



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:47 AM GMT

PDB ID : 2IQA  
Title : PFA2 FAB fragment, monoclinic apo form  
Authors : Gardberg, A.S.; Dealwis, C.  
Deposited on : 2006-10-13  
Resolution : 2.00 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

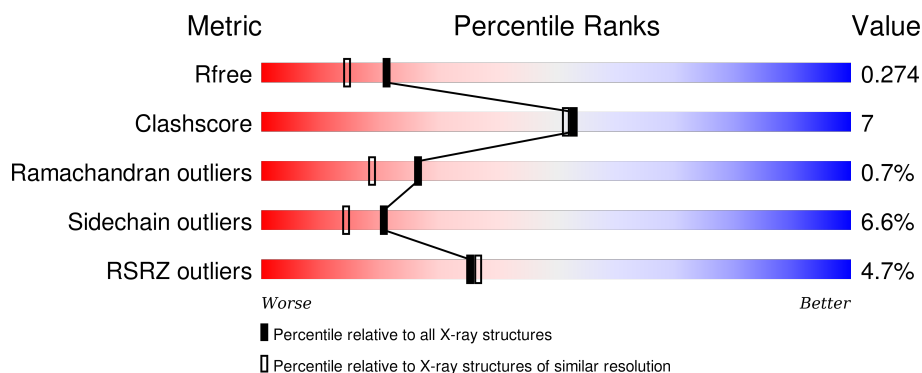
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	219	<div> <div>3%</div> <div>88%</div> <div>9%</div> <div>.</div> </div>
1	L	219	<div> <div>3%</div> <div>80%</div> <div>16%</div> <div>.</div> </div>
2	B	223	<div> <div>7%</div> <div>78%</div> <div>17%</div> <div>..</div> </div>
2	H	223	<div> <div>5%</div> <div>84%</div> <div>13%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACM	A	1219	-	-	-	X
5	GOL	H	408	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7057 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 IgG2a Fab fragment PFA2 Kappa light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	219	Total	C	N	O	S	0	5	0
			1701	1066	285	343	7			
1	A	219	Total	C	N	O	S	0	7	0
			1703	1064	287	345	7			

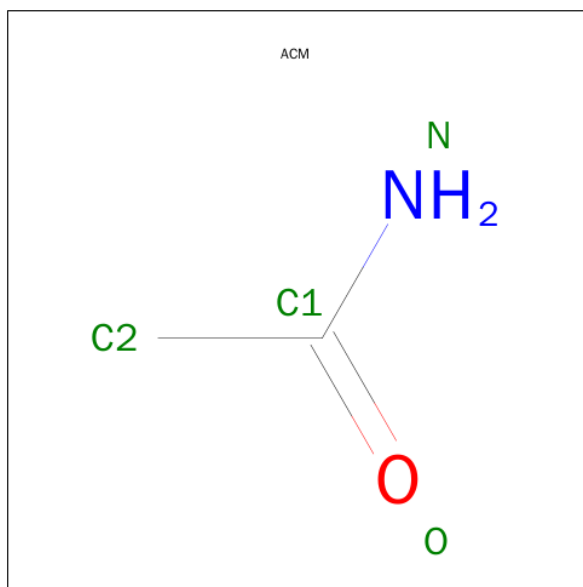
- Molecule 2 is a protein called IgG2a Fab fragment PFA2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	221	Total	C	N	O	S	0	2	0
			1671	1062	280	323	6			
2	B	220	Total	C	N	O	S	0	2	0
			1653	1052	277	318	6			

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	1	Total	Cl	0	0
			1	1		

- Molecule 4 is ACETAMIDE (three-letter code: ACM) (formula: C<sub>2</sub>H<sub>5</sub>NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	L	1	Total	C	N	O	0	0
			4	2	1	1		
4	A	1	Total	C	N	O	0	0
			4	2	1	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	1	Total	C	O	0	0
			6	3	3		
5	L	1	Total	C	O	0	0
			6	3	3		

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

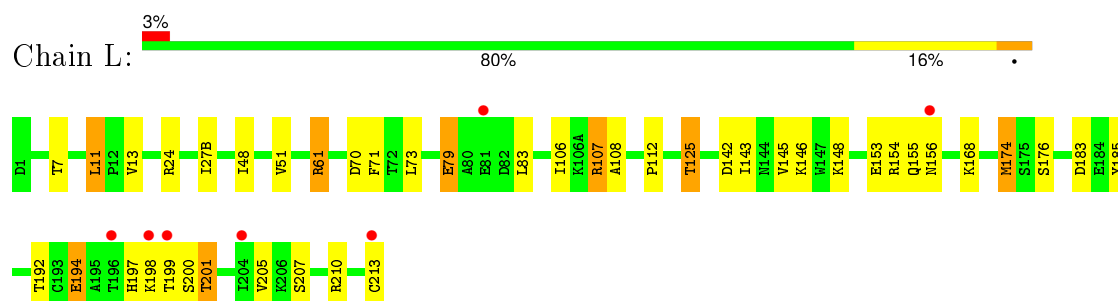
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	L	82	Total	O	0	0
			82	82		
6	H	59	Total	O	0	0
			59	59		
6	A	80	Total	O	0	0
			80	80		
6	B	51	Total	O	0	0
			51	51		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: IgG2a Fab fragment PFA2 Kappa light chain







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.98Å 73.41Å 93.51Å 90.00° 99.97° 90.00°	Depositor
Resolution (Å)	33.45 – 2.00 33.45 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (33.45-2.00) 99.6 (33.45-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.230 , 0.279 0.228 , 0.274	Depositor DCC
$R_{free}$ test set	3560 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.9	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	1 of 70336 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7057	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ACM, CL

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	0.53	0/1744	0.66	1/2365 (0.0%)
1	L	0.53	0/1748	0.69	0/2372
2	B	0.56	0/1698	0.70	0/2320
2	H	0.55	0/1719	0.66	0/2348
All	All	0.54	0/6909	0.68	1/9405 (0.0%)

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
2	B	0	1
2	H	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	LEU	CA-CB-CG	5.41	127.74	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	171	GLN	Peptide
2	H	171	GLN	Peptide

## 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	1703	0	1641	13	0
1	L	1701	0	1640	30	0
2	B	1653	0	1620	27	0
2	H	1671	0	1644	19	0
3	H	1	0	0	0	0
4	A	4	0	4	0	0
4	L	4	0	4	1	0
5	A	12	0	16	1	0
5	B	12	0	16	0	0
5	H	12	0	16	0	0
5	L	12	0	16	0	0
6	A	80	0	0	0	0
6	B	51	0	0	0	0
6	H	59	0	0	0	0
6	L	82	0	0	0	0
All	All	7057	0	6617	89	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 7.

All (89) 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:L:198:LYS:CG	1:L:199:THR:H	1.90	0.83
1:L:198:LYS:HG3	1:L:199:THR:H	1.44	0.82
1:L:200:SER:HA	1:L:201:THR:CB	2.11	0.81
1:L:48:ILE:HD12	1:L:73:LEU:HD13	1.66	0.78
4:L:1219:ACM:HN2	2:H:213:ARG:HH12	1.36	0.72
1:L:27(B):ILE:HD11	1:L:71:PHE:CE2	2.27	0.69
2:H:105:GLN:CD	2:H:105:GLN:H	1.97	0.68
1:A:107:ARG:HD3	1:A:108:ALA:O	1.94	0.67
1:L:194:GLU:HB3	1:L:205:VAL:HG22	1.74	0.67
1:L:145:VAL:HG11	1:L:174:MET:HE1	1.77	0.66
2:B:52:TRP:HE1	2:B:58:ASN:ND2	1.94	0.66
2:B:97:HIS:HD2	2:B:100(C):ASP:OD2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:107:ARG:HD3	1:L:108:ALA:O	1.99	0.62
2:B:52:TRP:HE1	2:B:58:ASN:HD21	1.47	0.62
2:B:12:LEU:HD13	2:B:82(C):VAL:HG21	1.81	0.62
1:A:18:GLN:HG2	1:A:76:SER:HA	1.82	0.62
2:H:97:HIS:HD2	2:H:100(C):ASP:OD1	1.82	0.61
2:B:171:GLN:HG2	2:B:171:GLN:O	2.01	0.60
1:L:145:VAL:CG1	1:L:174:MET:HE1	2.31	0.60
1:L:145:VAL:HG11	1:L:174:MET:CE	2.32	0.59
1:L:198:LYS:CG	1:L:199:THR:N	2.65	0.58
1:L:174:MET:HE3	1:L:176:SER:HB2	1.84	0.58
2:H:52:TRP:HE1	2:H:58:ASN:HD21	1.51	0.58
2:B:98:ASN:O	2:B:100:VAL:N	2.38	0.57
1:A:209:ASN:HD22	1:A:211:ASN:H	1.53	0.56
1:L:24:ARG:HD3	1:L:70:ASP:OD1	2.06	0.55
2:B:5:LYS:HD3	2:B:23:SER:O	2.07	0.55
1:L:48:ILE:CD1	1:L:73:LEU:HD13	2.36	0.55
2:H:189:PRO:HB3	2:H:212:PRO:HG3	1.89	0.54
2:H:52:TRP:HE1	2:H:58:ASN:ND2	2.07	0.53
1:L:148:LYS:HB2	1:L:192:THR:HB	1.91	0.52
1:L:61:ARG:CZ	1:L:79:GLU:HG3	2.40	0.51
2:B:4:LEU:C	2:B:5:LYS:HD2	2.31	0.51
2:H:105:GLN:N	2:H:105:GLN:CD	2.64	0.51
2:H:50:HIS:CE1	2:H:95:ARG:HB3	2.46	0.51
2:B:29:LEU:H	2:B:76:ASN:HD21	1.58	0.51
1:L:185:TYR:CE2	1:L:210:ARG:HD3	2.46	0.50
1:L:174:MET:CE	1:L:176:SER:HB2	2.42	0.50
1:A:211:ASN:OD1	1:A:212:GLU:HG3	2.12	0.50
2:B:184:THR:HG22	2:B:186:SER:H	1.77	0.49
2:H:29:LEU:H	2:H:76:ASN:HD21	1.60	0.48
1:A:106[A]:ILE:HG22	1:A:106(A):LYS:O	2.14	0.48
2:B:5:LYS:N	2:B:5:LYS:CD	2.77	0.47
2:B:34:MET:HE2	2:B:34:MET:HA	1.97	0.47
2:B:63:LEU:HD11	2:B:67:LEU:CD1	2.45	0.47
2:B:68:THR:HB	2:B:81:LYS:HB3	1.97	0.46
2:B:84:THR:HA	2:B:111:VAL:HB	1.96	0.46
1:A:149:ILE:HD11	1:A:178:LEU:HD21	1.97	0.46
1:L:106[B]:ILE:HD13	1:L:106[B]:ILE:HA	1.83	0.46
1:L:83:LEU:HD11	1:L:106[B]:ILE:HG12	1.97	0.46
1:L:200:SER:CA	1:L:201:THR:CB	2.89	0.46
2:H:16:GLN:O	2:H:82(C):VAL:HG22	2.17	0.45
2:H:189:PRO:CB	2:H:212:PRO:HG3	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ARG:HD2	1:A:139:TYR:CB	2.46	0.45
5:A:402:GOL:H32	2:B:178:SER:H	1.81	0.45
2:H:37:ILE:HD12	2:H:93:VAL:HG11	1.99	0.45
1:L:112:PRO:HG3	1:L:143:ILE:CD1	2.45	0.45
2:H:188:TRP:CG	2:H:189:PRO:HA	2.51	0.45
2:H:128:CYS:HA	2:H:129:GLY:HA2	1.56	0.45
2:B:33:GLY:HA2	2:B:53:TRP:CE3	2.52	0.45
2:B:54:ASP:OD1	2:B:56[A]:ASP:HB2	2.17	0.45
2:H:11:ILE:HD11	2:H:147:PRO:HG3	1.98	0.44
1:L:185:TYR:CZ	1:L:210:ARG:HD3	2.53	0.43
1:L:112:PRO:HG3	1:L:143:ILE:HD11	2.00	0.43
2:H:29:LEU:HD13	2:H:71:LYS:HD2	2.00	0.43
1:A:12:PRO:HB2	1:A:106(A):LYS:HG2	2.01	0.43
2:B:123:PRO:HG3	2:B:208:LYS:HE3	1.99	0.43
1:A:185:TYR:CZ	1:A:210:ARG:HD3	2.54	0.43
1:L:107:ARG:CD	1:L:108:ALA:O	2.65	0.43
2:H:76:ASN:HA	2:H:76:ASN:HD22	1.64	0.43
2:H:67:LEU:HD23	2:H:82:ILE:HG12	2.00	0.43
1:L:83:LEU:HD11	1:L:106[A]:ILE:HG12	2.00	0.42
2:B:63:LEU:HD11	2:B:67:LEU:HD11	2.00	0.42
2:B:87:THR:HG23	2:B:110:THR:HA	2.01	0.42
1:L:11:LEU:HD22	1:L:13:VAL:HG13	2.01	0.42
1:A:209:ASN:ND2	1:A:211:ASN:H	2.16	0.41
1:A:185:TYR:CE2	1:A:210:ARG:HD3	2.55	0.41
2:B:127:VAL:HA	2:B:213:ARG:HD2	2.02	0.41
2:B:128:CYS:HA	2:B:129:GLY:HA2	1.73	0.41
1:L:48:ILE:CD1	1:L:73:LEU:CD1	2.99	0.41
1:A:209:ASN:C	1:A:209:ASN:HD22	2.24	0.41
2:B:4:LEU:CA	2:B:5:LYS:HD2	2.51	0.41
2:B:39:GLN:HG3	2:B:44:GLY:O	2.20	0.41
2:B:64:LYS:CB	2:B:65:SER:HB2	2.51	0.41
1:L:146:LYS:HD3	1:L:153:GLU:HG3	2.04	0.40
2:H:32:SER:HA	2:H:33:GLY:HA2	1.89	0.40
2:B:147:PRO:HD2	2:B:201:ALA:HB3	2.04	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 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	218/219 (100%)	214 (98%)	4 (2%)	0	100	100
1	L	220/219 (100%)	212 (96%)	6 (3%)	2 (1%)	21	13
2	B	215/223 (96%)	203 (94%)	9 (4%)	3 (1%)	14	6
2	H	217/223 (97%)	208 (96%)	8 (4%)	1 (0%)	34	26
All	All	870/884 (98%)	837 (96%)	27 (3%)	6 (1%)	26	19

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	65	SER
1	L	201	THR
2	B	64	LYS
2	B	171	GLN
1	L	51	VAL
2	H	9	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 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	197/196 (100%)	182 (92%)	15 (8%)	16	10
1	L	196/196 (100%)	179 (91%)	17 (9%)	13	7
2	B	184/192 (96%)	174 (95%)	10 (5%)	27	21
2	H	188/192 (98%)	180 (96%)	8 (4%)	35	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	765/776 (99%)	715 (94%)	50 (6%)	21	15

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	7	THR
1	L	11	LEU
1	L	61	ARG
1	L	79	GLU
1	L	107	ARG
1	L	125	THR
1	L	142	ASP
1	L	154	ARG
1	L	155	GLN
1	L	156	ASN
1	L	168	LYS
1	L	174	MET
1	L	183	ASP
1	L	194	GLU
1	L	197	HIS
1	L	207	SER
1	L	213	CYS
2	H	2	VAL
2	H	9	PRO
2	H	29	LEU
2	H	73	THR
2	H	76	ASN
2	H	100(D)	TRP
2	H	158	SER
2	H	186	SER
1	A	11	LEU
1	A	18	GLN
1	A	43[A]	SER
1	A	77[A]	ARG
1	A	107	ARG
1	A	125	THR
1	A	154	ARG
1	A	179	THR
1	A	180	LEU
1	A	190	SER
1	A	200	SER
1	A	201	THR

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Mol	Chain	Res	Type
1	A	202	SER
1	A	209	ASN
1	A	211	ASN
2	B	5	LYS
2	B	12	LEU
2	B	34	MET
2	B	56[A]	ASP
2	B	64	LYS
2	B	74	SER
2	B	76	ASN
2	B	100(D)	TRP
2	B	177	LEU
2	B	196	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	189	ASN
2	H	58	ASN
2	H	76	ASN
2	H	97	HIS
2	H	98	ASN
1	A	27	GLN
1	A	209	ASN
2	B	58	ASN
2	B	76	ASN
2	B	97	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

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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
4	ACM	A	1219	1	3,3,3	0.88	0	3,3,3	0.60	0
5	GOL	A	402	-	5,5,5	0.29	0	5,5,5	0.28	0
5	GOL	A	403	-	5,5,5	0.30	0	5,5,5	0.35	0
5	GOL	B	404	-	5,5,5	0.27	0	5,5,5	0.33	0
5	GOL	B	406	-	5,5,5	0.30	0	5,5,5	0.44	0
5	GOL	H	405	-	5,5,5	0.29	0	5,5,5	0.41	0
5	GOL	H	408	-	5,5,5	0.28	0	5,5,5	0.47	0
4	ACM	L	1219	1	3,3,3	1.05	0	3,3,3	0.45	0
5	GOL	L	401	-	5,5,5	0.29	0	5,5,5	0.42	0
5	GOL	L	407	-	5,5,5	0.39	0	5,5,5	0.28	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
4	ACM	A	1219	1	-	0/0/0/0	0/0/0/0
5	GOL	A	402	-	-	0/4/4/4	0/0/0/0
5	GOL	A	403	-	-	0/4/4/4	0/0/0/0
5	GOL	B	404	-	-	0/4/4/4	0/0/0/0
5	GOL	B	406	-	-	0/4/4/4	0/0/0/0
5	GOL	H	405	-	-	0/4/4/4	0/0/0/0
5	GOL	H	408	-	-	0/4/4/4	0/0/0/0
4	ACM	L	1219	1	-	0/0/0/0	0/0/0/0
5	GOL	L	401	-	-	0/4/4/4	0/0/0/0
5	GOL	L	407	-	-	0/4/4/4	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	402	GOL	1	0
4	L	1219	ACM	1	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	219/219 (100%)	0.07	7 (3%)	51	52	22, 34, 48, 61	3 (1%)
1	L	219/219 (100%)	0.06	7 (3%)	51	52	22, 34, 49, 59	2 (0%)
2	B	220/223 (98%)	0.33	15 (6%)	20	22	22, 35, 48, 60	0
2	H	221/223 (99%)	0.18	12 (5%)	29	31	22, 33, 55, 69	0
All	All	879/884 (99%)	0.16	41 (4%)	35	37	22, 34, 51, 69	5 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	1	GLN	7.4
2	B	128	CYS	5.3
1	A	213	CYS	5.1
2	B	1	GLN	5.0
2	H	131	THR	4.6
2	B	132	THR	4.5
2	H	128	CYS	4.3
1	A	201	THR	4.2
2	H	191	GLN	4.0
1	L	213	CYS	3.8
1	A	211	ASN	3.3
2	H	159	LEU	3.2
2	B	129	GLY	3.1
2	B	15	SER	3.0
1	A	202	SER	2.9
2	B	186	SER	2.8
2	B	121	VAL	2.8
2	B	156	SER	2.8
1	A	29	GLY	2.7
2	H	2	VAL	2.6
1	L	204	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
2	H	158	SER	2.4
2	H	156	SER	2.4
1	A	106[A]	ILE	2.4
2	H	130	GLY	2.4
2	H	192	SER	2.2
1	L	156	ASN	2.2
2	B	64	LYS	2.2
1	L	198	LYS	2.2
1	L	196	THR	2.2
2	H	205	LYS	2.2
2	B	120	SER	2.2
1	L	199	THR	2.2
2	B	133	GLY	2.2
2	B	2	VAL	2.1
2	B	171	GLN	2.1
2	B	135	SER	2.1
1	A	27(E)	SER	2.1
2	H	134	SER	2.0
1	L	81	GLU	2.0
2	B	32	SER	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	GOL	H	408	6/6	0.65	0.28	12.29	54,55,55,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	ACM	A	1219	4/4	0.65	0.53	3.70	66,67,68,68	0
5	GOL	A	402	6/6	0.85	0.18	1.52	50,53,54,55	0
4	ACM	L	1219	4/4	0.62	0.23	1.45	60,60,60,61	0
5	GOL	L	401	6/6	0.85	0.14	1.32	35,40,41,44	0
5	GOL	A	403	6/6	0.85	0.18	1.28	57,59,60,60	0
5	GOL	H	405	6/6	0.85	0.12	1.14	47,51,52,54	0
5	GOL	B	404	6/6	0.78	0.15	0.73	62,63,63,63	0
5	GOL	L	407	6/6	0.88	0.17	0.60	61,61,62,63	0
3	CL	H	301	1/1	0.99	0.10	-1.17	33,33,33,33	0
5	GOL	B	406	6/6	0.80	0.19	-	63,64,64,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.