1:C:171:ASP:OD2	2.26	0.53
1:D:48:MET:HG3	1:D:88:GLN:HE22	1.73	0.53
1:C:278:ARG:O	1:C:278:ARG:HD2	2.08	0.52
1:A:284:LYS:HE3	1:A:342:GLU:CB	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:230:MET:HE2	1:D:242:ILE:HG21	1.91	0.52
1:A:161:ASP:OD1	1:A:199:ARG:NH2	2.36	0.52
3:A:414:HOH:O	1:B:266:ARG:HD2	2.09	0.52
1:C:134:ASP:O	1:C:146:ARG:NH2	2.43	0.52
1:D:198:GLN:HG3	3:D:1400:HOH:O	2.02	0.52
1:C:142:ALA:HB1	3:C:1151:HOH:O	2.03	0.51
1:D:102:GLN:O	1:D:102:GLN:HG2	2.10	0.51
1:D:308:ALA:CB	1:D:331:LEU:CD1	2.86	0.51
1:D:157:PRO:HD2	1:D:158:GLU:OE2	2.10	0.51
1:A:230:MET:CE	1:A:290:TYR:CD1	2.86	0.51
1:C:237:SER:HB3	1:C:240:LEU:HB2	1.92	0.51
1:C:67:SER:O	1:C:71:GLN:HG3	2.11	0.50
1:D:134:ASP:CG	1:D:146:ARG:HH22	2.20	0.50
1:A:198:GLN:CG	3:A:569:HOH:O	2.42	0.50
1:C:168:ARG:O	1:C:168:ARG:HG3	2.11	0.49
1:B:134:ASP:CG	1:B:146:ARG:HH22	2.20	0.49
1:C:13:ALA:HA	1:C:41:THR:O	2.13	0.49
1:D:309:ASP:HB2	1:D:310:PRO:HD3	1.95	0.49
1:B:317:HIS:HE1	1:B:322:ASP:OD2	1.96	0.49
1:B:230:MET:HE3	1:B:242:ILE:CG2	2.43	0.48
1:C:220:TYR:C	1:C:220:TYR:CD2	2.90	0.48
1:C:33:VAL:CG1	3:C:1102:HOH:O	2.60	0.48
1:D:220:TYR:CD1	1:D:220:TYR:C	2.91	0.48
1:C:31:ASN:OD1	1:C:34:ARG:NH2	2.41	0.48
1:A:284:LYS:HE3	1:A:342:GLU:HB3	1.94	0.48
1:B:42:ALA:HB2	1:B:46:MET:HE3	1.95	0.48
1:C:143:ASN:OD1	3:C:1031:HOH:O	2.05	0.48
1:D:7:ASP:OD1	1:D:7:ASP:N	2.46	0.48
1:A:266:ARG:O	1:A:266:ARG:HG3	2.14	0.48
1:B:308:ALA:HB2	1:B:331:LEU:CD1	2.44	0.48
1:A:84:HIS:N	1:A:85:PRO:CD	2.77	0.47
1:C:162:GLU:O	1:C:162:GLU:HG3	2.14	0.47
1:B:69:ALA:HB1	1:B:74:GLN:HB2	1.97	0.47
1:C:293:VAL:O	1:C:295:PRO:HD3	2.15	0.46
1:D:214:MET:HE1	1:D:226:ILE:HG23	1.96	0.46
1:A:227:ARG:HG3	1:A:227:ARG:HH11	1.79	0.46
1:C:143:ASN:HB2	3:C:1031:HOH:O	2.09	0.46
1:A:100:PHE:CB	1:A:153:GLN:NE2	2.76	0.46
1:C:334:LYS:HB3	1:C:335:PRO:HD2	1.97	0.46
1:B:217:MET:HG2	1:B:250:ARG:HB2	1.97	0.46
1:B:284:LYS:O	1:B:288:GLN:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:ILE:CG2	3:D:1379:HOH:O	2.55	0.46
1:C:69:ALA:HB1	1:C:74:GLN:HB2	1.96	0.46
1:A:130:PHE:CD2	1:A:141:SER:HB2	2.50	0.46
1:C:205:VAL:HG13	1:C:206:PRO:HD2	1.97	0.46
1:D:230:MET:HE3	1:D:242:ILE:CG2	2.44	0.46
1:C:83:TRP:CZ2	1:C:85:PRO:HG2	2.51	0.45
1:B:131:ASP:HB3	1:B:134:ASP:HB3	1.98	0.45
1:B:161:ASP:O	1:B:165:ARG:HG3	2.16	0.45
1:A:121:SER:HB3	1:A:175:GLU:HB2	1.99	0.45
1:C:223:ILE:HD12	3:C:950:HOH:O	2.16	0.45
1:A:52:TYR:OH	1:A:107:HIS:CD2	2.69	0.45
1:A:139:ARG:HB2	1:A:147:GLN:HB2	1.99	0.45
1:D:64:ARG:HG3	3:D:1356:HOH:O	2.16	0.45
1:D:315:TYR:OH	1:D:329:ASP:OD2	2.22	0.45
1:B:228:GLN:CG	3:B:842:HOH:O	2.65	0.44
1:A:84:HIS:N	1:A:85:PRO:HD3	2.32	0.44
1:B:46:MET:CE	1:B:65:LEU:HD23	2.47	0.44
1:A:154:PHE:CG	1:A:159:TYR:HB3	2.52	0.44
1:D:108:ILE:CD1	1:D:163:ALA:HA	2.46	0.44
1:B:308:ALA:HB2	1:B:331:LEU:HD12	2.00	0.44
1:C:171:ASP:OD1	1:C:173:THR:OG1	2.33	0.44
1:D:168:ARG:NH2	1:D:208:ASP:OD2	2.46	0.44
1:A:214:MET:HE1	1:A:226:ILE:HG23	2.00	0.43
1:C:196:LEU:C	1:C:196:LEU:HD23	2.44	0.43
1:C:213:GLN:O	1:C:214:MET:HB2	2.18	0.43
1:A:294:VAL:HA	1:A:295:PRO:HD3	1.86	0.43
1:B:196:LEU:C	1:B:196:LEU:HD23	2.43	0.43
1:A:33:VAL:CG1	3:A:548:HOH:O	2.66	0.43
1:B:237:SER:HB3	1:B:240:LEU:HB2	2.00	0.43
1:D:177:TYR:CE2	1:D:243:LYS:HB2	2.54	0.43
1:B:83:TRP:CZ2	1:B:85:PRO:HG2	2.54	0.43
1:A:223:ILE:HD12	1:A:223:ILE:N	2.34	0.42
1:B:217:MET:HE3	1:B:220:TYR:HB3	2.00	0.42
1:C:309:ASP:N	1:C:310:PRO:CD	2.82	0.42
1:A:33:VAL:CG2	3:A:548:HOH:O	2.66	0.42
1:B:139:ARG:HB2	1:B:147:GLN:HB2	2.01	0.42
1:A:148:SER:O	1:A:152:ARG:HG3	2.19	0.42
1:A:237:SER:HB3	1:A:240:LEU:HB2	2.01	0.42
1:B:195:ASN:HD22	1:B:195:ASN:HA	1.68	0.42
1:C:240:LEU:HD12	1:C:240:LEU:HA	1.68	0.42
1:D:99:ASN:ND2	3:D:1442:HOH:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:13:ALA:HB2	1:C:305:TRP:CE3	2.55	0.42
1:C:330:ASN:HB2	1:C:332:GLN:HG2	2.02	0.42
1:B:83:TRP:CD2	1:B:85:PRO:HD2	2.55	0.41
1:B:136:PRO:HD2	1:B:146:ARG:HH21	1.85	0.41
1:D:151:TYR:CZ	1:D:156:GLY:HA2	2.55	0.41
1:B:228:GLN:HG2	3:B:842:HOH:O	2.19	0.41
1:D:254:PRO:HA	3:D:1180:HOH:O	2.19	0.41
1:D:12:VAL:CG1	3:D:1379:HOH:O	2.67	0.41
1:C:284:LYS:HG3	1:C:343:ALA:HB2	2.03	0.41
1:A:11:GLY:HA2	1:A:39:GLN:O	2.20	0.41
1:A:295:PRO:HA	1:A:296:PRO:HD3	1.86	0.41
1:A:331:LEU:HD12	1:A:331:LEU:HA	1.80	0.41
1:A:230:MET:HE2	1:A:294:VAL:CG2	2.51	0.41
1:B:177:TYR:CE2	1:B:209:GLY:HA3	2.56	0.41
1:A:284:LYS:HE3	1:A:342:GLU:HB2	2.03	0.40
1:B:295:PRO:HA	1:B:296:PRO:HD3	1.95	0.40
1:A:151:TYR:CZ	1:A:156:GLY:HA2	2.56	0.40
1:A:318:GLN:NE2	3:A:737:HOH:O	2.42	0.40
1:A:33:VAL:HG11	3:A:548:HOH:O	2.22	0.40
1:C:89:LEU:HD23	1:C:89:LEU:HA	1.92	0.40
1:C:284:LYS:HE3	1:C:342:GLU:HB3	2.04	0.40
1:B:317:HIS:HB2	3:B:704:HOH:O	2.21	0.40
1:D:31:ASN:OD1	1:D:34:ARG:NH2	2.49	0.40
1:D:142:ALA:O	1:D:143:ASN:HB2	2.21	0.40
1:A:315:TYR:OH	1:A:329:ASP:OD2	2.21	0.40

All (20) 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)
3:A:622:HOH:O	3:D:1395:HOH:O[2_675]	0.78	1.42
3:A:477:HOH:O	3:A:546:HOH:O[3_646]	0.88	1.32
3:A:507:HOH:O	3:D:1354:HOH:O[3_656]	1.28	0.92
3:B:899:HOH:O	3:D:1286:HOH:O[3_656]	1.40	0.80
3:A:547:HOH:O	3:A:597:HOH:O[3_656]	1.47	0.73
3:A:601:HOH:O	3:B:754:HOH:O[3_656]	1.53	0.67
1:A:64:ARG:NH2	3:D:1422:HOH:O[3_656]	1.56	0.64
1:A:173:THR:O	3:B:754:HOH:O[3_656]	1.59	0.61
1:A:64:ARG:NH1	3:D:1422:HOH:O[3_656]	1.62	0.58
3:A:525:HOH:O	3:D:1450:HOH:O[3_656]	1.68	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:583:HOH:O	3:D:1318:HOH:O[2_675]	1.68	0.52
3:A:591:HOH:O	3:D:1281:HOH:O[3_656]	1.72	0.48
1:D:173:THR:CB	3:C:1151:HOH:O[4_466]	1.73	0.47
1:A:64:ARG:CZ	3:D:1422:HOH:O[3_656]	1.74	0.46
1:D:173:THR:CG2	3:C:1151:HOH:O[4_466]	1.84	0.36
1:A:175:GLU:CG	1:B:143:ASN:OD1[3_656]	1.99	0.21
1:A:239:THR:CG2	1:B:195:ASN:ND2[3_656]	1.99	0.21
1:D:173:THR:CA	3:C:1151:HOH:O[4_466]	2.04	0.16
1:C:143:ASN:ND2	1:D:208:ASP:OD1[4_566]	2.06	0.14
3:A:523:HOH:O	3:D:1454:HOH:O[3_656]	2.14	0.06

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	343/347 (99%)	331 (96%)	11 (3%)	1 (0%)	36	25
1	B	343/347 (99%)	332 (97%)	11 (3%)	0	100	100
1	C	343/347 (99%)	332 (97%)	11 (3%)	0	100	100
1	D	343/347 (99%)	330 (96%)	13 (4%)	0	100	100
All	All	1372/1388 (99%)	1325 (97%)	46 (3%)	1 (0%)	48	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	GLY

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.