



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:29 PM UTC

PDB ID : 1PAM / pdb_00001pam
Title : CYCLODEXTRIN GLUCANOTRANSFERASE
Authors : Harata, K.; Haga, K.; Nakamura, A.; Aoyagi, M.; Yamane, K.
Deposited on : 1996-07-08
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

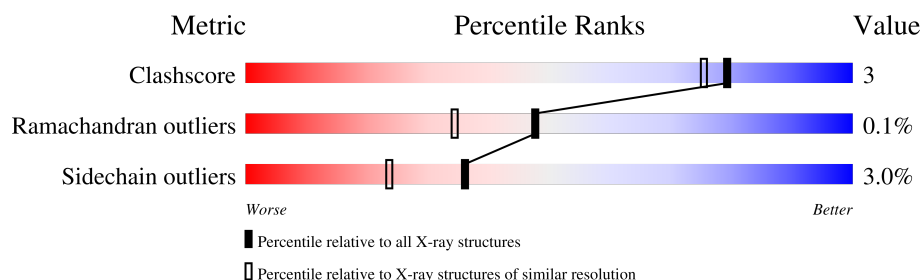
1 Overall quality at a glance

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)
Sidechain outliers	187428	8390 (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	686	
1	B	686	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11433 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 CYCLODEXTRIN GLUCANOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	686	Total	C	N	O	S	0	0	0
			5312	3354	906	1036	16			
1	B	686	Total	C	N	O	S	0	0	0
			5312	3354	906	1036	16			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	452	PRO	ARG	conflict	UNP P05618
A	454	GLY	ALA	conflict	UNP P05618
B	452	PRO	ARG	conflict	UNP P05618
B	454	GLY	ALA	conflict	UNP P05618

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

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

- Molecule 3 is water.

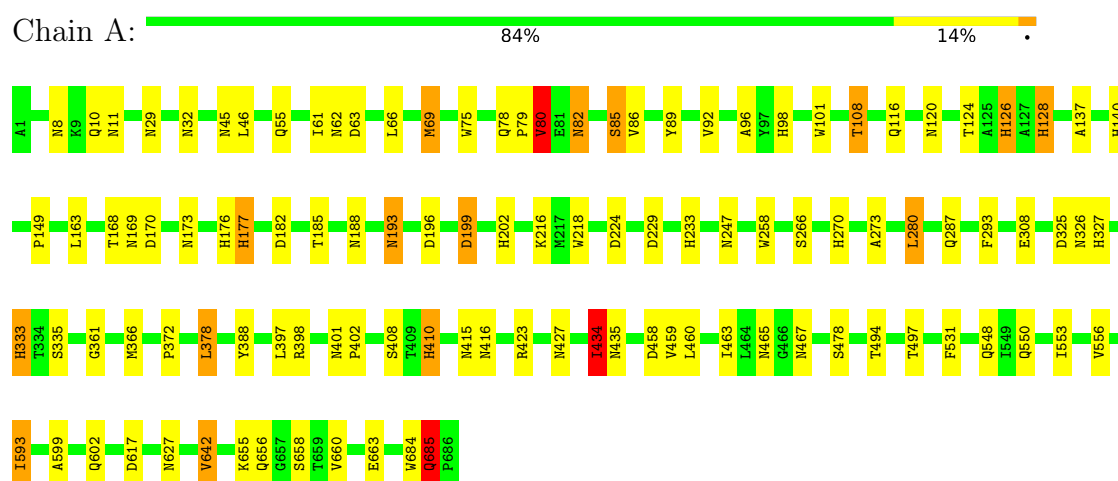
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	435	Total	O	0	0
			435	435		
3	B	370	Total	O	0	0
			370	370		

3 Residue-property plots

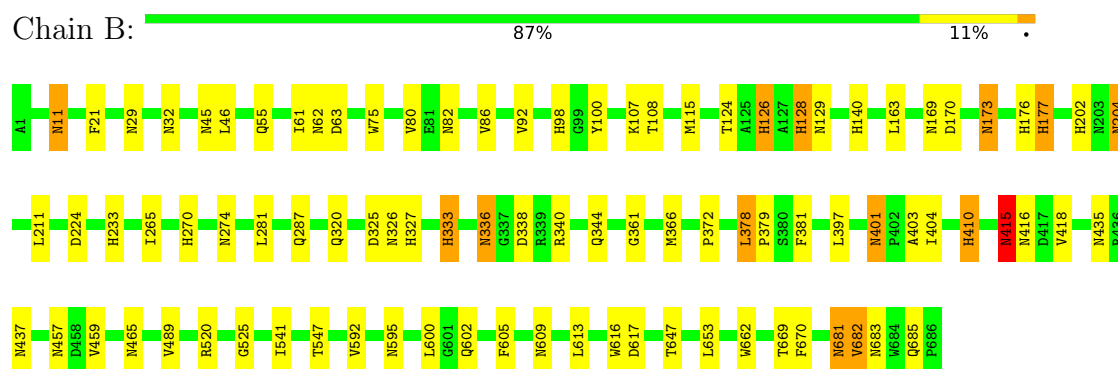
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



• Molecule 1: CYCLODEXTRIN GLUCANOTRANSFERASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.93Å 74.45Å 79.12Å 85.20° 105.00° 101.00°	Depositor
Resolution (Å)	10.00 – 1.80	Depositor
% Data completeness (in resolution range)	74.5 (10.00-1.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.161 , 0.211	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11433	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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	0.92	15/5446 (0.3%)	1.56	79/7429 (1.1%)
1	B	0.91	13/5446 (0.2%)	1.55	64/7429 (0.9%)
All	All	0.92	28/10892 (0.3%)	1.55	143/14858 (1.0%)

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	434	ILE	CA-CB	10.27	1.68	1.54
1	A	140	HIS	CD2-NE2	-7.57	1.29	1.37
1	B	98	HIS	CD2-NE2	-7.19	1.29	1.37
1	A	327	HIS	CD2-NE2	-7.19	1.29	1.37
1	A	333	HIS	CD2-NE2	-7.08	1.30	1.37
1	B	140	HIS	CD2-NE2	-7.04	1.30	1.37
1	A	126	HIS	CD2-NE2	-6.98	1.30	1.37
1	A	128	HIS	CD2-NE2	-6.83	1.30	1.37
1	B	128	HIS	CD2-NE2	-6.80	1.30	1.37
1	A	98	HIS	CD2-NE2	-6.61	1.30	1.37
1	A	177	HIS	CD2-NE2	-6.56	1.30	1.37
1	B	327	HIS	CD2-NE2	-6.50	1.30	1.37
1	B	410	HIS	CD2-NE2	-6.44	1.30	1.37
1	B	233	HIS	CD2-NE2	-6.30	1.30	1.37
1	B	333	HIS	CD2-NE2	-6.30	1.30	1.37
1	B	177	HIS	CD2-NE2	-6.28	1.30	1.37
1	A	176	HIS	CD2-NE2	-6.27	1.30	1.37
1	B	176	HIS	CD2-NE2	-6.25	1.30	1.37
1	B	270	HIS	CD2-NE2	-6.24	1.30	1.37
1	A	233	HIS	CD2-NE2	-6.21	1.31	1.37
1	B	126	HIS	CD2-NE2	-6.09	1.31	1.37
1	A	202	HIS	CD2-NE2	-5.83	1.31	1.37
1	A	270	HIS	CD2-NE2	-5.45	1.31	1.37
1	B	202	HIS	CD2-NE2	-5.38	1.31	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	410	HIS	CD2-NE2	-5.23	1.32	1.37
1	B	270	HIS	CG-ND1	-5.23	1.32	1.38
1	A	233	HIS	CG-ND1	-5.19	1.32	1.38
1	A	128	HIS	CG-ND1	-5.12	1.32	1.38

All (143) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	ARG	NE-CZ-NH2	-13.04	107.46	119.20
1	B	336	ASN	CA-CB-CG	10.76	123.36	112.60
1	B	415	ASN	CA-CB-CG	9.71	122.31	112.60
1	B	325	ASP	CA-CB-CG	9.12	121.72	112.60
1	A	642	VAL	N-CA-CB	-8.69	99.04	111.21
1	A	398	ARG	NE-CZ-NH1	8.66	130.16	121.50
1	A	11	ASN	OD1-CG-ND2	-8.55	114.05	122.60
1	A	435	ASN	OD1-CG-ND2	-8.35	114.25	122.60
1	B	410	HIS	CB-CG-CD2	-8.14	120.62	131.20
1	A	325	ASP	CA-CB-CG	8.13	120.73	112.60
1	A	69	MET	CG-SD-CE	-7.83	83.67	100.90
1	A	108	THR	N-CA-CB	-7.76	97.76	110.41
1	A	8	ASN	OD1-CG-ND2	-7.75	114.85	122.60
1	B	685	GLN	OE1-CD-NE2	-7.73	114.87	122.60
1	B	129	ASN	OD1-CG-ND2	-7.61	114.99	122.60
1	A	415	ASN	CA-CB-CG	7.46	120.06	112.60
1	B	98	HIS	CB-CG-CD2	-7.46	121.50	131.20
1	A	685	GLN	OE1-CD-NE2	-7.44	115.16	122.60
1	B	327	HIS	CB-CG-CD2	-7.38	121.60	131.20
1	A	327	HIS	CB-CG-CD2	-7.13	121.93	131.20
1	A	126	HIS	CB-CG-CD2	-7.10	121.97	131.20
1	A	82	ASN	OD1-CG-ND2	-7.07	115.53	122.60
1	B	401	ASN	OD1-CG-ND2	-7.03	115.57	122.60
1	A	627	ASN	OD1-CG-ND2	-7.03	115.58	122.60
1	B	100	TYR	N-CA-C	7.01	121.66	113.18
1	A	63	ASP	CA-CB-CG	6.98	119.58	112.60
1	B	415	ASN	OD1-CG-ND2	-6.96	115.64	122.60
1	B	32	ASN	CA-CB-CG	6.81	119.41	112.60
1	A	10	GLN	OE1-CD-NE2	-6.80	115.80	122.60
1	B	86	VAL	N-CA-C	-6.76	98.11	107.99
1	B	287	GLN	OE1-CD-NE2	-6.70	115.90	122.60
1	A	333	HIS	CB-CG-CD2	-6.66	122.55	131.20
1	B	55	GLN	OE1-CD-NE2	-6.64	115.96	122.60
1	A	398	ARG	CG-CD-NE	-6.61	97.46	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	685	GLN	CG-CD-NE2	6.58	126.27	116.40
1	B	63	ASP	CA-CB-CG	6.53	119.13	112.60
1	B	274	ASN	OD1-CG-ND2	-6.53	116.07	122.60
1	B	11	ASN	OD1-CG-ND2	-6.50	116.10	122.60
1	B	320	GLN	OE1-CD-NE2	-6.42	116.18	122.60
1	B	457	ASN	OD1-CG-ND2	-6.36	116.24	122.60
1	B	435	ASN	OD1-CG-ND2	-6.35	116.25	122.60
1	B	204	ASN	OD1-CG-ND2	-6.31	116.29	122.60
1	A	196	ASP	CA-CB-CG	6.31	118.91	112.60
1	A	247	ASN	OD1-CG-ND2	-6.28	116.33	122.60
1	A	98	HIS	CB-CG-CD2	-6.27	123.05	131.20
1	B	410	HIS	CB-CG-ND1	6.25	132.08	122.70
1	B	617	ASP	CA-CB-CG	6.24	118.84	112.60
1	A	80	VAL	N-CA-CB	-6.23	98.31	110.45
1	B	98	HIS	CB-CG-ND1	6.20	132.00	122.70
1	B	338	ASP	CA-CB-CG	6.20	118.80	112.60
1	A	120	ASN	OD1-CG-ND2	-6.16	116.44	122.60
1	B	602	GLN	N-CA-C	-6.16	99.62	109.96
1	B	173	ASN	CA-CB-CG	-6.11	106.49	112.60
1	B	682	VAL	N-CA-CB	-6.07	99.56	112.00
1	A	32	ASN	CA-CB-CG	6.03	118.63	112.60
1	A	467	ASN	OD1-CG-ND2	-6.03	116.57	122.60
1	B	61	ILE	N-CA-C	-6.02	104.98	110.82
1	A	11	ASN	CB-CG-ND2	6.01	125.42	116.40
1	A	266	SER	CA-C-N	6.01	125.72	119.05
1	A	266	SER	C-N-CA	6.01	125.72	119.05
1	B	662	TRP	CG-CD2-CE3	5.99	139.89	133.90
1	B	126	HIS	CB-CG-CD2	-5.97	123.44	131.20
1	B	415	ASN	CB-CG-ND2	5.92	125.29	116.40
1	B	29	ASN	CA-C-N	5.90	125.52	119.56
1	B	29	ASN	C-N-CA	5.90	125.52	119.56
1	A	531	PHE	N-CA-C	-5.89	97.56	107.99
1	B	62	ASN	N-CA-C	5.87	117.75	111.36
1	B	129	ASN	CA-CB-CG	-5.85	106.75	112.60
1	A	287	GLN	OE1-CD-NE2	-5.84	116.76	122.60
1	B	541	ILE	N-CA-C	-5.84	98.62	107.73
1	A	10	GLN	CG-CD-NE2	5.83	125.14	116.40
1	B	416	ASN	OD1-CG-ND2	-5.80	116.80	122.60
1	A	85	SER	N-CA-C	5.80	118.64	110.23
1	A	108	THR	CB-CA-C	5.78	119.39	109.51
1	A	80	VAL	CB-CA-C	5.75	119.22	111.28
1	A	270	HIS	CB-CG-CD2	-5.74	123.73	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	45	ASN	OD1-CG-ND2	-5.71	116.89	122.60
1	A	478	SER	N-CA-CB	-5.69	101.61	109.97
1	A	177	HIS	CB-CG-CD2	-5.68	123.81	131.20
1	A	29	ASN	CA-C-N	5.68	125.21	119.19
1	A	29	ASN	C-N-CA	5.68	125.21	119.19
1	B	327	HIS	CB-CG-ND1	5.67	131.20	122.70
1	A	465	ASN	OD1-CG-ND2	-5.66	116.94	122.60
1	B	333	HIS	CB-CG-CD2	-5.64	123.87	131.20
1	A	458	ASP	CA-CB-CG	5.61	118.21	112.60
1	A	685	GLN	CB-CG-CD	5.60	122.12	112.60
1	B	140	HIS	CB-CG-CD2	-5.59	123.93	131.20
1	A	62	ASN	OD1-CG-ND2	-5.55	117.05	122.60
1	A	61	ILE	N-CA-C	-5.54	105.45	110.82
1	A	202	HIS	CB-CG-CD2	-5.51	124.04	131.20
1	A	416	ASN	OD1-CG-ND2	-5.49	117.11	122.60
1	A	98	HIS	CB-CG-ND1	5.48	130.92	122.70
1	A	116	GLN	OE1-CD-NE2	-5.46	117.14	122.60
1	B	609	ASN	N-CA-C	5.44	119.55	113.02
1	B	681	ASN	OD1-CG-ND2	-5.44	117.16	122.60
1	B	176	HIS	CB-CG-CD2	-5.43	124.15	131.20
1	B	326	ASN	CA-CB-CG	5.42	118.02	112.60
1	A	553	ILE	CA-C-N	5.41	125.39	120.03
1	A	553	ILE	C-N-CA	5.41	125.39	120.03
1	B	685	GLN	CG-CD-NE2	5.38	124.48	116.40
1	A	548	GLN	OE1-CD-NE2	-5.34	117.25	122.60
1	A	140	HIS	CB-CG-CD2	-5.33	124.27	131.20
1	A	270	HIS	CA-CB-CG	-5.32	108.48	113.80
1	A	169	ASN	CA-CB-CG	-5.30	107.30	112.60
1	B	128	HIS	CB-CG-CD2	-5.29	124.32	131.20
1	B	662	TRP	CE2-CD2-CG	-5.28	100.87	107.20
1	B	685	GLN	N-CA-C	-5.27	101.91	109.24
1	B	437	ASN	CA-CB-CG	-5.24	107.36	112.60
1	A	69	MET	N-CA-CB	-5.24	102.23	110.46
1	B	617	ASP	CA-C-N	5.23	125.04	119.28
1	B	617	ASP	C-N-CA	5.23	125.04	119.28
1	A	216	LYS	CB-CG-CD	-5.23	99.28	111.30
1	A	8	ASN	CB-CG-ND2	5.20	124.20	116.40
1	B	75	TRP	CG-CD2-CE3	5.17	139.07	133.90
1	A	378	LEU	CA-CB-CG	5.17	134.38	116.30
1	A	55	GLN	OE1-CD-NE2	-5.15	117.45	122.60
1	A	556	VAL	CA-C-N	5.15	125.14	119.89
1	A	556	VAL	C-N-CA	5.15	125.14	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	75	TRP	CG-CD2-CE3	5.14	139.04	133.90
1	B	616	TRP	CG-CD2-CE3	5.13	139.03	133.90
1	A	550	GLN	OE1-CD-NE2	-5.11	117.49	122.60
1	B	233	HIS	CB-CG-CD2	-5.10	124.56	131.20
1	B	265	ILE	N-CA-C	-5.10	100.78	108.12
1	B	525	GLY	CA-C-O	-5.09	116.28	120.92
1	A	617	ASP	CA-C-N	5.09	124.88	119.28
1	A	617	ASP	C-N-CA	5.09	124.88	119.28
1	A	327	HIS	CB-CG-ND1	5.09	130.33	122.70
1	A	79	PRO	CA-C-N	5.08	128.17	120.75
1	A	79	PRO	C-N-CA	5.08	128.17	120.75
1	A	229	ASP	CA-CB-CG	5.07	117.67	112.60
1	B	21	PHE	N-CA-C	-5.07	99.07	107.99
1	A	193	ASN	OD1-CG-ND2	-5.06	117.54	122.60
1	A	182	ASP	CA-CB-CG	5.06	117.66	112.60
1	B	595	ASN	OD1-CG-ND2	-5.05	117.55	122.60
1	A	86	VAL	N-CA-C	-5.05	100.62	107.99
1	A	258	TRP	N-CA-C	-5.04	99.05	108.02
1	A	326	ASN	CA-CB-CG	5.04	117.64	112.60
1	B	281	LEU	N-CA-C	-5.03	102.41	109.96
1	B	416	ASN	CB-CG-ND2	5.03	123.95	116.40
1	B	344	GLN	CB-CA-C	-5.03	102.99	110.88
1	A	45	ASN	OD1-CG-ND2	-5.01	117.58	122.60
1	A	126	HIS	CB-CG-ND1	5.01	130.22	122.70
1	A	218	TRP	CG-CD2-CE3	5.00	138.90	133.90

There are no chirality outliers.

There are no planarity outliers.

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	5312	0	5050	33	0
1	B	5312	0	5050	24	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	435	0	0	4	0
3	B	370	0	0	5	0
All	All	11433	0	10100	56	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (56) 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:82:ASN:HD22	1:A:96:ALA:HB1	1.48	0.79
1:B:336:ASN:HB3	3:B:1038:HOH:O	1.89	0.72
1:A:185:THR:HG22	1:A:188:ASN:HB2	1.73	0.70
1:A:82:ASN:ND2	1:A:101:TRP:H	1.92	0.68
1:A:82:ASN:HD21	1:A:101:TRP:H	1.41	0.67
1:A:185:THR:HG23	1:A:188:ASN:H	1.64	0.62
1:A:397:LEU:HD11	1:A:459:VAL:HG11	1.84	0.59
1:B:459:VAL:HG22	1:B:489:VAL:HB	1.83	0.59
1:B:340:ARG:HH12	1:B:465:ASN:ND2	2.02	0.58
1:A:170:ASP:OD2	1:A:177:HIS:HE1	1.86	0.57
1:B:170:ASP:OD2	1:B:177:HIS:HE1	1.88	0.57
1:B:11:ASN:ND2	3:B:689:HOH:O	2.36	0.57
1:B:126:HIS:HE1	1:B:224:ASP:OD2	1.88	0.56
1:B:592:VAL:HB	1:B:681:ASN:HA	1.87	0.56
1:A:656:GLN:HB2	3:A:1018:HOH:O	2.07	0.54
1:A:177:HIS:HD2	3:A:825:HOH:O	1.93	0.52
1:A:333:HIS:HD2	3:A:813:HOH:O	1.93	0.51
1:B:333:HIS:HD2	3:B:790:HOH:O	1.95	0.50
1:B:401:ASN:HD22	1:B:403:ALA:H	1.58	0.50
1:A:126:HIS:HE1	1:A:224:ASP:OD2	1.94	0.50
1:B:177:HIS:HD2	3:B:789:HOH:O	1.94	0.49
1:A:599:ALA:H	1:A:602:GLN:HE21	1.59	0.49
1:A:124:THR:O	1:A:128:HIS:HD2	1.96	0.48
1:A:185:THR:HG22	1:A:188:ASN:CB	2.41	0.48
1:A:126:HIS:HD2	3:A:891:HOH:O	1.95	0.47
1:B:605:PHE:HB2	1:B:653:LEU:HG	1.97	0.47
1:A:293:PHE:HE1	1:A:434:ILE:HD11	1.80	0.46
1:B:124:THR:O	1:B:128:HIS:HD2	1.97	0.46
1:A:193:ASN:OD1	1:A:199:ASP:HB2	2.15	0.46
1:A:599:ALA:H	1:A:602:GLN:NE2	2.14	0.46
1:A:78:GLN:NE2	1:A:137:ALA:H	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:647:THR:HA	1:B:670:PHE:O	2.16	0.45
1:A:460:LEU:O	1:A:463:ILE:HG12	2.16	0.45
1:B:378:LEU:HD21	1:B:381:PHE:CZ	2.52	0.45
1:A:89:TYR:O	1:A:92:VAL:HG12	2.17	0.44
1:A:361:GLY:HA3	1:A:366:MET:SD	2.58	0.43
1:B:361:GLY:HA3	1:B:366:MET:SD	2.58	0.43
1:A:308:GLU:OE1	1:B:410:HIS:HE1	2.01	0.43
1:B:80:VAL:HA	1:B:107:LYS:O	2.18	0.43
1:B:397:LEU:HB3	1:B:404:ILE:HD12	2.01	0.42
1:B:520:ARG:HD3	1:B:547:THR:HG22	2.00	0.42
1:A:663:GLU:HB2	1:A:685:GLN:O	2.20	0.42
1:A:593:ILE:HD11	1:A:684:TRP:HA	2.01	0.42
1:B:401:ASN:ND2	1:B:403:ALA:H	2.17	0.42
1:A:427:ASN:HB2	1:A:494:THR:CG2	2.50	0.42
1:B:415:ASN:HD22	1:B:418:VAL:H	1.67	0.41
1:B:126:HIS:HD2	3:B:957:HOH:O	2.03	0.41
1:A:78:GLN:HG2	1:A:80:VAL:HB	2.03	0.41
1:A:149:PRO:HG3	1:A:168:THR:HG21	2.03	0.41
1:A:401:ASN:HA	1:A:402:PRO:HD2	1.88	0.41
1:A:655:LYS:HG2	1:A:660:VAL:HG22	2.03	0.41
1:B:378:LEU:HA	1:B:379:PRO:HD3	1.99	0.41
1:A:69:MET:HE3	1:A:388:TYR:CD2	2.56	0.40
1:A:273:ALA:HB2	1:A:280:LEU:HD22	2.01	0.40
1:A:408:SER:O	1:A:423:ARG:HA	2.21	0.40
1:B:108:THR:HG23	1:B:115:MET:HE2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	684/686 (100%)	666 (97%)	18 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	684/686 (100%)	668 (98%)	15 (2%)	1 (0%)	48	34
All	All	1368/1372 (100%)	1334 (98%)	33 (2%)	1 (0%)	48	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	600	LEU

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	564/564 (100%)	545 (97%)	19 (3%)	32	20
1	B	564/564 (100%)	549 (97%)	15 (3%)	39	27
All	All	1128/1128 (100%)	1094 (97%)	34 (3%)	36	24

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LEU
1	A	66	LEU
1	A	80	VAL
1	A	85	SER
1	A	108	THR
1	A	163	LEU
1	A	173	ASN
1	A	199	ASP
1	A	280	LEU
1	A	335	SER
1	A	372	PRO
1	A	378	LEU
1	A	410	HIS
1	A	434	ILE
1	A	497	THR

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Mol	Chain	Res	Type
1	A	593	ILE
1	A	642	VAL
1	A	658	SER
1	A	685	GLN
1	B	46	LEU
1	B	82	ASN
1	B	92	VAL
1	B	163	LEU
1	B	169	ASN
1	B	173	ASN
1	B	204	ASN
1	B	211	LEU
1	B	372	PRO
1	B	378	LEU
1	B	415	ASN
1	B	613	LEU
1	B	669	THR
1	B	682	VAL
1	B	683	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	55	GLN
1	A	62	ASN
1	A	78	GLN
1	A	82	ASN
1	A	116	GLN
1	A	126	HIS
1	A	128	HIS
1	A	177	HIS
1	A	263	ASN
1	A	333	HIS
1	A	392	GLN
1	A	435	ASN
1	A	550	GLN
1	A	602	GLN
1	A	632	GLN
1	B	10	GLN
1	B	62	ASN
1	B	126	HIS

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Mol	Chain	Res	Type
1	B	128	HIS
1	B	129	ASN
1	B	160	ASN
1	B	177	HIS
1	B	204	ASN
1	B	333	HIS
1	B	392	GLN
1	B	401	ASN
1	B	410	HIS
1	B	415	ASN
1	B	465	ASN
1	B	467	ASN
1	B	548	GLN
1	B	550	GLN
1	B	595	ASN
1	B	683	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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.