



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:53 PM GMT

PDB ID : 1MHH  
Title : Antibody-antigen complex  
Authors : Graille, M.; Stura, E.A.  
Deposited on : 2002-08-20  
Resolution : 2.10 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

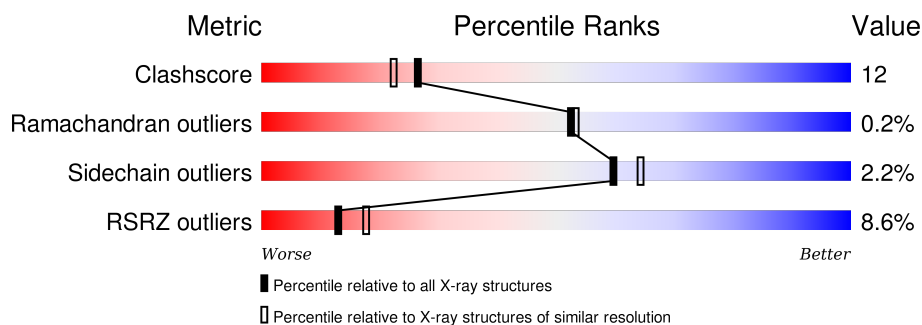
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	220	<div> <div>6%</div> <div>76%</div> <div>23%</div> <div>.</div> </div>
1	C	220	<div> <div>5%</div> <div>84%</div> <div>15%</div> <div>.</div> </div>
2	B	217	<div> <div>7%</div> <div>74%</div> <div>24%</div> <div>..</div> </div>
2	D	217	<div> <div>9%</div> <div>77%</div> <div>19%</div> <div>..</div> </div>
3	E	63	<div> <div>19%</div> <div>71%</div> <div>29%</div> </div>
3	F	63	<div> <div>17%</div> <div>79%</div> <div>19%</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
1	AEA	A	214	X	-	-	-
1	AEA	C	214	X	-	-	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8490 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 Fab, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	3	0
			1735	1079	298	350	8			
1	C	220	Total	C	N	O	S	0	3	0
			1735	1078	295	354	8			

- Molecule 2 is a protein called Fab, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	2	0
			1648	1051	266	323	8			
2	D	214	Total	C	N	O	S	0	2	0
			1642	1047	265	322	8			

- Molecule 3 is a protein called protein L domain C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	63	Total	C	N	O	S	0	1	0
			497	316	81	99	1			
3	F	62	Total	C	N	O	S	0	1	0
			486	310	79	96	1			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

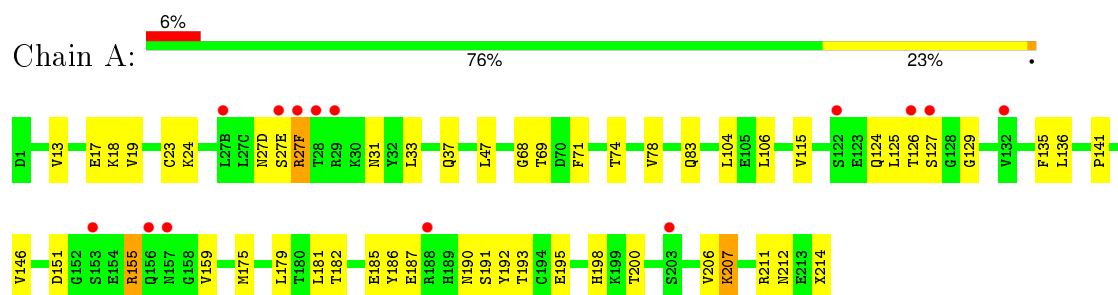
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	184	Total	O	0	0
			184	184		
5	B	149	Total	O	0	0
			149	149		
5	C	191	Total	O	0	0
			191	191		
5	D	164	Total	O	0	0
			164	164		
5	E	25	Total	O	0	0
			25	25		
5	F	26	Total	O	0	0
			26	26		

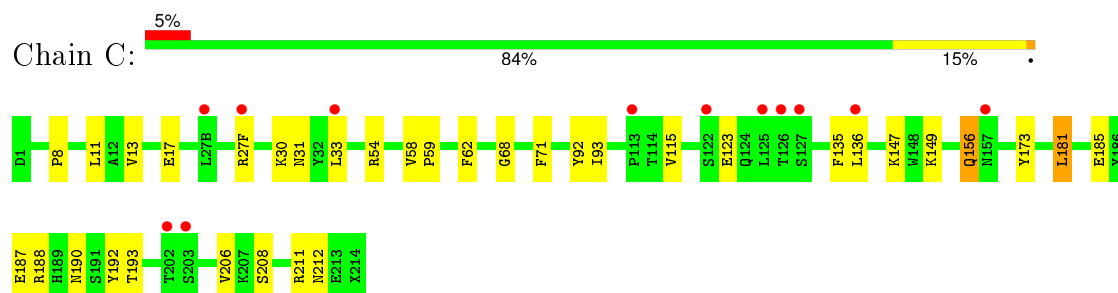
### 3 Residue-property plots [i](#)

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.

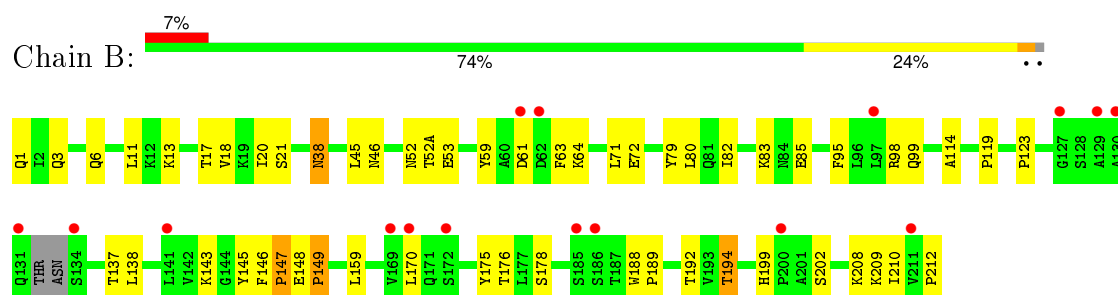
- Molecule 1: Fab, light chain



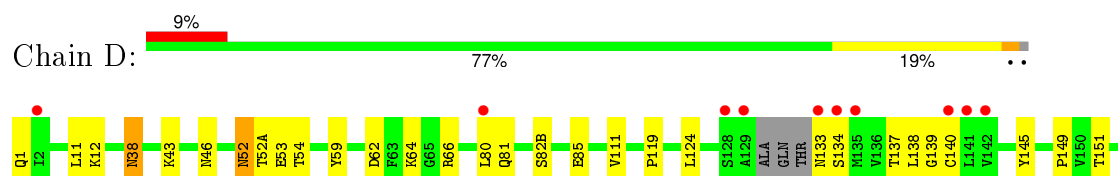
- Molecule 1: Fab, light chain

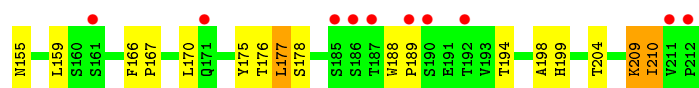


- Molecule 2: Fab, heavy chain

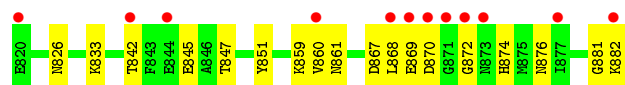


- Molecule 2: Fab, heavy chain

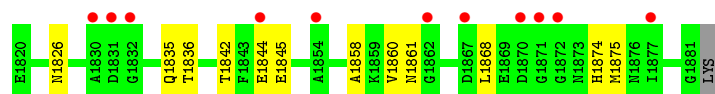
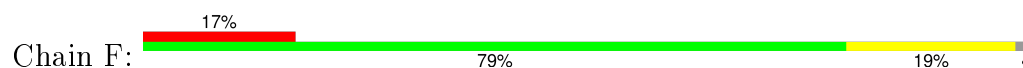




• Molecule 3: protein L domain C



• Molecule 3: protein L domain C



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.49Å 100.96Å 149.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.72 – 2.08	Depositor EDS
% Data completeness (in resolution range)	89.0 (20.00-2.10) 94.2 (19.72-2.08)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.33 (at 2.09Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.197 , 0.247 0.208 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	35.1	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 56.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 69722 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8490	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.12% 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: AEA, EDO

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	0.32	0/1762	0.61	0/2390
1	C	0.33	0/1762	0.61	0/2391
2	B	0.34	0/1694	0.62	0/2316
2	D	0.39	2/1688 (0.1%)	0.66	2/2308 (0.1%)
3	E	0.34	0/505	0.55	0/678
3	F	0.32	0/494	0.54	0/666
All	All	0.34	2/7905 (0.0%)	0.62	2/10749 (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
1	A	1	0
1	C	1	0
All	All	2	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	209	LYS	C-N	5.54	1.46	1.34
2	D	210	ILE	C-N	5.36	1.46	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	140[A]	CYS	CA-CB-SG	5.45	123.81	114.00
2	D	140[B]	CYS	CA-CB-SG	5.45	123.81	114.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	214	AEA	C1
1	C	214	AEA	C1

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	1735	0	1684	42	0
1	C	1735	0	1674	30	0
2	B	1648	0	1596	40	0
2	D	1642	0	1589	43	0
3	E	497	0	479	25	0
3	F	486	0	466	9	0
4	B	4	0	6	1	0
4	D	4	0	6	1	0
5	A	184	0	0	3	0
5	B	149	0	0	4	0
5	C	191	0	0	3	0
5	D	164	0	0	4	0
5	E	25	0	0	1	0
5	F	26	0	0	3	0
All	All	8490	0	7500	187	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 12.

All (187) 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:190:ASN:HD21	1:A:212:ASN:H	1.11	0.89
2:D:133:ASN:ND2	2:D:134:SER:H	1.72	0.86
1:A:31:ASN:HD21	1:A:68:GLY:H	1.23	0.86
3:E:842:THR:HG22	3:E:845[A]:GLU:HG2	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:194:THR:HG22	2:D:209:LYS:HA	1.61	0.82
1:A:190:ASN:ND2	1:A:212:ASN:H	1.77	0.82
2:B:123:PRO:HD3	2:B:208:LYS:HD3	1.68	0.75
3:E:842:THR:HG22	3:E:845[A]:GLU:CG	2.18	0.74
2:D:155:ASN:HB2	2:D:159:LEU:HD13	1.71	0.73
1:A:19:VAL:HG21	1:A:78[B]:VAL:HG21	1.73	0.71
1:A:195:GLU:HG2	1:A:206:VAL:HG22	1.72	0.71
1:C:31:ASN:HD21	1:C:68:GLY:H	1.38	0.70
2:B:85:GLU:CD	2:B:85:GLU:H	1.95	0.69
3:F:1868:LEU:HD23	3:F:1875:MET:HG3	1.74	0.69
1:A:31:ASN:ND2	1:A:68:GLY:H	1.91	0.68
1:A:206:VAL:O	1:A:207:LYS:HD2	1.94	0.68
1:A:13:VAL:HG21	1:A:19:VAL:HG22	1.75	0.67
2:D:52:ASN:HD22	2:D:53:GLU:H	1.41	0.67
2:D:119:PRO:HB3	2:D:145:TYR:HB3	1.77	0.67
1:A:155:ARG:HG2	1:A:155:ARG:HH11	1.58	0.66
2:B:119:PRO:HB3	2:B:145:TYR:HB3	1.78	0.66
2:B:194:THR:HG23	5:B:2725:HOH:O	1.95	0.66
2:D:194:THR:HG21	2:D:209:LYS:HG2	1.78	0.65
2:D:38:ASN:ND2	2:D:46[B]:ASN:HB2	2.12	0.65
1:A:19:VAL:CG2	1:A:78[B]:VAL:HG21	2.26	0.65
2:D:52:ASN:ND2	2:D:53:GLU:H	1.95	0.65
1:C:33:LEU:HD22	1:C:71:PHE:CG	2.34	0.63
5:A:2544:HOH:O	2:B:178:SER:HB3	1.98	0.63
1:A:190:ASN:HD21	1:A:212:ASN:N	1.91	0.62
1:C:193[A]:THR:HG22	1:C:208:SER:CB	2.29	0.62
2:B:147:PRO:O	2:B:199:HIS:HE1	1.82	0.62
2:D:38:ASN:HD21	2:D:46[B]:ASN:HB2	1.65	0.62
2:D:133:ASN:ND2	2:D:134:SER:N	2.48	0.61
1:A:151:ASP:HA	1:A:191:SER:HB3	1.82	0.61
1:A:23:CYS:C	1:A:24:LYS:HD3	2.21	0.61
2:B:148:GLU:OE2	2:B:149:PRO:HA	2.00	0.61
3:F:1842:THR:OG1	3:F:1845[B]:GLU:HG2	2.01	0.60
1:C:193[A]:THR:HG22	1:C:208:SER:HB3	1.83	0.60
3:F:1860:VAL:HG13	3:F:1861:ASN:ND2	2.17	0.59
2:B:38:ASN:ND2	2:B:46[A]:ASN:HB2	2.17	0.59
2:B:52:ASN:HA	4:B:4001:EDO:H11	1.86	0.58
2:D:194:THR:CG2	2:D:209:LYS:HG2	2.35	0.57
1:C:149:LYS:HB2	1:C:193[A]:THR:OG1	2.05	0.56
1:C:147:LYS:HE3	1:C:149:LYS:HE3	1.85	0.56
3:E:842:THR:HG23	3:E:845[A]:GLU:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:842:THR:HG22	3:E:845[B]:GLU:HB2	1.87	0.56
2:D:194:THR:HG23	5:D:2215:HOH:O	2.05	0.56
1:A:124:GLN:HG2	1:A:129:GLY:O	2.06	0.55
2:B:20:ILE:HD11	2:B:80:LEU:HD23	1.88	0.54
2:B:138:LEU:N	2:B:138:LEU:HD12	2.23	0.54
3:E:842:THR:HG23	3:E:845[B]:GLU:H	1.71	0.54
1:A:182:THR:OG1	1:A:185:GLU:HG3	2.07	0.54
2:D:133:ASN:HD22	2:D:134:SER:H	1.52	0.54
2:B:143:LYS:HB3	2:B:176:THR:HG23	1.90	0.54
1:C:31:ASN:ND2	1:C:68:GLY:H	2.05	0.53
1:A:37:GLN:HB2	1:A:47:LEU:HD11	1.90	0.53
2:B:137:THR:C	2:B:138:LEU:HD12	2.29	0.53
3:E:847:THR:HG22	3:E:851:TYR:CE2	2.43	0.53
2:B:194:THR:HB	2:B:209:LYS:HA	1.90	0.53
2:D:138:LEU:N	2:D:138:LEU:HD22	2.23	0.53
1:C:27(F):ARG:HB3	1:C:27(F):ARG:HH21	1.74	0.53
2:B:59:TYR:O	2:B:64:LYS:HE3	2.08	0.53
2:B:83:LYS:HB3	2:B:85:GLU:OE2	2.08	0.52
1:C:181:LEU:N	1:C:181:LEU:HD23	2.24	0.52
1:C:8:PRO:HG2	1:C:11:LEU:HD13	1.91	0.52
3:F:1826:ASN:HD22	3:F:1836:THR:HG22	1.74	0.52
2:B:13:LYS:HE2	5:B:2279:HOH:O	2.10	0.52
2:D:38:ASN:HD22	2:D:38:ASN:C	2.13	0.52
2:D:52:ASN:HD22	2:D:52:ASN:C	2.14	0.52
3:E:826:ASN:HB2	3:E:876:ASN:ND2	2.24	0.51
1:C:54:ARG:HD2	1:C:58:VAL:O	2.11	0.51
3:F:1874:HIS:HB2	5:F:2570:HOH:O	2.11	0.51
3:E:826:ASN:HB2	3:E:876:ASN:HD22	1.75	0.50
1:C:156:GLN:NE2	1:C:156:GLN:H	2.09	0.50
2:D:52:ASN:ND2	2:D:54:THR:H	2.09	0.50
2:B:61:ASP:HA	2:B:64:LYS:HD3	1.94	0.50
1:A:27(D):ASN:OD1	1:A:27(F):ARG:HB3	2.11	0.50
2:B:52:ASN:OD1	2:B:53:GLU:HB3	2.11	0.50
2:B:199:HIS:HD2	2:B:202:SER:OG	1.95	0.50
2:B:72:GLU:HB2	2:B:79:TYR:HE2	1.77	0.50
2:B:46[B]:ASN:ND2	2:B:63:PHE:HE2	2.10	0.50
1:A:17:GLU:OE2	3:E:833:LYS:HD3	2.11	0.50
1:C:13:VAL:HG22	1:C:17:GLU:HB2	1.94	0.50
1:A:141:PRO:O	1:A:198:HIS:HE1	1.94	0.50
1:A:198:HIS:HD2	1:A:200:THR:OG1	1.94	0.50
3:E:842:THR:CG2	3:E:845[A]:GLU:HG2	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:ASN:ND2	1:A:212:ASN:N	2.52	0.49
1:C:59:PRO:HG2	1:C:62:PHE:CD1	2.48	0.49
2:D:52:ASN:HD21	2:D:53:GLU:HB3	1.78	0.49
2:D:38:ASN:ND2	2:D:38:ASN:C	2.66	0.49
1:A:115:VAL:HA	1:A:135:PHE:O	2.13	0.49
1:A:187:GLU:HA	1:A:211:ARG:CZ	2.43	0.49
2:B:210:ILE:HD12	2:B:210:ILE:N	2.27	0.49
2:B:170:LEU:HB2	2:B:175:TYR:CE2	2.48	0.48
3:E:859:LYS:HE3	5:E:2710:HOH:O	2.13	0.48
1:A:24:LYS:HA	1:A:69:THR:O	2.14	0.48
1:C:92:TYR:CD1	1:C:93:ILE:HG13	2.48	0.48
2:D:194:THR:CG2	2:D:209:LYS:HA	2.38	0.48
2:B:46[B]:ASN:ND2	2:B:63:PHE:CE2	2.82	0.48
1:A:126:THR:HG22	1:A:126:THR:O	2.13	0.48
5:A:2213:HOH:O	3:E:860:VAL:HG11	2.12	0.47
3:E:882:LYS:HD2	3:E:882:LYS:N	2.29	0.47
2:B:114:ALA:HB3	2:B:146:PHE:CE2	2.49	0.47
2:D:124:LEU:HB2	2:D:139:GLY:CA	2.45	0.47
1:A:135:PHE:C	1:A:136:LEU:HD12	2.35	0.47
2:D:151:THR:OG1	2:D:198:ALA:HB3	2.15	0.47
1:A:159:VAL:HG22	1:A:179:LEU:HD23	1.96	0.47
2:D:199:HIS:HB3	2:D:204:THR:HB	1.98	0.46
1:A:18:LYS:HE3	1:A:74:THR:HG21	1.96	0.46
2:D:81:GLN:NE2	5:D:2613:HOH:O	2.48	0.46
2:D:170:LEU:HD13	2:D:170:LEU:C	2.35	0.46
2:D:170:LEU:HB2	2:D:175:TYR:CE2	2.51	0.46
1:C:187:GLU:O	1:C:211:ARG:NH2	2.48	0.46
1:C:30:LYS:NZ	5:C:2558:HOH:O	2.48	0.46
2:B:52(A):THR:HA	2:B:71:LEU:HD11	1.99	0.45
1:C:193[B]:THR:CG2	1:C:206:VAL:HG13	2.45	0.45
1:C:185:GLU:HA	1:C:188:ARG:NH2	2.32	0.45
1:C:173:TYR:HB3	5:C:2356:HOH:O	2.15	0.45
1:A:24:LYS:N	1:A:24:LYS:HD3	2.32	0.45
1:C:13:VAL:HG23	3:F:1835:GLN:HG2	1.99	0.45
2:D:177:LEU:HD23	2:D:177:LEU:C	2.38	0.45
2:B:1:GLN:O	2:B:3:GLN:HG2	2.17	0.45
1:A:193:THR:CG2	1:A:206:VAL:HG13	2.46	0.44
1:A:155:ARG:NH1	1:A:155:ARG:HG2	2.29	0.44
1:A:68:GLY:HA3	5:A:2261:HOH:O	2.15	0.44
1:C:192:TYR:O	1:C:208:SER:HB2	2.18	0.44
2:D:62:ASP:HB2	5:D:2629:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:LEU:HD22	1:A:71:PHE:CG	2.53	0.44
3:E:842:THR:CG2	3:E:845[A]:GLU:H	2.29	0.44
2:B:95:PHE:CZ	2:B:99:GLN:HA	2.52	0.44
3:F:1844:GLU:OE1	3:F:1844:GLU:N	2.48	0.44
2:D:137:THR:C	2:D:138:LEU:HD22	2.38	0.44
2:B:188:TRP:CH2	2:B:212:PRO:HG3	2.53	0.44
3:E:842:THR:CG2	3:E:845[B]:GLU:H	2.29	0.43
1:A:155:ARG:HH11	1:A:155:ARG:CG	2.30	0.43
2:D:177:LEU:HD23	2:D:178:SER:N	2.33	0.43
2:B:188:TRP:CG	2:B:189:PRO:HA	2.54	0.43
2:B:17:THR:HG22	2:B:18:VAL:N	2.34	0.43
1:A:186:TYR:HA	1:A:192:TYR:OH	2.18	0.43
2:B:6:GLN:HA	2:B:21:SER:O	2.19	0.43
2:D:38:ASN:HD21	2:D:46[A]:ASN:HB3	1.83	0.43
1:A:146:VAL:HB	1:A:175:MET:HE1	2.00	0.43
1:C:136:LEU:HD12	1:C:136:LEU:N	2.32	0.43
2:D:188:TRP:CG	2:D:189:PRO:HA	2.54	0.42
1:C:193[A]:THR:HA	1:C:208:SER:HB3	2.00	0.42
2:B:143:LYS:HE3	2:B:143:LYS:HB2	1.84	0.42
3:F:1826:ASN:ND2	5:F:2600:HOH:O	2.52	0.42
2:D:52(A):THR:H	4:D:3001:EDO:H22	1.83	0.42
3:E:881:GLY:O	3:E:882:LYS:HB2	2.19	0.42
5:C:2521:HOH:O	2:D:176:THR:HG21	2.18	0.42
2:B:38:ASN:HD21	2:B:46[A]:ASN:HB2	1.82	0.42
1:A:179:LEU:CD1	1:A:181:LEU:HG	2.49	0.42
2:D:52:ASN:HD22	2:D:53:GLU:N	2.12	0.42
2:D:59:TYR:HB2	2:D:64:LYS:HG2	2.02	0.42
3:E:870:ASP:C	3:E:872:GLY:N	2.73	0.42
3:E:867:ASP:OD1	3:E:876:ASN:HB2	2.19	0.42
1:C:190:ASN:ND2	1:C:212:ASN:ND2	2.68	0.42
3:E:869:GLU:OE2	3:E:874:HIS:HD2	2.03	0.41
2:D:85:GLU:CD	2:D:85:GLU:H	2.23	0.41
1:A:125:LEU:C	1:A:127:SER:H	2.23	0.41
2:B:146:PHE:CE2	2:B:147:PRO:HB3	2.55	0.41
2:D:138:LEU:HD12	2:D:210:ILE:HG21	2.01	0.41
3:E:826:ASN:HD22	3:E:826:ASN:HA	1.68	0.41
3:F:1858:ALA:HB3	5:F:2611:HOH:O	2.19	0.41
1:A:214:AEA:H41	1:A:214:AEA:H11	1.89	0.41
1:C:193[B]:THR:OG1	1:C:208:SER:HB3	2.21	0.41
2:D:43:LYS:HB3	5:D:2027:HOH:O	2.21	0.41
1:A:136:LEU:N	1:A:136:LEU:HD12	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:12:LYS:O	2:D:111:VAL:HA	2.20	0.41
3:E:842:THR:HG22	3:E:845[A]:GLU:CD	2.41	0.41
1:A:193:THR:HG23	1:A:206:VAL:HG13	2.03	0.41
2:D:38:ASN:ND2	2:D:46[A]:ASN:HB3	2.35	0.41
1:C:193[B]:THR:HA	1:C:208:SER:HB3	2.02	0.41
3:E:860:VAL:HG13	3:E:861:ASN:ND2	2.36	0.41
3:E:868:LEU:O	3:E:869:GLU:HG3	2.21	0.41
1:C:59:PRO:HG2	1:C:62:PHE:CE1	2.56	0.41
2:B:17:THR:HG23	2:B:82:ILE:O	2.21	0.41
3:E:868:LEU:C	3:E:869:GLU:HG3	2.41	0.41
1:A:83:GLN:HG2	1:A:106:LEU:HD23	2.03	0.41
3:E:842:THR:HG22	3:E:845[A]:GLU:OE1	2.21	0.40
1:C:123:GLU:N	1:C:123:GLU:OE1	2.41	0.40
2:B:192:THR:HG22	5:B:2725:HOH:O	2.21	0.40
2:B:98:ARG:HG3	5:B:2056:HOH:O	2.21	0.40
2:D:66:ARG:HD2	2:D:82(B):SER:HB2	2.03	0.40
2:B:38:ASN:ND2	2:B:46[B]:ASN:HB3	2.36	0.40
1:C:115:VAL:HA	1:C:135:PHE:O	2.22	0.40
2:D:166:PHE:HA	2:D:167:PRO:HD3	1.94	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	220/220 (100%)	212 (96%)	6 (3%)	2 (1%)	21	15
1	C	220/220 (100%)	214 (97%)	6 (3%)	0	100	100
2	B	213/217 (98%)	199 (93%)	14 (7%)	0	100	100
2	D	212/217 (98%)	200 (94%)	12 (6%)	0	100	100
3	E	62/63 (98%)	59 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
All	All	988/1000 (99%)	943 (95%)	43 (4%)	2 (0%)	52	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27(F)	ARG
1	A	27(E)	SER

### 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	197/194 (102%)	194 (98%)	3 (2%)	72	78
1	C	197/194 (102%)	195 (99%)	2 (1%)	82	87
2	B	186/186 (100%)	179 (96%)	7 (4%)	40	40
2	D	186/186 (100%)	179 (96%)	7 (4%)	40	40
3	E	48/47 (102%)	48 (100%)	0	100	100
3	F	47/47 (100%)	47 (100%)	0	100	100
All	All	861/854 (101%)	842 (98%)	19 (2%)	60	64

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	LEU
1	A	155	ARG
1	A	207	LYS
2	B	11	LEU
2	B	38	ASN
2	B	45	LEU
2	B	147	PRO
2	B	149	PRO
2	B	159	LEU

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Mol	Chain	Res	Type
2	B	194	THR
1	C	156	GLN
1	C	181	LEU
2	D	1	GLN
2	D	11	LEU
2	D	38	ASN
2	D	52	ASN
2	D	80	LEU
2	D	149	PRO
2	D	177	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	42	GLN
1	A	79	GLN
1	A	137	ASN
1	A	190	ASN
1	A	198	HIS
1	A	210	ASN
2	B	3	GLN
2	B	38	ASN
2	B	84	ASN
2	B	199	HIS
1	C	31	ASN
1	C	37	GLN
1	C	42	GLN
1	C	83	GLN
1	C	156	GLN
1	C	212	ASN
2	D	38	ASN
2	D	52	ASN
2	D	133	ASN
3	E	826	ASN
3	E	874	HIS
3	E	876	ASN
3	F	1826	ASN
3	F	1861	ASN
3	F	1874	HIS
3	F	1876	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z  > 2$
1	AEA	A	214	1	9,9,10	1.84	2 (22%)	7,10,12	1.52	1 (14%)
1	AEA	C	214	1	9,9,10	2.02	3 (33%)	7,10,12	1.53	1 (14%)

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
1	AEA	A	214	1	1/1/2/3	0/7/9/10	0/0/0/0
1	AEA	C	214	1	1/1/2/3	0/7/9/10	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	214	AEA	C2-N2	-3.80	1.25	1.32
1	A	214	AEA	C2-N2	-3.69	1.25	1.32
1	C	214	AEA	C4-S1	-2.77	1.79	1.81
1	C	214	AEA	O1-C5	3.45	1.42	1.19
1	A	214	AEA	O1-C5	3.46	1.42	1.19

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	214	AEA	C1-C3-S1	-3.53	104.49	112.84
1	A	214	AEA	C1-C3-S1	-3.36	104.91	112.84

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	214	AEA	C1
1	C	214	AEA	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	214	AEA	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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	EDO	B	4001	-	3,3,3	0.69	0	2,2,2	0.52	0
4	EDO	D	3001	-	3,3,3	0.68	0	2,2,2	0.33	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	EDO	B	4001	-	-	0/1/1/1	0/0/0/0
4	EDO	D	3001	-	-	0/1/1/1	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
4	B	4001	EDO	1	0
4	D	3001	EDO	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	219/220 (99%)	0.37	14 (6%)	23 30	22, 35, 63, 70	0
1	C	219/220 (99%)	0.31	12 (5%)	29 37	21, 35, 55, 63	0
2	B	215/217 (99%)	0.42	16 (7%)	17 24	23, 42, 61, 91	0
2	D	214/217 (98%)	0.48	20 (9%)	11 15	22, 40, 64, 74	0
3	E	63/63 (100%)	1.02	12 (19%)	2 2	27, 41, 67, 78	0
3	F	62/63 (98%)	1.09	11 (17%)	2 3	29, 44, 65, 72	0
All	All	992/1000 (99%)	0.48	85 (8%)	13 18	21, 38, 62, 91	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	126	THR	6.6
2	D	133	ASN	6.5
2	D	211	VAL	6.1
3	E	872	GLY	5.8
3	F	1871	GLY	5.6
2	D	187	THR	5.5
3	E	870	ASP	5.5
2	B	131	GLN	5.5
1	A	27(F)	ARG	4.9
1	A	28	THR	4.8
1	A	27(E)	SER	4.8
2	D	129	ALA	4.6
3	E	860	VAL	4.6
2	B	211	VAL	4.5
3	E	871	GLY	4.3
3	E	877	ILE	4.3
1	C	33	LEU	4.2
3	F	1832	GLY	4.1
2	B	170	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
3	F	1870	ASP	3.9
2	D	185	SER	3.8
3	F	1877	ILE	3.8
1	A	157	ASN	3.7
3	E	820	GLU	3.7
2	D	134	SER	3.7
1	C	136	LEU	3.7
1	C	27(B)	LEU	3.6
2	B	185	SER	3.6
2	D	212	PRO	3.6
3	E	869	GLU	3.5
2	D	186	SER	3.4
3	F	1862	GLY	3.4
1	C	127	SER	3.4
2	D	135	MET	3.3
1	A	122	SER	3.3
1	C	203	SER	3.3
2	B	186	SER	3.3
2	B	134	SER	3.1
1	A	203	SER	3.1
2	D	161	SER	3.1
3	E	882	LYS	3.0
2	B	172	SER	3.0
1	A	126	THR	3.0
2	D	141	LEU	3.0
2	D	190	SER	3.0
1	A	29	ARG	2.9
2	B	129	ALA	2.9
2	D	140[A]	CYS	2.9
2	D	80	LEU	2.9
1	A	188	ARG	2.8
1	A	127	SER	2.8
3	F	1844	GLU	2.8
2	D	128	SER	2.7
1	A	153	SER	2.7
3	E	873	ASN	2.7
1	A	132	VAL	2.7
2	D	142	VAL	2.6
1	C	125	LEU	2.6
1	C	157	ASN	2.6
2	B	130	ALA	2.5
1	C	202	THR	2.5

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Mol	Chain	Res	Type	RSRZ
2	D	189	PRO	2.5
3	F	1872	GLY	2.5
2	B	169	VAL	2.5
3	E	844	GLU	2.4
2	B	97	LEU	2.4
1	C	122	SER	2.4
3	F	1854	ALA	2.4
2	B	200	PRO	2.4
2	B	61	ASP	2.4
2	B	141	LEU	2.4
2	B	127	GLY	2.3
1	A	27(B)	LEU	2.3
3	E	842	THR	2.2
3	F	1867	ASP	2.2
2	D	2	ILE	2.2
3	F	1830	ALA	2.2
3	F	1831	ASP	2.2
2	B	62	ASP	2.2
1	C	113	PRO	2.2
2	D	171	GLN	2.1
1	A	156	GLN	2.1
1	C	27(F)	ARG	2.1
2	D	192	THR	2.0
3	E	868	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	AEA	A	214	10/11	0.62	0.33	-	60,64,66,67	0
1	AEA	C	214	10/11	0.74	0.19	-	54,55,58,59	0

## 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( $\text{\AA}^2$ )	Q<0.9
4	EDO	D	3001	4/4	0.76	0.14	1.34	28,32,38,40	0
4	EDO	B	4001	4/4	0.82	0.17	1.25	25,33,38,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.