



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2024 – 02:05 PM EDT

PDB ID : 8SVE  
Title : Structure of Monomeric Interleukin-10 Grafted into and Antibody CDR  
Authors : DiDonato, M.; Spraggon, G.  
Deposited on : 2023-05-16  
Resolution : 2.40 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

<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>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

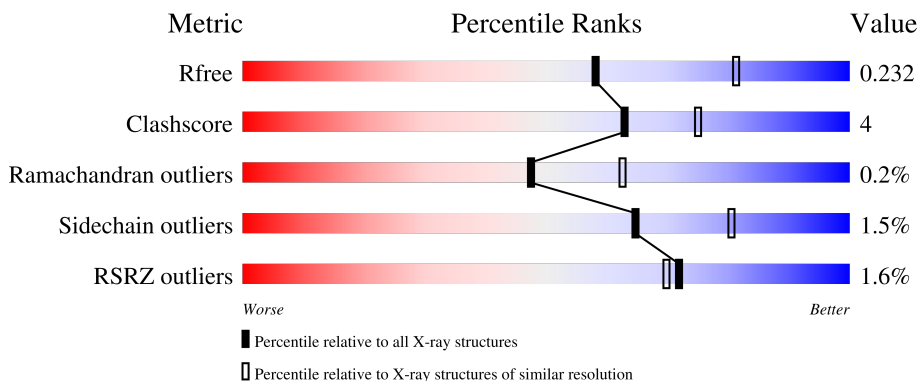
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	H	227	 87% 10% .
1	I	227	 86% 11% .
2	L	379	 2% 86% 8% . . .
2	M	379	 3% 81% 12% . 7%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9252 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 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	220	Total	C	N	O	S	0	1	0
			1666	1056	276	327	7			
1	I	220	Total	C	N	O	S	0	0	0
			1655	1050	272	326	7			

- Molecule 2 is a protein called Interleukin-10,Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	362	Total	C	N	O	S	0	3	0
			2878	1817	485	558	18			
2	M	354	Total	C	N	O	S	0	1	0
			2796	1770	472	536	18			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	1	ASP	-	expression tag	UNP P22301
L	2	ILE	-	expression tag	UNP P22301
L	3	GLN	-	expression tag	UNP P22301
L	4	MET	-	expression tag	UNP P22301
L	5	THR	-	expression tag	UNP P22301
L	6	GLN	-	expression tag	UNP P22301
L	7	SER	-	expression tag	UNP P22301
L	8	PRO	-	expression tag	UNP P22301
L	9	SER	-	expression tag	UNP P22301
L	10	THR	-	expression tag	UNP P22301
L	11	LEU	-	expression tag	UNP P22301
L	12	SER	-	expression tag	UNP P22301
L	13	ALA	-	expression tag	UNP P22301
L	14	SER	-	expression tag	UNP P22301
L	15	VAL	-	expression tag	UNP P22301
L	16	GLY	-	expression tag	UNP P22301

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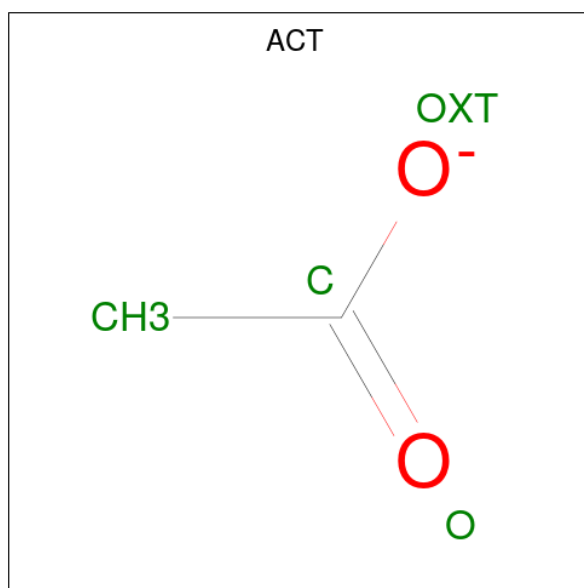
Chain	Residue	Modelled	Actual	Comment	Reference
L	17	ASP	-	expression tag	UNP P22301
L	18	ARG	-	expression tag	UNP P22301
L	19	VAL	-	expression tag	UNP P22301
L	20	THR	-	expression tag	UNP P22301
L	21	ILE	-	expression tag	UNP P22301
L	22	THR	-	expression tag	UNP P22301
L	23	CYS	-	expression tag	UNP P22301
L	24	LYS	-	expression tag	UNP P22301
L	25	ALA	-	expression tag	UNP P22301
L	26	GLN	-	expression tag	UNP P22301
L	27	LEU	-	expression tag	UNP P22301
L	28	SER	-	expression tag	UNP P22301
L	145	GLY	-	insertion	UNP P22301
L	146	GLY	-	insertion	UNP P22301
L	147	GLY	-	insertion	UNP P22301
L	148	SER	-	insertion	UNP P22301
L	149	GLY	-	insertion	UNP P22301
L	150	GLY	-	insertion	UNP P22301
M	1	ASP	-	expression tag	UNP P22301
M	2	ILE	-	expression tag	UNP P22301
M	3	GLN	-	expression tag	UNP P22301
M	4	MET	-	expression tag	UNP P22301
M	5	THR	-	expression tag	UNP P22301
M	6	GLN	-	expression tag	UNP P22301
M	7	SER	-	expression tag	UNP P22301
M	8	PRO	-	expression tag	UNP P22301
M	9	SER	-	expression tag	UNP P22301
M	10	THR	-	expression tag	UNP P22301
M	11	LEU	-	expression tag	UNP P22301
M	12	SER	-	expression tag	UNP P22301
M	13	ALA	-	expression tag	UNP P22301
M	14	SER	-	expression tag	UNP P22301
M	15	VAL	-	expression tag	UNP P22301
M	16	GLY	-	expression tag	UNP P22301
M	17	ASP	-	expression tag	UNP P22301
M	18	ARG	-	expression tag	UNP P22301
M	19	VAL	-	expression tag	UNP P22301
M	20	THR	-	expression tag	UNP P22301
M	21	ILE	-	expression tag	UNP P22301
M	22	THR	-	expression tag	UNP P22301
M	23	CYS	-	expression tag	UNP P22301
M	24	LYS	-	expression tag	UNP P22301

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Chain	Residue	Modelled	Actual	Comment	Reference
M	25	ALA	-	expression tag	UNP P22301
M	26	GLN	-	expression tag	UNP P22301
M	27	LEU	-	expression tag	UNP P22301
M	28	SER	-	expression tag	UNP P22301
M	145	GLY	-	insertion	UNP P22301
M	146	GLY	-	insertion	UNP P22301
M	147	GLY	-	insertion	UNP P22301
M	148	SER	-	insertion	UNP P22301
M	149	GLY	-	insertion	UNP P22301
M	150	GLY	-	insertion	UNP P22301

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	C	O	0	0
			4	2	2		

- 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	I	1	Total C O 4 2 2	0	0
4	L	1	Total C O 4 2 2	0	0
4	M	1	Total C O 4 2 2	0	0
4	M	1	Total C O 4 2 2	0	0
4	M	1	Total C O 4 2 2	0	0


- Molecule 5 is water.

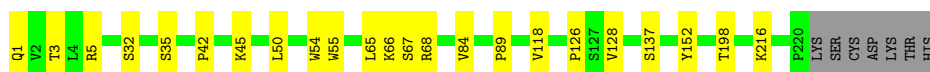
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	72	Total O 72 72	0	0
5	I	54	Total O 54 54	0	0
5	L	56	Total O 56 56	0	0
5	M	51	Total O 51 51	0	0

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


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: Fab Heavy chain

Chain H:  87% 10%




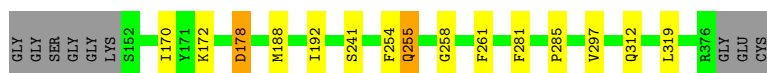
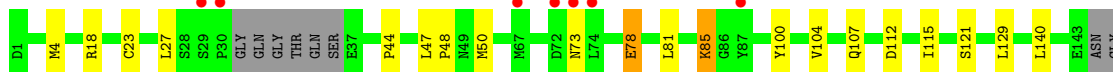
- Molecule 1: Fab Heavy chain

Chain I:  86% 11%




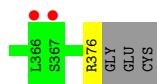
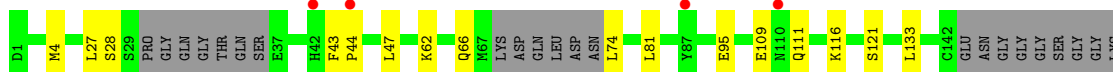
- Molecule 2: Interleukin-10,Fab light chain

Chain L:  86% 8%



- Molecule 2: Interleukin-10,Fab light chain

Chain M:  81% 12% 7%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.64Å 104.66Å 82.83Å 90.00° 115.29° 90.00°	Depositor
Resolution (Å)	42.90 – 2.40 42.90 – 2.40	Depositor EDS
% Data completeness (in resolution range)	82.9 (42.90-2.40) 77.5 (42.90-2.40)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.61 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.188 , 0.232 0.188 , 0.232	Depositor DCC
$R_{free}$ test set	2219 reflections (5.48%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.0	Xtrriage
Anisotropy	0.084	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 37.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.021 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9252	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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, 0.333 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: EDO, ACT, PCA

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	H	0.29	0/1702	0.58	0/2332
1	I	0.29	0/1691	0.58	0/2318
2	L	0.32	0/2937	0.57	0/3963
2	M	0.31	0/2853	0.56	0/3847
All	All	0.31	0/9183	0.57	0/12460

There are no bond length outliers.

There are no bond angle outliers.

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	H	1666	0	1647	14	0
1	I	1655	0	1635	16	0
2	L	2878	0	2822	22	0
2	M	2796	0	2757	33	0
3	H	4	0	3	0	0
4	I	4	0	6	1	0
4	L	4	0	6	0	0
4	M	12	0	18	0	0
5	H	72	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	54	0	0	0	0
5	L	56	0	0	0	0
5	M	51	0	0	0	0
All	All	9252	0	8894	77	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 4.

All (77) 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)
2:M:44:PRO:HG2	2:M:192:ILE:HD12	1.54	0.89
2:M:288:GLU:HA	2:M:291:LYS:NZ	1.87	0.88
2:M:288:GLU:HA	2:M:291:LYS:HZ3	1.54	0.72
2:M:44:PRO:HB3	2:M:47:LEU:HD13	1.73	0.69
1:H:66:LYS:O	1:H:67:SER:OG	2.10	0.69
2:M:288:GLU:HA	2:M:291:LYS:HZ1	1.59	0.65
2:L:4:MET:HG2	2:L:23[B]:CYS:SG	2.37	0.64
1:H:3:THR:HG22	1:I:198:THR:HG21	1.81	0.62
2:L:50:MET:HE3	2:L:129:LEU:HD13	1.81	0.61
2:L:73:ASN:O	2:L:172:LYS:HE3	2.03	0.59
2:M:152:SER:O	2:M:154:ALA:N	2.35	0.59
2:L:112:ASP:HB2	2:L:115:ILE:HD12	1.87	0.57
2:L:100:TYR:HA	2:L:104:VAL:HG13	1.85	0.57
1:H:50:LEU:HD22	1:H:65:LEU:HD11	1.85	0.57
2:M:226:ARG:NH1	2:M:247:ASP:OD2	2.34	0.55
2:M:285:PRO:HD3	2:M:297:VAL:HG22	1.88	0.55
1:I:156:PRO:HG3	4:I:301:EDO:H21	1.88	0.55
1:H:198:THR:HG23	1:I:5:ARG:HB2	1.88	0.55
1:H:5[B]:ARG:HB2	1:I:198:THR:HG23	1.88	0.53
2:L:255:GLN:OE1	2:L:258:GLY:N	2.36	0.53
2:M:255:GLN:OE1	2:M:258:GLY:N	2.40	0.53
2:L:312:GLN:HB3	2:L:319:LEU:HD11	1.90	0.53
2:L:107:GLN:HB2	2:L:170:ILE:HD13	1.91	0.53
2:M:153:LYS:HG3	2:M:154:ALA:N	2.24	0.53
2:M:351:TYR:O	2:M:357:TYR:OH	2.22	0.52
2:L:18:ARG:HG3	2:L:241:SER:HA	1.91	0.52
2:M:192:ILE:HG12	2:M:192:ILE:O	2.10	0.51
2:M:226:ARG:HH12	2:M:247:ASP:CG	2.14	0.51
2:L:44:PRO:HB2	2:L:192:ILE:HD12	1.92	0.51
1:I:35:SER:HB2	1:I:54:TRP:CE3	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:348:LYS:HE2	2:M:352:GLU:OE2	2.10	0.50
2:L:47:LEU:HD11	2:L:188:MET:HG3	1.93	0.49
2:M:153:LYS:HG3	2:M:154:ALA:H	1.77	0.49
1:H:5[A]:ARG:HB2	1:I:198:THR:HG23	1.94	0.49
2:L:47:LEU:HD11	2:L:188:MET:CG	2.43	0.49
2:M:95:GLU:HB3	2:M:155:VAL:HG11	1.95	0.48
2:L:50:MET:CE	2:L:129:LEU:HD13	2.43	0.48
2:M:62:LYS:HE2	2:M:66:GLN:NE2	2.29	0.47
2:M:270:GLU:HG2	2:M:271:ILE:N	2.29	0.47
1:H:68:ARG:O	1:H:84:VAL:HA	2.15	0.47
2:L:285:PRO:HD3	2:L:297:VAL:HG22	1.98	0.46
1:H:42:PRO:HB2	1:H:45:LYS:HD3	1.98	0.46
2:L:47:LEU:HB3	2:L:48:PRO:HD3	1.99	0.45
1:H:35:SER:HB2	1:H:54:TRP:CE3	2.52	0.45
1:I:134:SER:O	1:I:138:THR:HG23	2.17	0.45
1:H:126:PRO:HB3	1:H:152:TYR:HB3	1.99	0.45
1:I:188:VAL:HG11	2:M:300:LEU:CD2	2.48	0.44
1:H:128:VAL:O	1:H:216:LYS:HE3	2.18	0.44
1:I:166:LEU:HD21	1:I:189:VAL:HG21	2.00	0.44
2:L:107:GLN:HB2	2:L:170:ILE:CD1	2.47	0.44
2:L:78:GLU:O	2:L:78:GLU:HG3	2.17	0.44
2:M:74:LEU:HD23	2:M:172:LYS:CE	2.48	0.44
1:I:188:VAL:HG11	2:M:300:LEU:HD22	1.99	0.43
1:H:32:SER:HA	1:H:55:TRP:CD1	2.54	0.43
1:H:137:SER:HA	2:L:281:PHE:HB3	2.00	0.43
1:I:137:SER:HA	2:M:281:PHE:HB3	2.00	0.43
2:M:27:LEU:HG	2:M:28:SER:N	2.32	0.43
1:I:41:GLN:HB2	1:I:47:LEU:HD23	2.00	0.43
2:M:224:PRO:HD2	2:M:227:PHE:CD1	2.53	0.43
2:L:81:LEU:O	2:L:85:LYS:HG3	2.18	0.43
2:L:178[B]:ASP:OD1	2:L:178[B]:ASP:N	2.51	0.43
1:I:169:GLY:O	1:I:189:VAL:HA	2.19	0.43
1:I:63:PRO:HA	1:I:66:LYS:HB2	2.01	0.42
2:L:254:PHE:CE1	2:L:261:PHE:HB3	2.54	0.42
2:M:351:TYR:CE2	2:M:376:ARG:HD3	2.54	0.42
2:L:140:LEU:HD23	2:L:140:LEU:HA	1.93	0.42
2:M:74:LEU:HD23	2:M:172:LYS:HE2	2.01	0.41
2:M:81:LEU:HB2	2:M:183:TYR:CE1	2.55	0.41
2:M:287:ASP:O	2:M:291:LYS:HG3	2.20	0.41
2:M:109:GLU:OE1	2:M:116:LYS:NZ	2.53	0.41
1:I:68:ARG:O	1:I:84:VAL:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:190:MET:O	2:M:194:ASN:ND2	2.52	0.41
1:I:22:CYS:HB2	1:I:38:TRP:CZ2	2.56	0.41
2:M:43:PHE:HZ	2:M:133:LEU:HD23	1.86	0.40
2:M:81:LEU:HD13	2:M:183:TYR:CD1	2.56	0.40
2:M:305:TYR:CG	2:M:306:PRO:HA	2.57	0.40
1:H:89:PRO:HA	1:H:118:VAL:HB	2.04	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	H	219/227 (96%)	212 (97%)	7 (3%)	0	100	100
1	I	218/227 (96%)	210 (96%)	8 (4%)	0	100	100
2	L	359/379 (95%)	350 (98%)	9 (2%)	0	100	100
2	M	347/379 (92%)	334 (96%)	11 (3%)	2 (1%)	25	36
All	All	1143/1212 (94%)	1106 (97%)	35 (3%)	2 (0%)	47	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	153	LYS
2	M	111	GLN

### 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	H	191/197 (97%)	191 (100%)	0	100	100
1	I	190/197 (96%)	187 (98%)	3 (2%)	62	79
2	L	324/330 (98%)	317 (98%)	7 (2%)	52	71
2	M	314/330 (95%)	308 (98%)	6 (2%)	57	75
All	All	1019/1054 (97%)	1003 (98%)	16 (2%)	65	79

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	65	LEU
1	I	142	THR
1	I	204	ASN
2	L	27	LEU
2	L	78	GLU
2	L	85	LYS
2	L	121	SER
2	L	178[A]	ASP
2	L	178[B]	ASP
2	L	255	GLN
2	M	4	MET
2	M	121	SER
2	M	190	MET
2	M	224	PRO
2	M	255	GLN
2	M	329	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	PCA	I	1	1	7,8,9	1.86	1 (14%)	9,10,12	2.11	6 (66%)
1	PCA	H	1	1	7,8,9	1.75	1 (14%)	9,10,12	1.96	4 (44%)

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	PCA	I	1	1	-	0/0/11/13	0/1/1/1
1	PCA	H	1	1	-	0/0/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	1	PCA	CD-N	4.73	1.47	1.34
1	H	1	PCA	CD-N	4.48	1.46	1.34

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	1	PCA	OE-CD-CG	-3.02	121.48	126.76
1	H	1	PCA	CB-CA-N	3.01	111.94	103.30
1	H	1	PCA	CA-N-CD	-3.00	103.30	113.58
1	I	1	PCA	CA-N-CD	-2.76	104.14	113.58
1	H	1	PCA	CG-CD-N	2.56	115.01	108.39
1	I	1	PCA	CB-CA-N	2.50	110.47	103.30
1	H	1	PCA	OE-CD-CG	-2.42	122.54	126.76
1	I	1	PCA	O-C-CA	-2.32	118.71	124.78
1	I	1	PCA	CG-CD-N	2.31	114.38	108.39
1	I	1	PCA	CB-CA-C	-2.21	109.67	112.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

6 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	I	301	-	3,3,3	0.50	0	2,2,2	0.29	0
4	EDO	L	401	-	3,3,3	0.58	0	2,2,2	0.08	0
4	EDO	M	402	-	3,3,3	0.50	0	2,2,2	0.32	0
4	EDO	M	401	-	3,3,3	0.52	0	2,2,2	0.30	0
3	ACT	H	301	-	3,3,3	1.54	1 (33%)	3,3,3	1.34	0
4	EDO	M	403	-	3,3,3	0.45	0	2,2,2	0.37	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	I	301	-	-	1/1/1/1	-
4	EDO	L	401	-	-	0/1/1/1	-
4	EDO	M	402	-	-	0/1/1/1	-
4	EDO	M	401	-	-	0/1/1/1	-
4	EDO	M	403	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	301	ACT	CH3-C	2.35	1.58	1.49

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	301	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	301	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	H	219/227 (96%)	-0.54	0 <b>100</b> <b>100</b>	20, 35, 54, 79	0
1	I	219/227 (96%)	-0.39	1 (0%) <b>91</b> <b>89</b>	21, 37, 56, 93	0
2	L	362/379 (95%)	-0.18	7 (1%) <b>66</b> <b>64</b>	27, 45, 73, 120	0
2	M	354/379 (93%)	-0.01	10 (2%) <b>53</b> <b>51</b>	24, 48, 86, 115	0
All	All	1154/1212 (95%)	-0.24	18 (1%) <b>72</b> <b>70</b>	20, 42, 77, 120	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	87	TYR	6.6
2	M	87	TYR	5.9
2	L	30	PRO	4.1
2	M	44	PRO	4.0
2	L	29	SER	3.8
2	L	73	ASN	3.7
2	M	319	LEU	3.3
2	M	366	LEU	3.3
2	M	110	ASN	2.8
2	M	367	SER	2.5
2	M	356	VAL	2.4
2	M	167	GLU	2.2
2	M	164	LYS	2.2
2	L	67	MET	2.2
2	M	42	HIS	2.2
2	L	72	ASP	2.1
1	I	66	LYS	2.0
2	L	74	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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
1	PCA	H	1	8/9	0.80	0.20	39,46,51,61	0
1	PCA	I	1	8/9	0.82	0.27	51,53,55,59	0

## 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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
3	ACT	H	301	4/4	0.58	0.33	47,53,59,64	0
4	EDO	L	401	4/4	0.81	0.31	36,37,38,40	0
4	EDO	M	402	4/4	0.85	0.20	47,47,51,53	0
4	EDO	M	403	4/4	0.85	0.14	47,51,52,59	0
4	EDO	M	401	4/4	0.88	0.14	30,39,42,48	0
4	EDO	I	301	4/4	0.93	0.16	40,42,44,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.