



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2024 – 10:06 AM EDT

PDB ID : 5C14
Title : Crystal structure of PECAM-1 D1D2 domain
Authors : Zhou, D.; Paddock, C.; Newman, P.; Zhu, J.
Deposited on : 2015-06-12
Resolution : 2.80 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

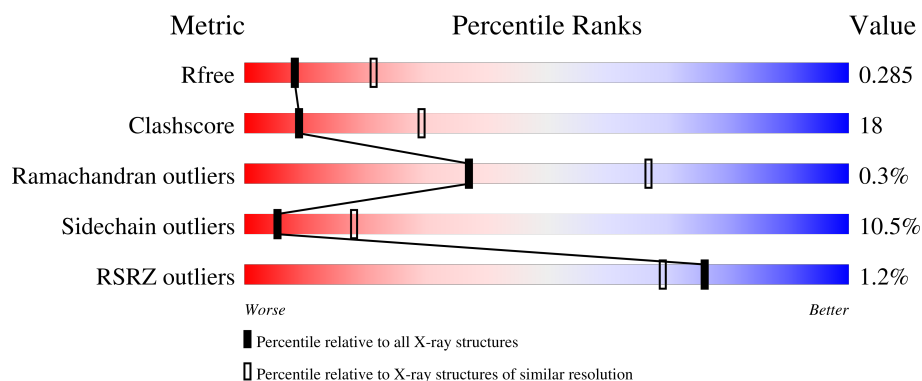
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

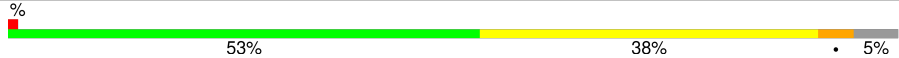

The reported resolution of this entry is 2.80 Å.

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))
R_{free}	164625	3657 (2.80-2.80)
Clashscore	180529	4123 (2.80-2.80)
Ramachandran outliers	177936	4071 (2.80-2.80)
Sidechain outliers	177891	4073 (2.80-2.80)
RSRZ outliers	164620	3659 (2.80-2.80)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	212	
2	B	212	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3368 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 Platelet endothelial cell adhesion molecule.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	201	Total	C	N	O	S	Se	0	0	0
			1616	1020	274	313	8	1			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ARG	-	expression tag	UNP P16284
A	0	SER	-	expression tag	UNP P16284
A	203	SER	-	expression tag	UNP P16284
A	204	ARG	-	expression tag	UNP P16284
A	205	GLU	-	expression tag	UNP P16284
A	206	ASN	-	expression tag	UNP P16284
A	207	LEU	-	expression tag	UNP P16284
A	208	TYR	-	expression tag	UNP P16284
A	209	PHE	-	expression tag	UNP P16284
A	210	GLN	-	expression tag	UNP P16284

- Molecule 2 is a protein called Platelet endothelial cell adhesion molecule.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	201	Total	C	N	O	S	0	0	0
			1616	1020	274	313	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	ARG	-	expression tag	UNP P16284
B	0	SER	-	expression tag	UNP P16284
B	203	SER	-	expression tag	UNP P16284
B	204	ARG	-	expression tag	UNP P16284
B	205	GLU	-	expression tag	UNP P16284
B	206	ASN	-	expression tag	UNP P16284

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Chain	Residue	Modelled	Actual	Comment	Reference
B	207	LEU	-	expression tag	UNP P16284
B	208	TYR	-	expression tag	UNP P16284
B	209	PHE	-	expression tag	UNP P16284
B	210	GLN	-	expression tag	UNP P16284

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

- Molecule 4 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cu 1 1	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:

C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).

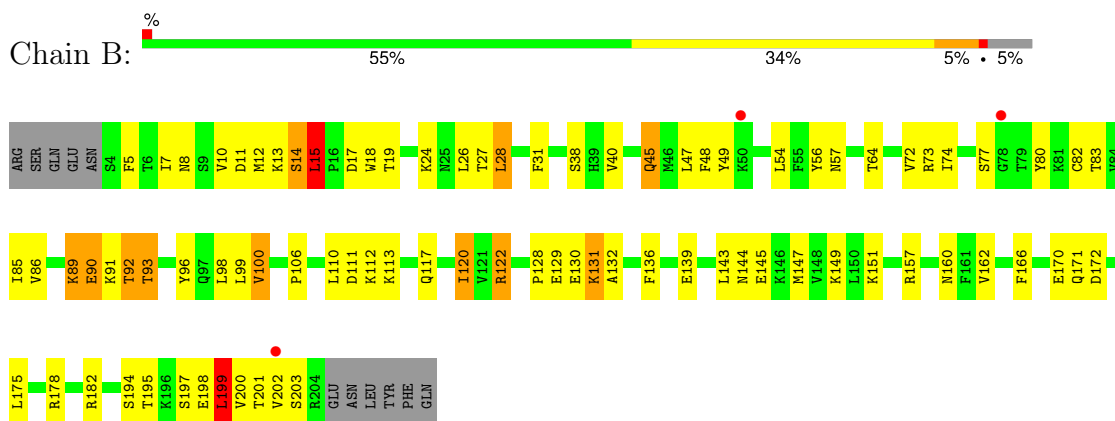


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	15	Total	O	0	0
			15	15		
7	B	12	Total	O	0	0
			12	12		

- Molecule 1: Platelet endothelial cell adhesion molecule



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	104.01Å 104.01Å 281.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.79 – 2.80 19.79 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.79-2.80) 99.5 (19.79-2.80)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.79Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.238 , 0.279 0.239 , 0.285	Depositor DCC
R_{free} test set	537 reflections (2.75%)	wwPDB-VP
Wilson B-factor (Å ²)	62.6	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3368	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CU, NAG, TRS

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	0.71	0/1643	0.83	1/2217 (0.0%)
2	B	0.69	0/1644	0.81	2/2220 (0.1%)
All	All	0.70	0/3287	0.82	3/4437 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	GLU	N-CA-C	-5.73	95.53	111.00
2	B	199	LEU	N-CA-C	5.46	125.73	111.00
2	B	15	LEU	CA-CB-CG	5.33	127.56	115.30

There are no chirality outliers.

There are no planarity outliers.

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	1616	0	1621	63	0
2	B	1616	0	1621	68	0
3	A	18	0	24	1	0
3	B	12	0	16	3	0
4	A	1	0	0	0	0
5	A	42	0	39	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	28	0	26	0	0
6	A	8	0	12	2	0
7	A	15	0	0	2	0
7	B	12	0	0	0	0
All	All	3368	0	3359	121	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 18.

All (121) 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:152:ARG:NH1	1:A:165:GLU:O	2.02	0.93
1:A:184:ILE:H	1:A:184:ILE:HD12	1.38	0.89
1:A:86:VAL:HG23	1:A:87:ASN:H	1.46	0.79
2:B:111:ASP:HB3	2:B:122:ARG:HE	1.51	0.75
1:A:117:GLN:NE2	1:A:170:GLU:O	2.20	0.75
1:A:97:GLN:H	6:A:308:TRS:H31	1.55	0.71
2:B:139:GLU:OE1	2:B:178:ARG:NH2	2.24	0.71
1:A:7:ILE:HG12	1:A:91:LYS:HE2	1.73	0.70
1:A:122:ARG:NH1	1:A:165:GLU:OE2	2.25	0.69
1:A:85:ILE:HG23	1:A:90:GLU:HB3	1.73	0.68
2:B:83:THR:HG22	2:B:92:THR:OG1	1.95	0.67
1:A:10:VAL:HG22	1:A:93:THR:HG22	1.77	0.67
2:B:14:SER:OG	2:B:17:ASP:O	2.15	0.64
2:B:132:ALA:HB1	2:B:157:ARG:O	1.99	0.63
2:B:85:ILE:HG22	2:B:90:GLU:HB2	1.80	0.62
1:A:184:ILE:HD12	1:A:184:ILE:N	2.13	0.62
2:B:145:GLU:O	2:B:147:MET:N	2.33	0.61
1:A:139:GLU:OE2	1:A:151:LYS:NZ	2.33	0.61
1:A:197:SER:HB2	2:B:110:LEU:HD11	1.83	0.61
1:A:87:ASN:O	1:A:88:ASN:ND2	2.34	0.60
1:A:184:ILE:HD11	7:A:401:HOH:O	2.02	0.60
2:B:90:GLU:HG2	2:B:91:LYS:N	2.16	0.60
1:A:130:GLU:HG3	1:A:131:LYS:H	1.67	0.60
1:A:200:VAL:HG13	2:B:175:LEU:HB2	1.84	0.59
2:B:117:GLN:CD	2:B:170:GLU:HA	2.22	0.59
1:A:97:GLN:N	6:A:308:TRS:H31	2.17	0.59
1:A:22:ASN:OD1	1:A:73:ARG:NH1	2.36	0.59
2:B:74:ILE:HA	2:B:100:VAL:HG11	1.86	0.57
1:A:50:LYS:HD2	1:A:80:TYR:OH	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:7:ILE:HD11	2:B:86:VAL:HG13	1.87	0.57
2:B:73:ARG:HH12	3:B:301:GOL:H2	1.69	0.57
1:A:14:SER:OG	1:A:17:ASP:O	2.22	0.57
1:A:125:CYS:HB2	1:A:138:ILE:HD11	1.86	0.56
2:B:48:PHE:HB2	2:B:56:TYR:HB3	1.86	0.56
1:A:48:PHE:HB3	1:A:55:PHE:CZ	2.40	0.56
2:B:24:LYS:O	2:B:72:VAL:HG12	2.06	0.56
2:B:131:LYS:HD2	2:B:132:ALA:H	1.71	0.55
2:B:139:GLU:OE2	2:B:151:LYS:NZ	2.26	0.55
2:B:17:ASP:OD1	2:B:18:TRP:N	2.38	0.54
1:A:7:ILE:HB	1:A:34:VAL:HG22	1.89	0.54
2:B:12:MET:HB3	2:B:96:TYR:CE2	2.43	0.54
1:A:137:THR:HG23	1:A:153:GLU:HG2	1.91	0.53
1:A:184:ILE:H	1:A:184:ILE:CD1	2.16	0.53
1:A:25:ASN:OD1	1:A:70:PRO:O	2.27	0.52
1:A:198:GLU:HG3	2:B:113:LYS:NZ	2.24	0.52
2:B:10:VAL:HG12	2:B:93:THR:HG23	1.92	0.52
1:A:116:ILE:HD12	1:A:117:GLN:O	2.10	0.52
2:B:77:SER:HB2	2:B:100:VAL:HG12	1.92	0.52
2:B:89:LYS:HD3	2:B:90:GLU:N	2.25	0.52
1:A:122:ARG:HG2	1:A:165:GLU:HG2	1.92	0.51
1:A:31:PHE:HB3	1:A:64:THR:HB	1.92	0.51
1:A:43:GLN:N	1:A:43:GLN:OE1	2.42	0.51
1:A:7:ILE:HD11	1:A:91:LYS:HB3	1.92	0.51
1:A:15:LEU:HB2	1:A:27:THR:CG2	2.40	0.51
2:B:145:GLU:O	2:B:145:GLU:HG2	2.10	0.51
1:A:116:ILE:HG22	2:B:203:SER:HB2	1.93	0.51
2:B:74:ILE:N	2:B:130:GLU:OE2	2.42	0.51
1:A:45:GLN:NE2	1:A:59:SER:OG	2.38	0.50
2:B:198:GLU:HG3	2:B:199:LEU:N	2.27	0.50
2:B:14:SER:HB2	2:B:28:LEU:HD12	1.93	0.50
1:A:86:VAL:HG23	1:A:87:ASN:N	2.21	0.49
2:B:136:PHE:CD2	2:B:162:VAL:HG13	2.47	0.49
1:A:15:LEU:O	1:A:26:LEU:HD12	2.12	0.49
2:B:38:SER:HB2	2:B:40:VAL:HG12	1.95	0.48
2:B:74:ILE:HA	2:B:100:VAL:CG1	2.43	0.48
1:A:81:LYS:HE3	3:A:301:GOL:H12	1.95	0.48
1:A:65:GLU:HG3	1:A:66:SER:H	1.78	0.47
1:A:195:THR:HG23	2:B:106:PRO:HG2	1.96	0.47
1:A:72:VAL:HG22	1:A:100:VAL:HG21	1.96	0.47
1:A:7:ILE:HG23	1:A:89:LYS:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:45:GLN:HE21	2:B:45:GLN:HB2	1.52	0.46
2:B:12:MET:HB2	2:B:93:THR:HG21	1.97	0.46
1:A:132:ALA:HB1	1:A:157:ARG:O	2.16	0.45
1:A:134:ILE:HG23	1:A:183:ILE:HG12	1.99	0.45
1:A:116:ILE:O	1:A:168:VAL:HG21	2.16	0.45
1:A:10:VAL:HG21	1:A:84:VAL:HG12	1.97	0.45
1:A:191:THR:HG22	2:B:182:ARG:HG3	1.97	0.45
2:B:149:LYS:NZ	2:B:171:GLN:HE21	2.14	0.45
1:A:200:VAL:HA	2:B:113:LYS:O	2.17	0.45
2:B:120:ILE:HG13	2:B:166:PHE:O	2.16	0.45
2:B:26:LEU:HD13	2:B:27:THR:N	2.32	0.45
2:B:128:PRO:HA	2:B:160:ASN:ND2	2.31	0.45
2:B:131:LYS:HD2	2:B:132:ALA:N	2.32	0.45
1:A:50:LYS:O	1:A:53:VAL:HG12	2.16	0.44
2:B:12:MET:HB3	2:B:96:TYR:CD2	2.53	0.44
1:A:150:LEU:HD12	7:A:408:HOH:O	2.18	0.44
2:B:171:GLN:CD	2:B:171:GLN:H	2.22	0.44
1:A:43:GLN:HG3	1:A:61:MET:HE1	2.00	0.43
2:B:26:LEU:CD1	2:B:28:LEU:HD13	2.48	0.43
2:B:80:TYR:CD2	2:B:98:LEU:HD22	2.53	0.43
2:B:82:CYS:N	2:B:93:THR:OG1	2.40	0.43
2:B:131:LYS:CD	2:B:132:ALA:H	2.31	0.43
2:B:15:LEU:HB2	2:B:27:THR:HG23	2.01	0.43
2:B:49:TYR:O	2:B:80:TYR:HA	2.19	0.42
1:A:145:GLU:C	1:A:147:MET:H	2.22	0.42
1:A:168:VAL:HG23	1:A:168:VAL:O	2.19	0.42
2:B:13:LYS:HG3	2:B:15:LEU:HD12	2.01	0.42
2:B:47:LEU:HB2	2:B:83:THR:OG1	2.19	0.42
2:B:85:ILE:HD12	2:B:86:VAL:O	2.19	0.42
2:B:98:LEU:H	2:B:98:LEU:HD23	1.84	0.42
2:B:131:LYS:HD2	2:B:131:LYS:HA	1.68	0.42
1:A:202:VAL:HG11	2:B:172:ASP:HB3	2.02	0.42
2:B:201:THR:OG1	2:B:202:VAL:N	2.53	0.42
2:B:8:ASN:N	2:B:8:ASN:OD1	2.53	0.41
1:A:14:SER:HB2	1:A:28:LEU:HD23	2.03	0.41
2:B:73:ARG:NH1	3:B:301:GOL:H2	2.34	0.41
1:A:113:LYS:HD2	2:B:198:GLU:O	2.21	0.41
1:A:146:LYS:HA	1:A:146:LYS:HD2	1.57	0.41
2:B:54:LEU:HD11	2:B:57:ASN:HB2	2.03	0.41
2:B:175:LEU:HA	2:B:175:LEU:HD23	1.85	0.41
1:A:75:TYR:CD2	1:A:131:LYS:HD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:15:LEU:O	2:B:26:LEU:HD22	2.21	0.41
1:A:154:LYS:HG2	1:A:155:ASN:N	2.36	0.41
2:B:129:GLU:OE2	3:B:301:GOL:H11	2.21	0.40
2:B:145:GLU:C	2:B:147:MET:H	2.21	0.40
2:B:26:LEU:HD11	2:B:28:LEU:HD13	2.02	0.40
1:A:12:MSE:HA	1:A:29:GLN:O	2.21	0.40
1:A:136:PHE:CD1	1:A:162:VAL:HG13	2.57	0.40
1:A:11:ASP:HB2	1:A:31:PHE:CE1	2.56	0.40
1:A:178:ARG:HA	2:B:195:THR:O	2.20	0.40
2:B:80:TYR:HE2	2:B:98:LEU:HD21	1.86	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	199/212 (94%)	190 (96%)	9 (4%)	0	100	100
2	B	199/212 (94%)	185 (93%)	13 (6%)	1 (0%)	25	56
All	All	398/424 (94%)	375 (94%)	22 (6%)	1 (0%)	37	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	89	LYS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/200 (95%)	174 (92%)	16 (8%)	9	28
2	B	190/201 (94%)	166 (87%)	24 (13%)	3	12
All	All	380/401 (95%)	340 (90%)	40 (10%)	5	18

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	7	ILE
1	A	39	HIS
1	A	60	SER
1	A	63	SER
1	A	77	SER
1	A	85	ILE
1	A	111	ASP
1	A	145	GLU
1	A	146	LYS
1	A	174	VAL
1	A	184	ILE
1	A	194	SER
1	A	195	THR
1	A	200	VAL
1	A	202	VAL
2	B	5	PHE
2	B	11	ASP
2	B	14	SER
2	B	15	LEU
2	B	19	THR
2	B	28	LEU
2	B	31	PHE
2	B	45	GLN
2	B	64	THR
2	B	90	GLU
2	B	92	THR
2	B	93	THR
2	B	99	LEU
2	B	100	VAL
2	B	112	LYS
2	B	120	ILE
2	B	122	ARG

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Mol	Chain	Res	Type
2	B	131	LYS
2	B	143	LEU
2	B	144	ASN
2	B	194	SER
2	B	197	SER
2	B	199	LEU
2	B	200	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	ASN
2	B	45	GLN
2	B	171	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	B	302	-	5,5,5	0.37	0	5,5,5	0.35	0
3	GOL	A	302	-	5,5,5	0.37	0	5,5,5	0.83	0
5	NAG	A	305	1	14,14,15	0.76	1 (7%)	17,19,21	0.80	0
5	NAG	B	303	-	14,14,15	0.40	0	17,19,21	0.77	1 (5%)
3	GOL	A	301	-	5,5,5	0.36	0	5,5,5	0.63	0
5	NAG	B	304	2	14,14,15	0.62	0	17,19,21	0.77	0
3	GOL	B	301	-	5,5,5	0.31	0	5,5,5	0.42	0
3	GOL	A	303	-	5,5,5	0.33	0	5,5,5	0.36	0
5	NAG	A	306	1	14,14,15	0.97	0	17,19,21	1.26	1 (5%)
6	TRS	A	308	-	7,7,7	0.48	0	9,9,9	0.84	0
5	NAG	A	307	1	14,14,15	1.10	2 (14%)	17,19,21	0.68	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	302	-	-	0/4/4/4	-
3	GOL	A	302	-	-	2/4/4/4	-
5	NAG	A	305	1	-	0/6/23/26	0/1/1/1
5	NAG	B	303	-	-	0/6/23/26	0/1/1/1
3	GOL	A	301	-	-	4/4/4/4	-
5	NAG	B	304	2	-	0/6/23/26	0/1/1/1
3	GOL	B	301	-	-	0/4/4/4	-
3	GOL	A	303	-	-	2/4/4/4	-
5	NAG	A	306	1	-	0/6/23/26	0/1/1/1
6	TRS	A	308	-	-	5/9/9/9	-
5	NAG	A	307	1	-	4/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	307	NAG	O5-C1	-3.10	1.38	1.43
5	A	307	NAG	C2-N2	-2.31	1.42	1.46
5	A	305	NAG	O5-C1	-2.30	1.39	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	306	NAG	C1-O5-C5	3.22	116.50	112.19
5	B	303	NAG	C1-O5-C5	2.42	115.43	112.19

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	GOL	O1-C1-C2-C3
3	A	302	GOL	O1-C1-C2-C3
5	A	307	NAG	O5-C5-C6-O6
5	A	307	NAG	C4-C5-C6-O6
5	A	307	NAG	C8-C7-N2-C2
5	A	307	NAG	O7-C7-N2-C2
3	A	303	GOL	O1-C1-C2-C3
3	A	301	GOL	O1-C1-C2-O2
3	A	302	GOL	O1-C1-C2-O2
3	A	303	GOL	O1-C1-C2-O2
6	A	308	TRS	C3-C-C1-O1
6	A	308	TRS	N-C-C1-O1
3	A	301	GOL	O2-C2-C3-O3
6	A	308	TRS	C1-C-C3-O3
6	A	308	TRS	C2-C-C1-O1
3	A	301	GOL	C1-C2-C3-O3
6	A	308	TRS	N-C-C3-O3

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	GOL	1	0
3	B	301	GOL	3	0
6	A	308	TRS	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	200/212 (94%)	-0.43	2 (1%) 79 73	50, 68, 135, 169	0
2	B	201/212 (94%)	-0.17	3 (1%) 71 64	50, 79, 123, 182	0
All	All	401/424 (94%)	-0.30	5 (1%) 76 69	50, 73, 129, 182	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	78	GLY	4.8
2	B	202	VAL	3.0
1	A	89	LYS	2.8
1	A	204	ARG	2.2
2	B	50	LYS	2.1

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	B	304	14/15	0.77	0.10	83,100,103,105	0
3	GOL	A	302	6/6	0.81	0.14	77,87,91,93	0
5	NAG	A	305	14/15	0.82	0.12	100,117,124,125	0
6	TRS	A	308	8/8	0.82	0.13	84,90,102,107	0
5	NAG	B	303	14/15	0.84	0.14	85,93,116,124	0
5	NAG	A	306	14/15	0.85	0.12	54,100,116,120	0
3	GOL	B	301	6/6	0.85	0.12	72,85,89,89	0
3	GOL	A	301	6/6	0.88	0.12	90,97,99,100	0
5	NAG	A	307	14/15	0.90	0.10	72,87,97,98	0
3	GOL	A	303	6/6	0.91	0.14	85,87,94,100	0
3	GOL	B	302	6/6	0.93	0.13	109,110,110,112	0
4	CU	A	304	1/1	0.98	0.08	101,101,101,101	0

6.5 Other polymers [i](#)

There are no such residues in this entry.