



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:29 PM UTC

PDB ID : 1IV5 / pdb_00001iv5
Title : New Crystal Form of Human CD81 Large Extracellular Loop.
Authors : Kitadokoro, K.; Bolognesi, M.; Grandi, G.; Marco, P.; Galli, G.; Petracca, R.; Fabiana, F.
Deposited on : 2002-03-14
Resolution : 2.60 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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

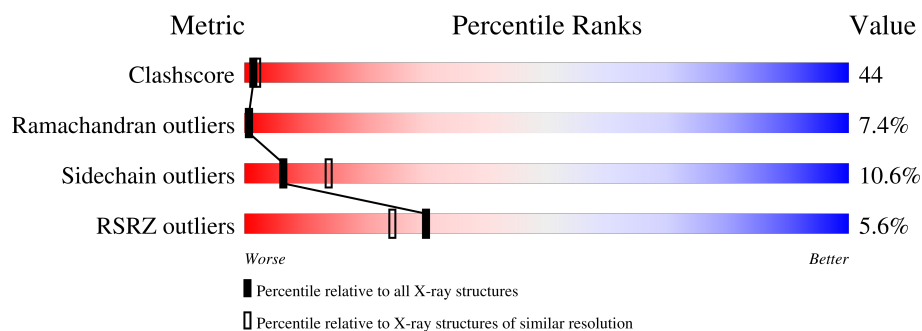
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	90	4% 50% 36% 14%
1	B	90	7% 34% 46% 14% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1403 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 CD81 antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	90	Total	C	N	O	S	1	0	0
			694	430	118	142	4			
1	B	90	Total	C	N	O	S	14	0	0
			694	430	118	142	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	HIS	-	expression tag	UNP P60033
B	302	HIS	-	expression tag	UNP P60033

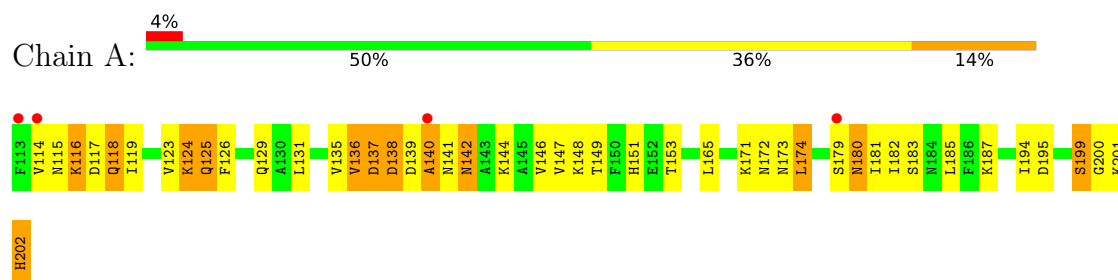
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	8	Total	O	0	0
			8	8		
2	B	7	Total	O	0	0
			7	7		

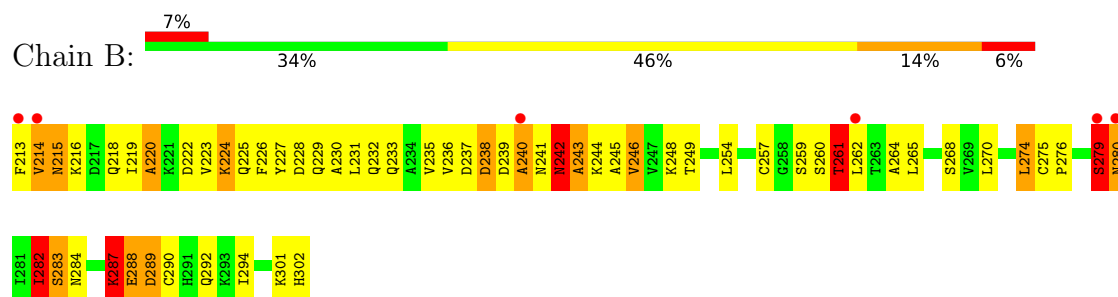
3 Residue-property plots

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: CD81 antigen



• Molecule 1: CD81 antigen



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	102.05Å 102.05Å 35.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	18.73 – 2.60 18.73 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.1 (18.73-2.60) 98.0 (18.73-2.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.229 , 0.282 0.228 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	64.1	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.052 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1403	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.85% 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

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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.49	5/703 (0.7%)	1.42	2/948 (0.2%)
1	B	1.63	9/703 (1.3%)	2.41	20/948 (2.1%)
All	All	1.56	14/1406 (1.0%)	1.98	22/1896 (1.2%)

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	B	0	1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	283	SER	CA-C	-14.74	1.35	1.53
1	B	246	VAL	CA-CB	-8.44	1.44	1.54
1	B	280	ASN	N-CA	8.40	1.57	1.46
1	A	140	ALA	CA-CB	6.95	1.64	1.53
1	A	125	GLN	CA-C	-6.85	1.44	1.52
1	B	289	ASP	N-CA	-5.74	1.39	1.45
1	A	153	THR	C-O	-5.53	1.17	1.24
1	B	224	LYS	CA-CB	-5.45	1.44	1.53
1	B	223	VAL	CA-CB	5.33	1.61	1.54
1	A	194	ILE	CA-CB	-5.27	1.47	1.54
1	B	280	ASN	CA-C	5.20	1.59	1.52
1	B	220	ALA	C-O	5.13	1.30	1.24
1	A	194	ILE	N-CA	-5.10	1.40	1.46
1	B	220	ALA	CA-CB	-5.02	1.45	1.53

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	283	SER	CA-C-O	-47.50	64.94	122.41
1	B	283	SER	N-CA-C	-16.16	80.40	108.52
1	B	282	ILE	CA-C-N	15.16	146.51	122.26
1	B	282	ILE	C-N-CA	15.16	146.51	122.26
1	B	283	SER	N-CA-CB	11.21	126.72	110.58
1	B	279	SER	CA-C-N	9.91	140.48	121.54
1	B	279	SER	C-N-CA	9.91	140.48	121.54
1	A	118	GLN	OE1-CD-NE2	-8.33	114.27	122.60
1	B	280	ASN	N-CA-C	8.22	128.32	110.80
1	A	199	SER	N-CA-C	-7.44	102.19	112.30
1	B	215	ASN	N-CA-C	6.69	119.92	109.96
1	B	223	VAL	N-CA-C	-5.66	103.85	111.44
1	B	227	TYR	N-CA-C	-5.61	105.25	111.36
1	B	287	LYS	N-CA-C	5.54	122.61	110.80
1	B	260	SER	N-CA-C	-5.54	105.32	111.36
1	B	230	ALA	N-CA-C	-5.48	105.46	111.82
1	B	243	ALA	N-CA-C	-5.28	104.77	111.11
1	B	230	ALA	CA-C-N	5.13	127.42	120.65
1	B	230	ALA	C-N-CA	5.13	127.42	120.65
1	B	261	THR	CA-C-N	-5.06	114.97	122.35
1	B	261	THR	C-N-CA	-5.06	114.97	122.35
1	B	257	CYS	CB-CA-C	-5.01	105.21	111.43

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	283	SER	Mainchain

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	694	0	672	61	0
1	B	694	0	672	68	4
2	A	8	0	0	2	4
2	B	7	0	0	3	0
All	All	1403	0	1344	119	4

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 44.

All (119) 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:115:ASN:HD22	1:A:118:GLN:HB2	1.05	1.16
1:B:287:LYS:O	1:B:288:GLU:HB2	1.50	1.04
1:A:114:VAL:HG12	1:B:229:GLN:NE2	1.78	0.98
1:B:287:LYS:O	1:B:288:GLU:CB	2.10	0.97
1:A:180:ASN:CG	1:A:181:ILE:H	1.74	0.96
1:A:114:VAL:HG12	1:B:229:GLN:HE22	1.30	0.95
1:A:116:LYS:C	1:A:116:LYS:HD2	1.93	0.94
1:A:115:ASN:ND2	1:A:118:GLN:HB2	1.83	0.93
1:A:116:LYS:HD2	1:A:116:LYS:O	1.70	0.92
1:B:242:ASN:HA	2:B:7:HOH:O	1.73	0.89
1:B:240:ALA:HB1	1:B:244:LYS:HG3	1.54	0.87
1:A:180:ASN:ND2	1:A:183:SER:H	1.75	0.83
1:A:115:ASN:HD22	1:A:118:GLN:CB	1.90	0.83
1:A:202:HIS:HB2	1:B:249:THR:HG23	1.59	0.82
1:A:180:ASN:CG	1:A:181:ILE:N	2.34	0.82
1:A:138:ASP:O	1:A:139:ASP:HB2	1.80	0.81
1:A:174:LEU:CD1	1:A:174:LEU:N	2.44	0.81
1:B:215:ASN:HD22	1:B:216:LYS:N	1.79	0.79
1:A:174:LEU:N	1:A:174:LEU:HD12	1.96	0.78
1:B:287:LYS:HG3	1:B:288:GLU:N	1.98	0.78
1:B:287:LYS:HG3	1:B:288:GLU:H	1.48	0.78
1:B:261:THR:O	1:B:262:LEU:HB2	1.83	0.75
1:A:180:ASN:HD22	1:A:183:SER:H	1.33	0.73
1:B:241:ASN:C	1:B:243:ALA:H	1.98	0.71
1:A:116:LYS:C	1:A:116:LYS:CD	2.64	0.71
1:B:282:ILE:O	1:B:284:ASN:N	2.24	0.70
1:A:140:ALA:C	1:A:142:ASN:H	2.00	0.70
1:B:242:ASN:HB2	1:B:245:ALA:HB3	1.74	0.69
1:B:215:ASN:HB3	1:B:218:GLN:HB3	1.76	0.68
1:B:220:ALA:O	1:B:224:LYS:HD2	1.94	0.67
1:B:215:ASN:O	1:B:219:ILE:HG13	1.96	0.66
1:B:240:ALA:HB2	1:B:244:LYS:HE3	1.79	0.65
1:B:225:GLN:O	1:B:229:GLN:HG3	1.96	0.65
1:B:289:ASP:HB3	2:B:8:HOH:O	1.97	0.63
1:B:213:PHE:O	1:B:214:VAL:C	2.41	0.63
1:B:225:GLN:HG2	1:B:229:GLN:OE1	1.98	0.63
1:A:180:ASN:HD21	1:A:182:ILE:N	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:ASN:O	1:B:246:VAL:N	2.28	0.62
1:A:117:ASP:HA	2:A:2:HOH:O	2.00	0.62
1:A:174:LEU:H	1:A:174:LEU:HD13	1.64	0.62
1:B:241:ASN:O	1:B:243:ALA:N	2.34	0.61
1:B:215:ASN:HD22	1:B:215:ASN:C	2.06	0.60
1:B:287:LYS:CG	1:B:288:GLU:H	2.14	0.60
1:B:287:LYS:CG	1:B:288:GLU:N	2.63	0.60
1:A:174:LEU:CD1	1:A:174:LEU:H	2.14	0.60
1:A:140:ALA:O	1:A:141:ASN:HB2	2.02	0.60
1:B:270:LEU:C	1:B:270:LEU:HD23	2.27	0.60
1:B:242:ASN:O	1:B:245:ALA:N	2.35	0.59
1:B:236:VAL:HG13	1:B:236:VAL:O	2.03	0.59
1:B:231:LEU:C	1:B:233:GLN:H	2.11	0.59
1:A:148:LYS:HZ2	1:A:173:ASN:HD21	1.49	0.59
1:A:173:ASN:HB3	2:A:15:HOH:O	2.03	0.58
1:B:242:ASN:CB	1:B:245:ALA:HB3	2.34	0.58
1:B:215:ASN:C	1:B:215:ASN:ND2	2.62	0.57
1:B:259:SER:HA	1:B:289:ASP:HB2	1.84	0.57
1:B:290:CYS:O	1:B:294:ILE:HG13	2.04	0.57
1:A:114:VAL:HG12	1:B:229:GLN:CD	2.31	0.56
1:A:180:ASN:HD21	1:A:182:ILE:HB	1.69	0.56
1:A:115:ASN:O	1:A:119:ILE:HG22	2.05	0.56
1:A:124:LYS:NZ	1:A:195:ASP:OD1	2.39	0.56
1:A:119:ILE:HD13	1:B:222:ASP:HB3	1.87	0.55
1:B:241:ASN:C	1:B:243:ALA:N	2.59	0.55
1:A:136:VAL:HG23	1:A:137:ASP:N	2.20	0.55
1:A:144:LYS:O	1:A:148:LYS:HG3	2.06	0.55
1:B:287:LYS:O	1:B:288:GLU:CG	2.54	0.55
1:A:147:VAL:HG13	1:A:151:HIS:CE1	2.42	0.55
1:A:180:ASN:ND2	1:A:181:ILE:N	2.54	0.55
1:A:114:VAL:HG13	1:A:114:VAL:O	2.06	0.54
1:A:138:ASP:O	1:A:139:ASP:CB	2.54	0.54
1:B:215:ASN:O	1:B:216:LYS:C	2.50	0.54
1:A:182:ILE:O	1:A:185:LEU:HB3	2.08	0.54
1:B:237:ASP:O	1:B:240:ALA:N	2.41	0.53
1:B:282:ILE:C	1:B:284:ASN:N	2.53	0.53
1:A:136:VAL:O	1:A:138:ASP:N	2.43	0.52
1:B:274:LEU:C	1:B:276:PRO:HD3	2.36	0.51
1:B:275:CYS:N	1:B:276:PRO:HD3	2.26	0.50
1:B:261:THR:O	1:B:262:LEU:CB	2.50	0.50
1:A:148:LYS:NZ	1:A:173:ASN:OD1	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:237:ASP:O	1:B:238:ASP:C	2.55	0.49
1:A:114:VAL:HG11	1:B:226:PHE:HA	1.93	0.49
1:B:287:LYS:O	1:B:288:GLU:HG3	2.12	0.49
1:A:180:ASN:ND2	1:A:182:ILE:N	2.61	0.49
1:A:140:ALA:O	1:A:142:ASN:N	2.44	0.49
1:A:114:VAL:O	1:A:114:VAL:CG1	2.62	0.48
1:B:228:ASP:O	1:B:231:LEU:HB3	2.13	0.48
1:B:264:ALA:O	1:B:265:LEU:C	2.55	0.48
1:A:125:GLN:O	1:A:129:GLN:HG2	2.12	0.48
1:A:202:HIS:HB2	1:B:249:THR:CG2	2.36	0.47
1:B:282:ILE:HD11	1:B:288:GLU:OE1	2.14	0.47
1:A:115:ASN:ND2	1:A:118:GLN:H	2.13	0.47
1:B:292:GLN:NE2	1:B:292:GLN:HA	2.29	0.47
1:A:165:LEU:HD11	1:A:185:LEU:HD13	1.96	0.46
1:B:215:ASN:ND2	1:B:216:LYS:N	2.56	0.46
1:A:114:VAL:HB	1:B:225:GLN:NE2	2.30	0.46
1:A:146:VAL:HG23	1:A:147:VAL:N	2.30	0.46
1:A:136:VAL:CG2	1:A:137:ASP:N	2.77	0.45
1:A:126:PHE:HB2	1:B:219:ILE:CD1	2.46	0.45
1:B:240:ALA:CB	1:B:244:LYS:HE3	2.46	0.45
1:A:131:LEU:HA	1:A:147:VAL:HG21	1.99	0.45
1:B:235:VAL:HG12	1:B:268:SER:OG	2.17	0.44
1:A:135:VAL:O	1:A:171:LYS:HE3	2.17	0.44
1:A:199:SER:O	1:A:200:GLY:C	2.58	0.44
1:A:147:VAL:CG1	1:A:151:HIS:CE1	3.00	0.44
1:A:116:LYS:HE3	1:A:117:ASP:OD2	2.18	0.44
1:B:242:ASN:C	1:B:245:ALA:H	2.25	0.44
1:A:114:VAL:HB	1:B:225:GLN:HE21	1.83	0.44
1:B:231:LEU:C	1:B:233:GLN:N	2.76	0.43
1:B:239:ASP:O	1:B:241:ASN:N	2.52	0.43
1:A:146:VAL:CG2	1:A:147:VAL:N	2.78	0.43
1:B:274:LEU:HA	1:B:274:LEU:HD12	1.82	0.42
1:A:119:ILE:O	1:A:123:VAL:HG23	2.19	0.42
1:A:148:LYS:NZ	1:A:173:ASN:HD21	2.16	0.42
1:B:287:LYS:HD2	2:B:8:HOH:O	2.19	0.42
1:B:231:LEU:HD12	1:B:231:LEU:HA	1.51	0.42
1:A:173:ASN:ND2	1:A:173:ASN:C	2.76	0.41
1:B:239:ASP:C	1:B:241:ASN:N	2.78	0.41
1:B:292:GLN:HA	1:B:292:GLN:HE21	1.84	0.41
1:B:240:ALA:O	1:B:241:ASN:OD1	2.38	0.41
1:A:173:ASN:C	1:A:173:ASN:HD22	2.28	0.41

All (4) 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)
1:B:302:HIS:CE1	2:A:12:HOH:O[6_664]	1.82	0.38
1:B:279:SER:OG	2:A:1:HOH:O[1_554]	1.88	0.32
1:B:302:HIS:NE2	2:A:12:HOH:O[6_664]	2.03	0.17
1:B:279:SER:CB	2:A:1:HOH:O[1_554]	2.11	0.09

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	88/90 (98%)	71 (81%)	13 (15%)	4 (4%)	2	2
1	B	88/90 (98%)	67 (76%)	12 (14%)	9 (10%)	0	0
All	All	176/180 (98%)	138 (78%)	25 (14%)	13 (7%)	1	1

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	ASP
1	B	242	ASN
1	B	280	ASN
1	A	136	VAL
1	A	138	ASP
1	B	240	ALA
1	B	279	SER
1	B	232	GLN
1	B	287	LYS
1	B	238	ASP
1	B	301	LYS
1	A	142	ASN
1	B	288	GLU

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	80/80 (100%)	70 (88%)	10 (12%)	4	9
1	B	80/80 (100%)	73 (91%)	7 (9%)	9	21
All	All	160/160 (100%)	143 (89%)	17 (11%)	6	14

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	LYS
1	A	124	LYS
1	A	149	THR
1	A	172	ASN
1	A	174	LEU
1	A	179	SER
1	A	180	ASN
1	A	187	LYS
1	A	201	LYS
1	A	202	HIS
1	B	214	VAL
1	B	242	ASN
1	B	248	LYS
1	B	254	LEU
1	B	261	THR
1	B	274	LEU
1	B	282	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	A	118	GLN
1	A	142	ASN
1	A	180	ASN
1	A	202	HIS

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Mol	Chain	Res	Type
1	B	215	ASN
1	B	218	GLN
1	B	225	GLN
1	B	232	GLN
1	B	233	GLN
1	B	272	ASN
1	B	284	ASN
1	B	292	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](#)

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 [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	90/90 (100%)	0.13	4 (4%) 39 33	39, 59, 96, 97	1 (1%)
1	B	90/90 (100%)	0.23	6 (6%) 24 19	32, 62, 97, 97	4 (4%)
All	All	180/180 (100%)	0.18	10 (5%) 30 24	32, 60, 97, 97	5 (2%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	240	ALA	5.0
1	A	113	PHE	3.5
1	B	214	VAL	3.4
1	B	279	SER	3.0
1	B	280	ASN	2.9
1	B	213	PHE	2.8
1	A	140	ALA	2.6
1	B	262	LEU	2.1
1	A	179	SER	2.0
1	A	114	VAL	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.