



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Aug 13, 2018 – 05:28 PM EDT

PDB ID : 6DRV  
EMDB ID: : EMD-8908  
Title : Beta-galactosidase  
Authors : Cianfrocco, M.A.; Lahiri, I.; DiMaio, F.; Leschziner, A.E.  
Deposited on : 2018-06-13  
Resolution : 2.20 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031172

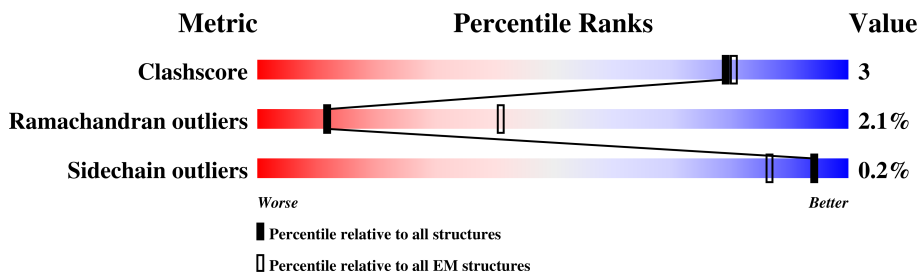
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.20 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)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1024	 93%7%
1	B	1024	 93%7%
1	C	1024	 93%7%
1	D	1024	 93%7%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 32888 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

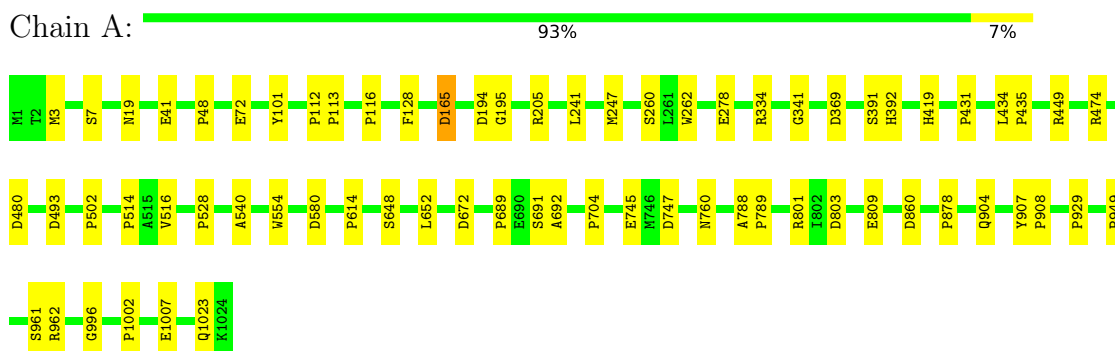
- Molecule 1 is a protein called Beta-galactosidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1024	Total	C	N	O	S	0	0
			8222	5199	1454	1529	40		
1	B	1024	Total	C	N	O	S	0	0
			8222	5199	1454	1529	40		
1	C	1024	Total	C	N	O	S	0	0
			8222	5199	1454	1529	40		
1	D	1024	Total	C	N	O	S	0	0
			8222	5199	1454	1529	40		

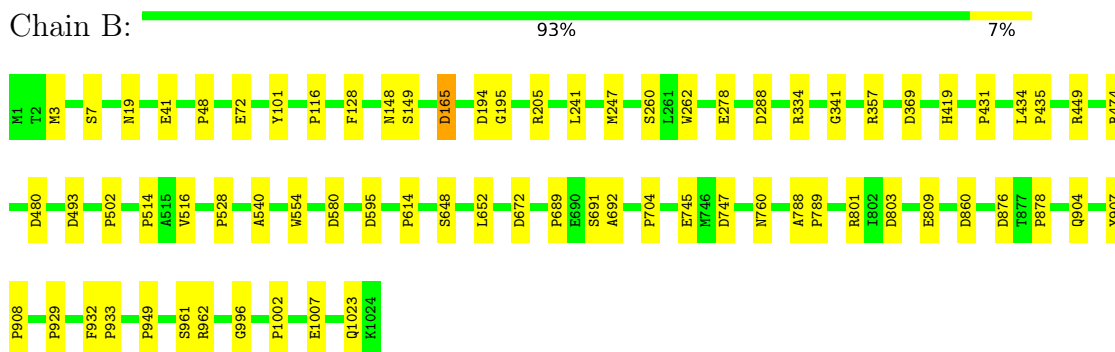
### 3 Residue-property plots

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.

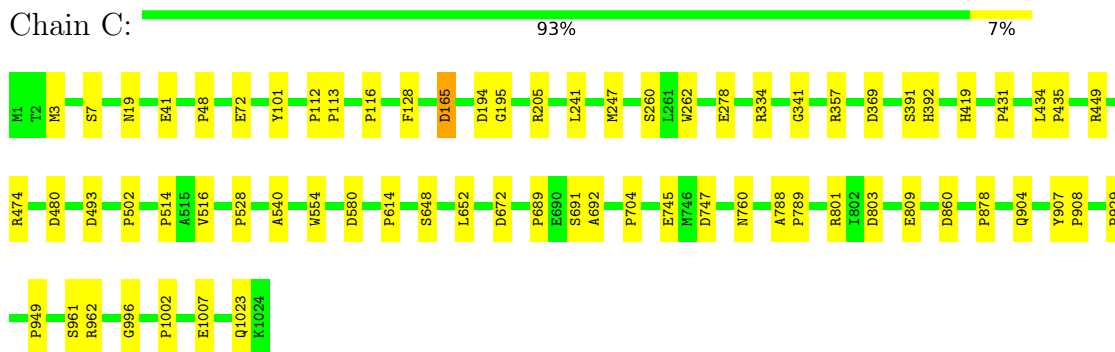
- Molecule 1: Beta-galactosidase



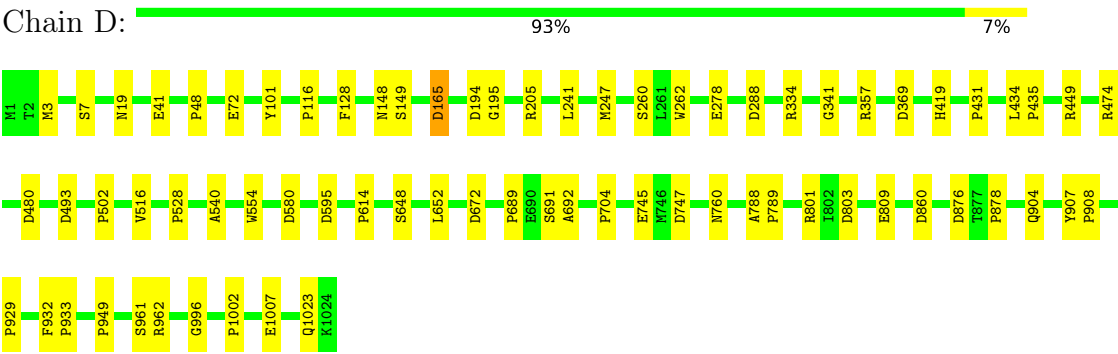
- Molecule 1: Beta-galactosidase



- Molecule 1: Beta-galactosidase



- Molecule 1: Beta-galactosidase



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	106237	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	45	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

## 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  >2	RMSZ	# Z  >2
1	A	0.94	0/8464	0.67	1/11546 (0.0%)
1	B	0.94	0/8464	0.67	2/11546 (0.0%)
1	C	0.94	0/8464	0.67	2/11546 (0.0%)
1	D	0.94	0/8464	0.67	2/11546 (0.0%)
All	All	0.94	0/33856	0.67	7/46184 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	357	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	C	357	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	B	554	TRP	CA-CB-CG	-5.07	104.07	113.70
1	D	357	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	C	554	TRP	CA-CB-CG	-5.04	104.12	113.70
1	A	554	TRP	CA-CB-CG	-5.03	104.14	113.70
1	D	554	TRP	CA-CB-CG	-5.01	104.18	113.70

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	8222	0	7822	46	0
1	B	8222	0	7822	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	8222	0	7822	46	0
1	D	8222	0	7822	48	0
All	All	32888	0	31288	189	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 (189) 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:D:652:LEU:O	1:D:652:LEU:HD12	1.64	0.98
1:B:652:LEU:HD12	1:B:652:LEU:O	1.65	0.97
1:C:652:LEU:HD12	1:C:652:LEU:O	1.64	0.96
1:A:652:LEU:HD12	1:A:652:LEU:O	1.64	0.96
1:D:809:GLU:OE1	1:D:809:GLU:HA	1.74	0.86
1:B:809:GLU:HA	1:B:809:GLU:OE1	1.74	0.86
1:C:809:GLU:OE1	1:C:809:GLU:HA	1.74	0.86
1:A:809:GLU:HA	1:A:809:GLU:OE1	1.74	0.86
1:D:904:GLN:OE1	1:D:904:GLN:N	2.14	0.80
1:B:904:GLN:OE1	1:B:904:GLN:N	2.14	0.80
1:C:904:GLN:OE1	1:C:904:GLN:N	2.14	0.79
1:A:904:GLN:OE1	1:A:904:GLN:N	2.14	0.79
1:A:72:GLU:N	1:A:72:GLU:OE1	2.17	0.74
1:C:652:LEU:C	1:C:652:LEU:HD12	2.08	0.74
1:A:652:LEU:C	1:A:652:LEU:HD12	2.08	0.74
1:C:72:GLU:OE1	1:C:72:GLU:N	2.17	0.74
1:D:72:GLU:N	1:D:72:GLU:OE1	2.17	0.74
1:B:72:GLU:OE1	1:B:72:GLU:N	2.17	0.74
1:D:652:LEU:HD12	1:D:652:LEU:C	2.08	0.73
1:B:652:LEU:HD12	1:B:652:LEU:C	2.08	0.73
1:A:41:GLU:HA	1:A:41:GLU:OE1	1.94	0.68
1:C:41:GLU:OE1	1:C:41:GLU:HA	1.94	0.68
1:D:41:GLU:HA	1:D:41:GLU:OE1	1.94	0.68
1:B:41:GLU:HA	1:B:41:GLU:OE1	1.94	0.68
1:B:369:ASP:O	1:B:369:ASP:OD1	2.12	0.68
1:D:369:ASP:OD1	1:D:369:ASP:O	2.12	0.68
1:C:369:ASP:OD1	1:C:369:ASP:C	2.32	0.67
1:A:369:ASP:OD1	1:A:369:ASP:C	2.32	0.67
1:D:369:ASP:OD1	1:D:369:ASP:C	2.32	0.67
1:B:369:ASP:C	1:B:369:ASP:OD1	2.32	0.66
1:A:369:ASP:O	1:A:369:ASP:OD1	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:369:ASP:OD1	1:C:369:ASP:O	2.12	0.66
1:A:419:HIS:O	1:A:419:HIS:HD2	1.79	0.66
1:C:419:HIS:HD2	1:C:419:HIS:O	1.78	0.66
1:D:419:HIS:O	1:D:419:HIS:HD2	1.78	0.66
1:B:419:HIS:HD2	1:B:419:HIS:O	1.79	0.65
1:B:1007:GLU:N	1:B:1007:GLU:OE1	2.23	0.65
1:B:745:GLU:OE1	1:B:745:GLU:N	2.23	0.65
1:D:745:GLU:N	1:D:745:GLU:OE1	2.23	0.65
1:D:1007:GLU:N	1:D:1007:GLU:OE1	2.23	0.65
1:C:474:ARG:HD3	1:C:474:ARG:O	1.98	0.64
1:A:474:ARG:HD3	1:A:474:ARG:O	1.98	0.64
1:D:474:ARG:O	1:D:474:ARG:HD3	1.98	0.63
1:A:1007:GLU:N	1:A:1007:GLU:OE1	2.23	0.63
1:A:278:GLU:N	1:A:278:GLU:OE1	2.26	0.63
1:A:745:GLU:N	1:A:745:GLU:OE1	2.23	0.63
1:B:474:ARG:O	1:B:474:ARG:HD3	1.98	0.63
1:D:101:TYR:CD2	1:D:101:TYR:O	2.52	0.63
1:B:101:TYR:O	1:B:101:TYR:CD2	2.52	0.63
1:C:1007:GLU:N	1:C:1007:GLU:OE1	2.23	0.63
1:C:278:GLU:OE1	1:C:278:GLU:N	2.26	0.63
1:C:745:GLU:OE1	1:C:745:GLU:N	2.23	0.63
1:A:101:TYR:O	1:A:101:TYR:CD2	2.52	0.62
1:D:961:SER:OG	1:D:962:ARG:N	2.32	0.62
1:B:961:SER:OG	1:B:962:ARG:N	2.32	0.62
1:C:101:TYR:CD2	1:C:101:TYR:O	2.52	0.62
1:A:961:SER:OG	1:A:962:ARG:N	2.32	0.61
1:C:961:SER:OG	1:C:962:ARG:N	2.32	0.61
1:B:516:VAL:O	1:B:516:VAL:HG12	2.02	0.60
1:D:516:VAL:HG12	1:D:516:VAL:O	2.02	0.60
1:A:205:ARG:HG3	1:A:205:ARG:HH11	1.67	0.60
1:B:278:GLU:N	1:B:278:GLU:OE1	2.26	0.60
1:C:205:ARG:HG3	1:C:205:ARG:HH11	1.66	0.60
1:D:278:GLU:N	1:D:278:GLU:OE1	2.26	0.60
1:D:205:ARG:HG3	1:D:205:ARG:HH11	1.66	0.60
1:C:516:VAL:HG12	1:C:516:VAL:O	2.02	0.60
1:A:516:VAL:O	1:A:516:VAL:HG12	2.01	0.59
1:B:205:ARG:HG3	1:B:205:ARG:HH11	1.66	0.59
1:A:419:HIS:CD2	1:A:419:HIS:O	2.57	0.58
1:C:419:HIS:CD2	1:C:419:HIS:O	2.57	0.58
1:D:803:ASP:OD1	1:D:803:ASP:C	2.44	0.56
1:B:803:ASP:OD1	1:B:803:ASP:C	2.44	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:HIS:CD2	1:B:419:HIS:O	2.57	0.56
1:D:419:HIS:O	1:D:419:HIS:CD2	2.57	0.56
1:A:803:ASP:OD1	1:A:803:ASP:C	2.44	0.55
1:C:803:ASP:C	1:C:803:ASP:OD1	2.44	0.55
1:A:648:SER:O	1:A:648:SER:OG	2.24	0.55
1:C:648:SER:OG	1:C:648:SER:O	2.24	0.55
1:A:652:LEU:CD1	1:A:652:LEU:C	2.77	0.53
1:C:652:LEU:C	1:C:652:LEU:CD1	2.77	0.53
1:A:760:ASN:OD1	1:A:760:ASN:C	2.48	0.52
1:B:19:ASN:C	1:B:19:ASN:OD1	2.48	0.52
1:C:760:ASN:C	1:C:760:ASN:OD1	2.48	0.52
1:D:19:ASN:OD1	1:D:19:ASN:C	2.48	0.52
1:B:288:ASP:N	1:B:288:ASP:OD1	2.35	0.52
1:B:72:GLU:CD	1:B:72:GLU:H	2.10	0.52
1:D:72:GLU:CD	1:D:72:GLU:H	2.10	0.52
1:B:101:TYR:O	1:B:101:TYR:CG	2.61	0.51
1:D:101:TYR:CG	1:D:101:TYR:O	2.61	0.51
1:B:760:ASN:OD1	1:B:760:ASN:C	2.48	0.51
1:D:760:ASN:OD1	1:D:760:ASN:C	2.48	0.51
1:D:672:ASP:OD1	1:D:672:ASP:C	2.49	0.50
1:B:672:ASP:C	1:B:672:ASP:OD1	2.49	0.50
1:B:205:ARG:NH1	1:B:205:ARG:HG3	2.27	0.50
1:D:205:ARG:HG3	1:D:205:ARG:NH1	2.27	0.50
1:A:19:ASN:OD1	1:A:19:ASN:C	2.48	0.49
1:C:72:GLU:CD	1:C:72:GLU:H	2.10	0.49
1:A:205:ARG:NH1	1:A:205:ARG:HG3	2.27	0.49
1:A:672:ASP:C	1:A:672:ASP:OD1	2.49	0.49
1:C:19:ASN:C	1:C:19:ASN:OD1	2.48	0.49
1:C:205:ARG:HG3	1:C:205:ARG:NH1	2.27	0.49
1:C:672:ASP:C	1:C:672:ASP:OD1	2.49	0.49
1:A:72:GLU:CD	1:A:72:GLU:H	2.10	0.49
1:B:652:LEU:CD1	1:B:652:LEU:C	2.77	0.49
1:D:652:LEU:CD1	1:D:652:LEU:C	2.77	0.49
1:B:247:MET:C	1:B:247:MET:SD	2.91	0.49
1:D:247:MET:C	1:D:247:MET:SD	2.91	0.49
1:B:595:ASP:OD1	1:B:595:ASP:N	2.44	0.48
1:D:595:ASP:OD1	1:D:595:ASP:N	2.44	0.48
1:C:247:MET:SD	1:C:247:MET:C	2.91	0.48
1:A:480:ASP:O	1:A:480:ASP:CG	2.51	0.48
1:C:480:ASP:CG	1:C:480:ASP:O	2.51	0.48
1:A:247:MET:SD	1:A:247:MET:C	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:648:SER:O	1:D:648:SER:OG	2.24	0.48
1:A:101:TYR:O	1:A:101:TYR:CG	2.61	0.47
1:B:648:SER:OG	1:B:648:SER:O	2.24	0.47
1:C:101:TYR:CG	1:C:101:TYR:O	2.61	0.47
1:B:128:PHE:CD2	1:B:128:PHE:N	2.83	0.47
1:D:128:PHE:N	1:D:128:PHE:CD2	2.83	0.47
1:C:128:PHE:N	1:C:128:PHE:CD2	2.83	0.46
1:A:128:PHE:CD2	1:A:128:PHE:N	2.83	0.46
1:C:434:LEU:HD12	1:C:434:LEU:O	2.16	0.46
1:D:480:ASP:O	1:D:480:ASP:CG	2.51	0.46
1:A:434:LEU:HD12	1:A:434:LEU:O	2.16	0.46
1:B:480:ASP:O	1:B:480:ASP:CG	2.51	0.46
1:C:480:ASP:OD1	1:C:480:ASP:C	2.53	0.46
1:A:480:ASP:C	1:A:480:ASP:OD1	2.53	0.46
1:D:241:LEU:C	1:D:241:LEU:HD23	2.37	0.46
1:D:480:ASP:C	1:D:480:ASP:OD1	2.53	0.46
1:B:434:LEU:O	1:B:434:LEU:HD12	2.16	0.45
1:D:288:ASP:OD1	1:D:288:ASP:N	2.35	0.45
1:B:241:LEU:C	1:B:241:LEU:HD23	2.37	0.45
1:D:434:LEU:O	1:D:434:LEU:HD12	2.16	0.45
1:D:260:SER:HG	1:D:262:TRP:HE1	1.64	0.45
1:B:260:SER:HG	1:B:262:TRP:HE1	1.64	0.45
1:C:260:SER:HG	1:C:262:TRP:HE1	1.63	0.45
1:A:241:LEU:C	1:A:241:LEU:HD23	2.37	0.45
1:C:241:LEU:HD23	1:C:241:LEU:C	2.37	0.45
1:D:165:ASP:OD1	1:D:165:ASP:C	2.55	0.45
1:A:260:SER:HG	1:A:262:TRP:HE1	1.63	0.45
1:B:165:ASP:C	1:B:165:ASP:OD1	2.56	0.45
1:B:860:ASP:OD1	1:B:860:ASP:C	2.55	0.44
1:D:860:ASP:OD1	1:D:860:ASP:C	2.55	0.44
1:C:165:ASP:C	1:C:165:ASP:OD1	2.56	0.44
1:A:580:ASP:OD1	1:A:580:ASP:C	2.55	0.44
1:A:860:ASP:OD1	1:A:860:ASP:C	2.55	0.44
1:D:580:ASP:OD1	1:D:580:ASP:C	2.55	0.44
1:A:165:ASP:C	1:A:165:ASP:OD1	2.56	0.44
1:B:580:ASP:C	1:B:580:ASP:OD1	2.55	0.44
1:C:580:ASP:C	1:C:580:ASP:OD1	2.55	0.44
1:C:860:ASP:C	1:C:860:ASP:OD1	2.55	0.43
1:D:148:ASN:HA	1:D:149:SER:HA	1.84	0.43
1:B:3:MET:O	1:B:7:SER:N	2.51	0.43
1:D:3:MET:O	1:D:7:SER:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:MET:O	1:A:7:SER:N	2.51	0.43
1:B:148:ASN:HA	1:B:149:SER:HA	1.84	0.43
1:C:3:MET:O	1:C:7:SER:N	2.51	0.43
1:A:419:HIS:C	1:A:419:HIS:CD2	2.92	0.43
1:C:419:HIS:CD2	1:C:419:HIS:C	2.92	0.43
1:B:480:ASP:C	1:B:480:ASP:OD1	2.53	0.43
1:D:876:ASP:C	1:D:876:ASP:OD1	2.58	0.42
1:B:876:ASP:OD1	1:B:876:ASP:C	2.58	0.42
1:B:907:TYR:HB3	1:B:908:PRO:HD2	2.01	0.42
1:D:907:TYR:HB3	1:D:908:PRO:HD2	2.02	0.42
1:A:907:TYR:HB3	1:A:908:PRO:HD2	2.01	0.42
1:C:493:ASP:OD1	1:C:493:ASP:C	2.58	0.42
1:C:907:TYR:HB3	1:C:908:PRO:HD2	2.02	0.42
1:A:493:ASP:C	1:A:493:ASP:OD1	2.58	0.42
1:A:747:ASP:C	1:A:747:ASP:OD1	2.58	0.41
1:C:747:ASP:OD1	1:C:747:ASP:C	2.58	0.41
1:C:391:SER:HA	1:C:392:HIS:HA	1.87	0.41
1:B:747:ASP:C	1:B:747:ASP:OD1	2.58	0.41
1:D:691:SER:OG	1:D:692:ALA:N	2.54	0.41
1:C:691:SER:OG	1:C:692:ALA:N	2.54	0.41
1:D:747:ASP:OD1	1:D:747:ASP:C	2.58	0.41
1:B:691:SER:OG	1:B:692:ALA:N	2.54	0.41
1:A:691:SER:OG	1:A:692:ALA:N	2.54	0.41
1:B:194:ASP:OD1	1:B:195:GLY:N	2.54	0.41
1:C:194:ASP:OD1	1:C:195:GLY:N	2.54	0.41
1:A:194:ASP:OD1	1:A:195:GLY:N	2.54	0.41
1:A:391:SER:HA	1:A:392:HIS:HA	1.87	0.41
1:D:194:ASP:OD1	1:D:195:GLY:N	2.54	0.41
1:D:493:ASP:C	1:D:493:ASP:OD1	2.58	0.41
1:B:493:ASP:C	1:B:493:ASP:OD1	2.58	0.41
1:D:932:PHE:HA	1:D:933:PRO:HD3	1.94	0.41
1:B:932:PHE:HA	1:B:933:PRO:HD3	1.94	0.40
1:A:112:PRO:HA	1:A:113:PRO:HA	1.97	0.40
1:B:419:HIS:CD2	1:B:419:HIS:C	2.92	0.40
1:C:112:PRO:HA	1:C:113:PRO:HA	1.97	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	1022/1024 (100%)	931 (91%)	69 (7%)	22 (2%)	7	4
1	B	1022/1024 (100%)	931 (91%)	69 (7%)	22 (2%)	7	4
1	C	1022/1024 (100%)	931 (91%)	69 (7%)	22 (2%)	7	4
1	D	1022/1024 (100%)	931 (91%)	70 (7%)	21 (2%)	8	4
All	All	4088/4096 (100%)	3724 (91%)	277 (7%)	87 (2%)	12	4

All (87) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	949	PRO
1	B	949	PRO
1	C	949	PRO
1	D	949	PRO
1	A	502	PRO
1	A	801	ARG
1	B	502	PRO
1	B	801	ARG
1	C	502	PRO
1	C	801	ARG
1	D	502	PRO
1	D	801	ARG
1	A	48	PRO
1	A	528	PRO
1	A	540	ALA
1	A	788	ALA
1	A	1002	PRO
1	A	1023	GLN
1	B	48	PRO
1	B	528	PRO
1	B	540	ALA
1	B	788	ALA

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Mol	Chain	Res	Type
1	B	1002	PRO
1	B	1023	GLN
1	C	48	PRO
1	C	528	PRO
1	C	540	ALA
1	C	788	ALA
1	C	1002	PRO
1	C	1023	GLN
1	D	48	PRO
1	D	528	PRO
1	D	540	ALA
1	D	788	ALA
1	D	1002	PRO
1	D	1023	GLN
1	A	165	ASP
1	A	689	PRO
1	B	165	ASP
1	B	689	PRO
1	C	165	ASP
1	C	689	PRO
1	D	165	ASP
1	D	689	PRO
1	A	449	ARG
1	A	878	PRO
1	B	449	ARG
1	B	878	PRO
1	C	449	ARG
1	C	878	PRO
1	D	449	ARG
1	D	878	PRO
1	A	341	GLY
1	B	341	GLY
1	C	341	GLY
1	C	704	PRO
1	D	341	GLY
1	A	116	PRO
1	A	431	PRO
1	A	704	PRO
1	A	929	PRO
1	B	116	PRO
1	B	431	PRO
1	B	704	PRO

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Mol	Chain	Res	Type
1	B	789	PRO
1	B	929	PRO
1	C	116	PRO
1	C	431	PRO
1	C	789	PRO
1	C	929	PRO
1	D	116	PRO
1	D	431	PRO
1	D	704	PRO
1	D	929	PRO
1	A	614	PRO
1	A	789	PRO
1	A	996	GLY
1	B	614	PRO
1	B	996	GLY
1	C	614	PRO
1	C	996	GLY
1	D	614	PRO
1	D	789	PRO
1	D	996	GLY
1	A	514	PRO
1	B	514	PRO
1	C	514	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	876/876 (100%)	874 (100%)	2 (0%)	94	98
1	B	876/876 (100%)	874 (100%)	2 (0%)	94	98
1	C	876/876 (100%)	874 (100%)	2 (0%)	94	98
1	D	876/876 (100%)	874 (100%)	2 (0%)	94	98
All	All	3504/3504 (100%)	3496 (100%)	8 (0%)	94	98

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	334	ARG
1	A	435	PRO
1	B	334	ARG
1	B	435	PRO
1	C	334	ARG
1	C	435	PRO
1	D	334	ARG
1	D	435	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	419	HIS
1	B	419	HIS
1	C	419	HIS
1	D	419	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 carbohydrates 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 ⓘ

There are no chain breaks in this entry.