



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 08:12 pm BST

PDB ID : 1PAM
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

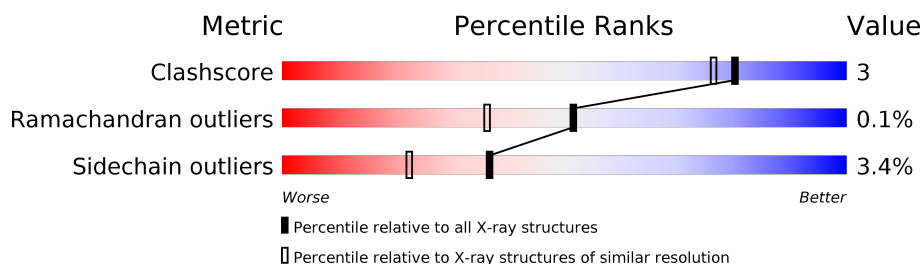
1 Overall quality at a glance

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	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (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 on 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 (three-letter code: CA) (formula: Ca).

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

- Molecule 3 is water.

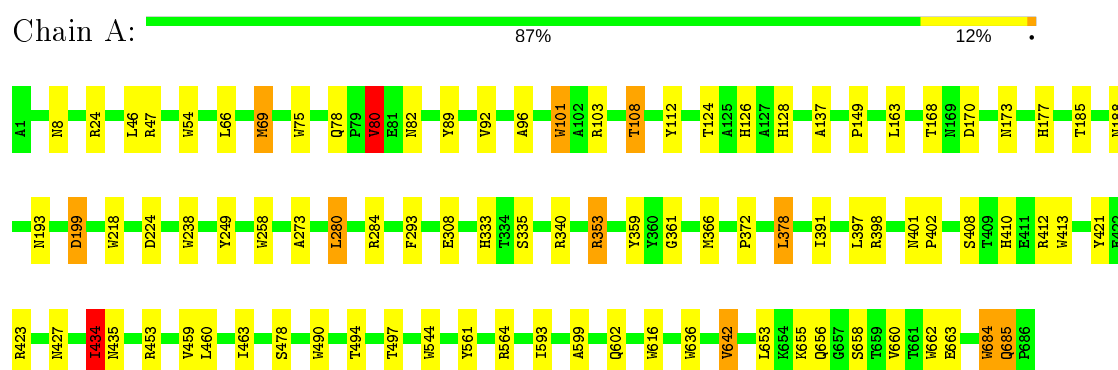
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	435	Total	O	0	0
			435	435		
3	B	370	Total	O	0	0
			370	370		

3 Residue-property plots

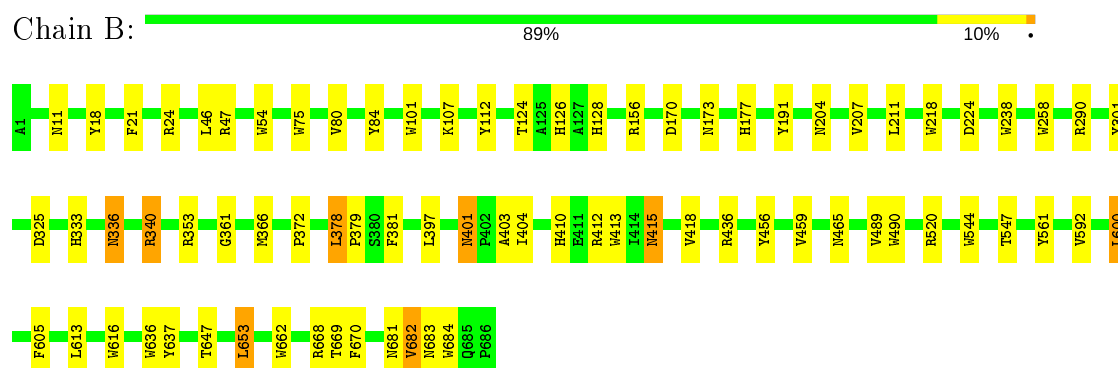
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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	64.93 Å 74.45 Å 79.12 Å 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	0.77	1/5446 (0.0%)	1.41	66/7429 (0.9%)
1	B	0.75	0/5446	1.34	57/7429 (0.8%)
All	All	0.76	1/10892 (0.0%)	1.37	123/14858 (0.8%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	434	ILE	CA-CB	5.76	1.68	1.54

All (123) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	ARG	NE-CZ-NH2	-25.68	107.46	120.30
1	A	398	ARG	NE-CZ-NH1	19.72	130.16	120.30
1	A	69	MET	CG-SD-CE	-10.33	83.67	100.20
1	A	112	TYR	CB-CG-CD2	-9.70	115.18	121.00
1	B	662	TRP	CD1-CG-CD2	8.74	113.29	106.30
1	A	662	TRP	CD1-CG-CD2	8.63	113.20	106.30
1	B	436	ARG	NE-CZ-NH2	-8.44	116.08	120.30
1	B	436	ARG	NE-CZ-NH1	8.37	124.48	120.30
1	A	378	LEU	CA-CB-CG	8.30	134.38	115.30
1	B	490	TRP	CD1-CG-CD2	8.29	112.93	106.30
1	A	490	TRP	CD1-CG-CD2	8.20	112.86	106.30
1	A	75	TRP	CD1-CG-CD2	8.16	112.83	106.30
1	A	544	TRP	CD1-CG-CD2	8.16	112.83	106.30
1	A	101	TRP	CD1-CG-CD2	8.12	112.80	106.30
1	A	616	TRP	CD1-CG-CD2	8.12	112.80	106.30
1	B	413	TRP	CD1-CG-CD2	8.04	112.73	106.30
1	B	662	TRP	CE2-CD2-CG	-8.04	100.87	107.30
1	B	238	TRP	CD1-CG-CD2	7.95	112.66	106.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	24	ARG	NE-CZ-NH1	7.83	124.21	120.30
1	B	47	ARG	NE-CZ-NH2	-7.76	116.42	120.30
1	A	636	TRP	CD1-CG-CD2	7.72	112.47	106.30
1	A	47	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	B	636	TRP	CD1-CG-CD2	7.66	112.43	106.30
1	A	413	TRP	CD1-CG-CD2	7.63	112.40	106.30
1	B	684	TRP	CD1-CG-CD2	7.61	112.39	106.30
1	B	668	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	A	47	ARG	NE-CZ-NH2	-7.53	116.53	120.30
1	A	684	TRP	CE2-CD2-CG	-7.49	101.31	107.30
1	A	544	TRP	CE2-CD2-CG	-7.45	101.34	107.30
1	A	218	TRP	CD1-CG-CD2	7.38	112.20	106.30
1	A	684	TRP	CD1-CG-CD2	7.38	112.20	106.30
1	B	616	TRP	CD1-CG-CD2	7.35	112.18	106.30
1	B	616	TRP	CE2-CD2-CG	-7.31	101.45	107.30
1	A	616	TRP	CE2-CD2-CG	-7.29	101.46	107.30
1	B	684	TRP	CE2-CD2-CG	-7.29	101.47	107.30
1	A	636	TRP	CE2-CD2-CG	-7.28	101.48	107.30
1	B	636	TRP	CE2-CD2-CG	-7.21	101.53	107.30
1	A	75	TRP	CE2-CD2-CG	-7.12	101.60	107.30
1	A	662	TRP	CE2-CD2-CG	-7.12	101.61	107.30
1	A	353	ARG	NE-CZ-NH2	-7.11	116.74	120.30
1	B	238	TRP	CE2-CD2-CG	-7.11	101.61	107.30
1	B	75	TRP	CD1-CG-CD2	7.11	111.98	106.30
1	B	412	ARG	NE-CZ-NH1	7.09	123.84	120.30
1	A	54	TRP	CE2-CD2-CG	-7.05	101.66	107.30
1	A	218	TRP	CE2-CD2-CG	-7.05	101.66	107.30
1	B	490	TRP	CE2-CD2-CG	-7.05	101.66	107.30
1	A	413	TRP	CE2-CD2-CG	-7.04	101.66	107.30
1	B	218	TRP	CD1-CG-CD2	7.04	111.93	106.30
1	B	413	TRP	CE2-CD2-CG	-6.98	101.71	107.30
1	B	75	TRP	CE2-CD2-CG	-6.98	101.72	107.30
1	A	258	TRP	CE2-CD2-CG	-6.93	101.76	107.30
1	A	490	TRP	CE2-CD2-CG	-6.84	101.83	107.30
1	A	398	ARG	CG-CD-NE	-6.83	97.46	111.80
1	B	101	TRP	CD1-CG-CD2	6.83	111.76	106.30
1	A	258	TRP	CD1-CG-CD2	6.83	111.76	106.30
1	B	544	TRP	CD1-CG-CD2	6.81	111.75	106.30
1	B	54	TRP	CE2-CD2-CG	-6.81	101.86	107.30
1	A	412	ARG	NE-CZ-NH1	6.79	123.69	120.30
1	A	112	TYR	CB-CG-CD1	6.77	125.06	121.00
1	A	101	TRP	CE2-CD2-CG	-6.72	101.92	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	258	TRP	CD1-CG-CD2	6.68	111.64	106.30
1	B	662	TRP	CG-CD2-CE3	6.66	139.89	133.90
1	B	54	TRP	CD1-CG-CD2	6.62	111.59	106.30
1	A	108	THR	N-CA-CB	-6.60	97.76	110.30
1	A	353	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	B	101	TRP	CE2-CD2-CG	-6.57	102.04	107.30
1	B	218	TRP	CE2-CD2-CG	-6.54	102.07	107.30
1	A	54	TRP	CD1-CG-CD2	6.50	111.50	106.30
1	B	544	TRP	CE2-CD2-CG	-6.49	102.11	107.30
1	A	238	TRP	CE2-CD2-CG	-6.44	102.15	107.30
1	A	238	TRP	CD1-CG-CD2	6.41	111.43	106.30
1	B	301	TYR	CB-CG-CD2	-6.41	117.15	121.00
1	B	47	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	B	112	TYR	CB-CG-CD2	-6.35	117.19	121.00
1	A	453	ARG	NE-CZ-NH2	-6.27	117.17	120.30
1	B	290	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	B	258	TRP	CE2-CD2-CG	-6.05	102.46	107.30
1	A	24	ARG	NE-CZ-NH2	-6.05	117.27	120.30
1	B	156	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	A	80	VAL	N-CA-CB	-6.00	98.31	111.50
1	A	478	SER	N-CA-CB	-5.93	101.61	110.50
1	A	249	TYR	CB-CG-CD1	-5.91	117.45	121.00
1	B	325	ASP	CB-CG-OD1	5.87	123.59	118.30
1	A	412	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	561	TYR	CB-CG-CD2	-5.80	117.52	121.00
1	A	284	ARG	NE-CZ-NH2	-5.79	117.41	120.30
1	B	18	TYR	CB-CG-CD2	-5.76	117.54	121.00
1	B	238	TRP	CG-CD1-NE1	-5.75	104.35	110.10
1	B	75	TRP	CG-CD2-CE3	5.74	139.07	133.90
1	B	456	TYR	CB-CG-CD1	-5.73	117.56	121.00
1	A	75	TRP	CG-CD2-CE3	5.71	139.04	133.90
1	B	616	TRP	CG-CD2-CE3	5.70	139.03	133.90
1	A	642	VAL	N-CA-CB	-5.66	99.04	111.50
1	B	340	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	A	218	TRP	CG-CD2-CE3	5.56	138.90	133.90
1	B	616	TRP	CB-CG-CD1	-5.56	119.78	127.00
1	B	84	TYR	CB-CG-CD1	-5.55	117.67	121.00
1	B	207	VAL	CG1-CB-CG2	-5.54	102.03	110.90
1	B	662	TRP	CB-CG-CD1	-5.53	119.81	127.00
1	A	75	TRP	CG-CD1-NE1	-5.49	104.61	110.10
1	B	682	VAL	N-CA-CB	-5.43	99.56	111.50
1	A	101	TRP	CG-CD1-NE1	-5.32	104.78	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	340	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	B	662	TRP	CG-CD1-NE1	-5.32	104.78	110.10
1	A	662	TRP	CG-CD1-NE1	-5.29	104.81	110.10
1	A	564	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	B	561	TYR	CB-CG-CD2	-5.27	117.84	121.00
1	B	191	TYR	CB-CG-CD2	-5.26	117.84	121.00
1	B	668	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	A	413	TRP	CB-CG-CD1	-5.20	120.25	127.00
1	A	24	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	A	684	TRP	CG-CD2-CE3	5.17	138.56	133.90
1	A	413	TRP	CG-CD1-NE1	-5.12	104.98	110.10
1	A	544	TRP	CG-CD2-CE3	5.12	138.50	133.90
1	A	616	TRP	CB-CG-CD1	-5.08	120.39	127.00
1	B	413	TRP	CG-CD1-NE1	-5.07	105.03	110.10
1	A	642	VAL	CG1-CB-CG2	5.06	119.00	110.90
1	A	103	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	B	684	TRP	CG-CD2-CE3	5.04	138.44	133.90
1	A	616	TRP	CG-CD1-NE1	-5.03	105.07	110.10
1	A	421	TYR	CB-CG-CD1	-5.03	117.98	121.00
1	B	637	TYR	CB-CG-CD2	-5.02	117.99	121.00
1	A	359	TYR	CB-CG-CD2	-5.01	117.99	121.00

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	23	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	435	0	0	4	0
3	B	370	0	0	5	0
All	All	11433	0	10100	55	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 (55) 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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:69:MET:HE1	1:A:391: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: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:A:78:GLN:HG2	1:A:80:VAL:HB	2.03	0.41
1:B:378:LEU:HA	1:B:379:PRO:HD3	1.99	0.41
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

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
1	B	684/686 (100%)	668 (98%)	15 (2%)	1 (0%)	51	36
All	All	1368/1372 (100%)	1334 (98%)	33 (2%)	1 (0%)	51	36

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%)	543 (96%)	21 (4%)	34	19
1	B	564/564 (100%)	547 (97%)	17 (3%)	41	27
All	All	1128/1128 (100%)	1090 (97%)	38 (3%)	37	22

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	46	LEU
1	A	66	LEU
1	A	80	VAL
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	353	ARG
1	A	372	PRO
1	A	378	LEU
1	A	410	HIS
1	A	434	ILE
1	A	435	ASN
1	A	497	THR
1	A	642	VAL
1	A	653	LEU
1	A	658	SER
1	A	685	GLN
1	B	21	PHE
1	B	46	LEU

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Mol	Chain	Res	Type
1	B	173	ASN
1	B	204	ASN
1	B	211	LEU
1	B	336	ASN
1	B	353	ARG
1	B	372	PRO
1	B	378	LEU
1	B	401	ASN
1	B	415	ASN
1	B	600	LEU
1	B	613	LEU
1	B	653	LEU
1	B	669	THR
1	B	682	VAL
1	B	683	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	55	GLN
1	A	78	GLN
1	A	82	ASN
1	A	126	HIS
1	A	128	HIS
1	A	177	HIS
1	A	239	GLN
1	A	247	ASN
1	A	333	HIS
1	A	435	ASN
1	A	594	ASN
1	A	602	GLN
1	B	11	ASN
1	B	55	GLN
1	B	126	HIS
1	B	128	HIS
1	B	177	HIS
1	B	204	ASN
1	B	239	GLN
1	B	320	GLN
1	B	333	HIS
1	B	364	GLN

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Mol	Chain	Res	Type
1	B	401	ASN
1	B	410	HIS
1	B	415	ASN
1	B	465	ASN
1	B	548	GLN

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 carbohydrates 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.