



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2021 – 10:03 PM EDT

PDB ID : 7KF0  
Title : Crystal structure of bH1 Fab variant (CDR H3 loop design 13\_0346) in complex with VEGF  
Authors : Shi, R.; Picard, M.-E.  
Deposited on : 2020-10-13  
Resolution : 2.32 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.

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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 : 2.23.2  
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) : 2.23.2

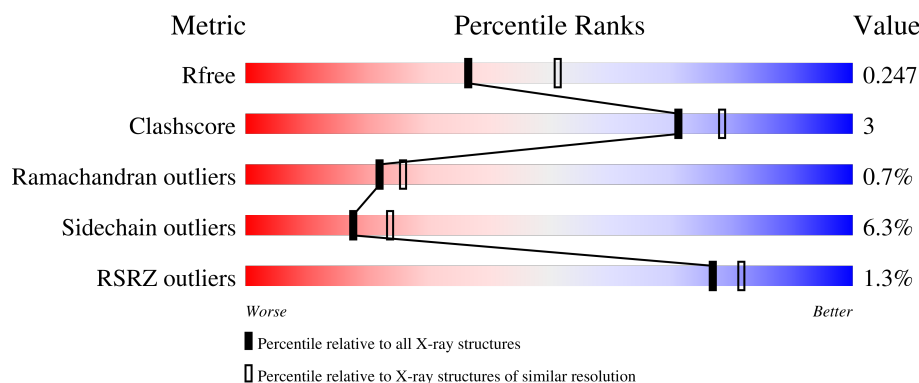
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.32 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	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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	A	236	<div> <div>5%</div> <div>81% 11% 6%</div> </div>
1	H	236	<div> <div>82% 9% 9%</div> </div>
2	B	218	<div> <div>93% 6% ..</div> </div>
2	L	218	<div> <div>89% 9% ..</div> </div>
3	C	116	<div> <div>5%</div> <div>64% 15% 18%</div> </div>

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Mol	Chain	Length	Quality of chain
3	V	116	<div><div><div>%</div><div><div></div></div><div>66%</div><div>15%</div><div>•</div><div>18%</div></div></div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8668 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 anti-VEGF-A Fab bH1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	215	Total	C	N	O	S	0	0	0
			1622	1031	272	313	6			
1	A	221	Total	C	N	O	S	0	0	0
			1663	1054	279	324	6			

- Molecule 2 is a protein called anti-VEGF-A Fab bH1 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	216	Total	C	N	O	S	0	0	0
			1670	1051	279	335	5			
2	B	216	Total	C	N	O	S	0	1	0
			1678	1056	282	335	5			

- Molecule 3 is a protein called Isoform L-VEGF206 of Vascular endothelial growth factor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	V	95	Total	C	N	O	S	0	0	0
			770	483	129	145	13			
3	C	95	Total	C	N	O	S	0	0	0
			770	483	129	145	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	111	HIS	-	expression tag	UNP P15692-14
V	112	HIS	-	expression tag	UNP P15692-14
V	113	HIS	-	expression tag	UNP P15692-14
V	114	HIS	-	expression tag	UNP P15692-14
V	115	HIS	-	expression tag	UNP P15692-14
V	116	HIS	-	expression tag	UNP P15692-14
C	111	HIS	-	expression tag	UNP P15692-14
C	112	HIS	-	expression tag	UNP P15692-14

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Chain	Residue	Modelled	Actual	Comment	Reference
C	113	HIS	-	expression tag	UNP P15692-14
C	114	HIS	-	expression tag	UNP P15692-14
C	115	HIS	-	expression tag	UNP P15692-14
C	116	HIS	-	expression tag	UNP P15692-14

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	96	Total	O	0	0
			96	96		
6	L	106	Total	O	0	0
			106	106		

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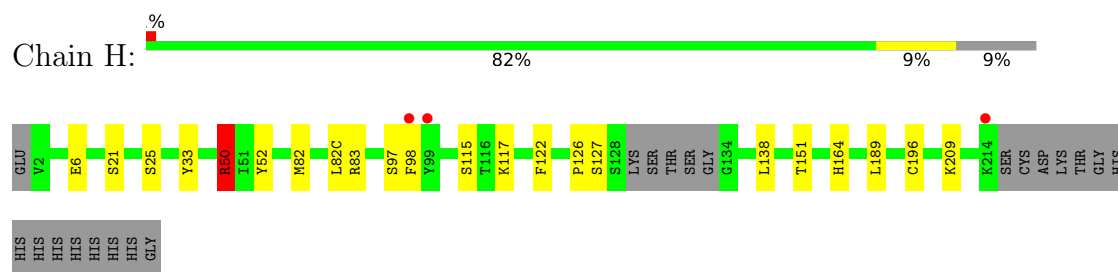
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	V	18	Total 18	O 18	0	0
6	A	109	Total 109	O 109	0	0
6	B	127	Total 127	O 127	0	0
6	C	30	Total 30	O 30	0	0

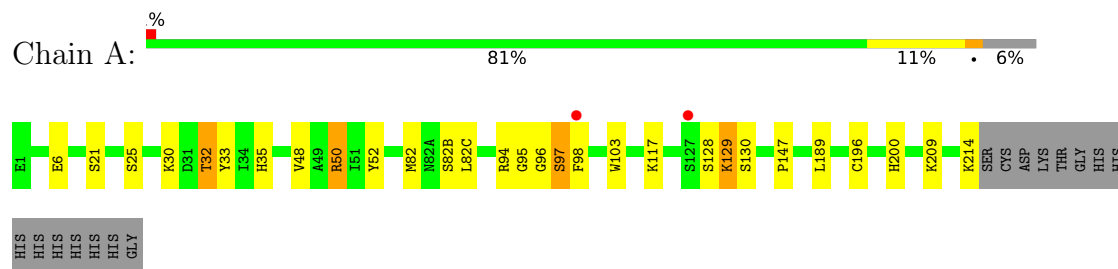
### 3 Residue-property plots [i](#)

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.

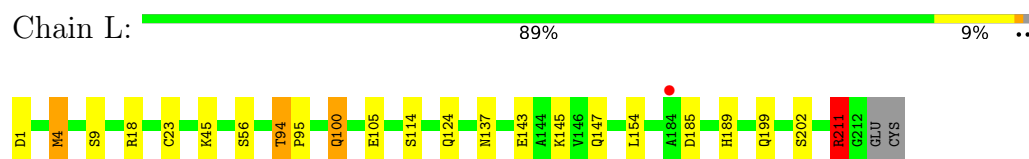
- Molecule 1: anti-VEGF-A Fab bH1 heavy chain



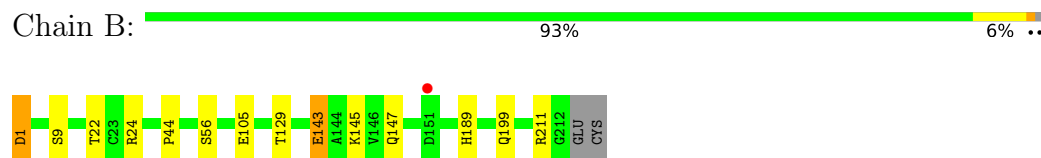
- Molecule 1: anti-VEGF-A Fab bH1 heavy chain



- Molecule 2: anti-VEGF-A Fab bH1 light chain



- Molecule 2: anti-VEGF-A Fab bH1 light chain



- Molecule 3: Isoform L-VEGF206 of Vascular endothelial growth factor A





● Molecule 3: Isoform L-VEGF206 of Vascular endothelial growth factor A





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.46Å 99.41Å 191.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.61 – 2.32 48.96 – 2.32	Depositor EDS
% Data completeness (in resolution range)	99.5 (95.61-2.32) 99.6 (48.96-2.32)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.58 (at 2.32Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.192 , 0.246 0.197 , 0.247	Depositor DCC
$R_{free}$ test set	3148 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.2	Xtriage
Anisotropy	0.333	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 35.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8668	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.63 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9847e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CL, 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	0.83	0/1705	0.90	2/2324 (0.1%)
1	H	0.79	0/1663	0.93	4/2267 (0.2%)
2	B	0.78	0/1722	0.87	1/2341 (0.0%)
2	L	0.82	0/1711	0.89	5/2327 (0.2%)
3	C	0.75	0/788	0.98	4/1062 (0.4%)
3	V	0.72	0/788	0.94	2/1062 (0.2%)
All	All	0.79	0/8377	0.91	18/11383 (0.2%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	50	ARG	NE-CZ-NH1	8.54	124.57	120.30
3	C	56	ARG	NE-CZ-NH1	-8.44	116.08	120.30
1	H	50	ARG	NE-CZ-NH2	-8.11	116.25	120.30
3	C	104	CYS	CA-CB-SG	-7.97	99.65	114.00
3	C	61	CYS	CA-CB-SG	-7.82	99.92	114.00
3	V	56	ARG	NE-CZ-NH2	7.61	124.10	120.30
3	C	56	ARG	NE-CZ-NH2	7.57	124.08	120.30
2	L	211	ARG	NE-CZ-NH1	7.18	123.89	120.30
1	A	50	ARG	NE-CZ-NH2	-6.51	117.04	120.30
3	V	56	ARG	NE-CZ-NH1	-6.32	117.14	120.30
2	L	154	LEU	CB-CG-CD2	-5.69	101.32	111.00
2	L	211	ARG	N-CA-C	5.68	126.33	111.00
1	H	83	ARG	NE-CZ-NH1	-5.67	117.47	120.30
1	A	50	ARG	NE-CZ-NH1	5.42	123.01	120.30
2	L	4	MET	CG-SD-CE	5.35	108.76	100.20
2	L	211	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	H	83	ARG	NE-CZ-NH2	5.10	122.85	120.30
2	B	1	ASP	CB-CG-OD2	5.05	122.84	118.30

There are no chirality outliers.

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	1663	0	1629	22	0
1	H	1622	0	1586	8	0
2	B	1678	0	1632	4	0
2	L	1670	0	1619	13	0
3	C	770	0	732	8	0
3	V	770	0	732	10	0
4	B	4	0	6	0	0
4	L	4	0	6	1	0
5	A	1	0	0	0	0
6	A	109	0	0	2	0
6	B	127	0	0	2	0
6	C	30	0	0	1	0
6	H	96	0	0	0	0
6	L	106	0	0	2	0
6	V	18	0	0	0	0
All	All	8668	0	7942	56	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 3.

All (56) 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:L:100:GLN:HG3	6:L:418:HOH:O	1.74	0.87
1:H:50:ARG:HH22	2:L:94:THR:HG21	1.42	0.83
1:A:32:THR:HG22	1:A:97:SER:CA	2.11	0.80
1:A:32:THR:CG2	1:A:97:SER:HA	2.11	0.80
1:A:33:TYR:CD2	1:A:50:ARG:HD3	2.22	0.75
2:L:45:LYS:HE2	4:L:301:EDO:O1	1.87	0.74
1:A:32:THR:HG22	1:A:97:SER:HA	1.66	0.73
1:A:32:THR:CG2	1:A:95:GLY:O	2.38	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:THR:HG21	1:A:95:GLY:O	1.92	0.70
1:A:32:THR:HG22	1:A:97:SER:N	2.10	0.67
1:A:30:LYS:HE3	6:A:498:HOH:O	1.94	0.66
1:H:50:ARG:NH2	2:L:94:THR:HG21	2.10	0.65
1:A:35:HIS:CE1	1:A:50:ARG:HG3	2.35	0.61
1:A:32:THR:HG23	1:A:97:SER:HA	1.82	0.60
3:C:61:CYS:O	3:C:62:ASN:ND2	2.35	0.60
1:H:33:TYR:CD2	1:H:50:ARG:HD2	2.38	0.58
1:A:32:THR:CG2	1:A:96:GLY:C	2.72	0.58
1:A:52:TYR:CE1	1:A:98:PHE:CD2	2.93	0.56
2:L:189:HIS:O	2:L:211:ARG:HD3	2.05	0.56
2:B:189:HIS:O	2:B:211:ARG:NH1	2.40	0.55
2:L:94:THR:HG23	3:V:87:GLN:HA	1.89	0.55
2:B:24:ARG:HD2	6:B:484:HOH:O	2.08	0.53
1:A:147:PRO:O	1:A:200:HIS:HE1	1.92	0.53
1:A:50:ARG:HD2	6:A:467:HOH:O	2.07	0.53
3:V:79:GLN:HG3	3:C:17:PHE:N	2.24	0.52
3:C:44:GLU:HG2	3:C:84:LYS:HE2	1.91	0.52
1:H:52:TYR:CE2	1:H:98:PHE:CE1	3.00	0.49
1:A:32:THR:CG2	1:A:97:SER:N	2.74	0.49
1:H:122:PHE:CE1	2:L:124:GLN:HG3	2.49	0.48
2:L:18:ARG:NE	6:L:403:HOH:O	2.40	0.47
3:V:103:GLU:OE2	3:V:105:ARG:NH1	2.46	0.47
1:A:52:TYR:HE1	1:A:98:PHE:CD2	2.32	0.47
3:V:79:GLN:HG2	3:C:15:VAL:O	2.15	0.47
3:C:56:ARG:NH2	3:C:97:LEU:O	2.43	0.46
1:A:32:THR:CG2	1:A:97:SER:CA	2.79	0.46
1:H:6:GLU:HA	1:H:21:SER:O	2.16	0.46
3:V:56:ARG:NH2	3:V:97:LEU:O	2.45	0.46
1:A:32:THR:HG21	1:A:96:GLY:C	2.35	0.45
1:A:6:GLU:HA	1:A:21:SER:O	2.15	0.45
3:V:69:VAL:HB	3:V:70:PRO:HD2	1.99	0.45
3:V:23:ARG:HD2	6:C:229:HOH:O	2.16	0.45
3:C:69:VAL:HB	3:C:70:PRO:HD2	1.98	0.44
1:H:82:MET:HB3	1:H:82(C):LEU:HD21	1.99	0.44
1:A:82:MET:HB3	1:A:82(C):LEU:HD21	2.00	0.43
1:A:52:TYR:CE1	1:A:98:PHE:CE2	3.07	0.42
3:V:35:ILE:HD11	3:V:52:VAL:HG13	2.02	0.42
3:C:21:TYR:OH	3:C:62:ASN:ND2	2.53	0.42
2:L:94:THR:HG23	3:V:87:GLN:O	2.20	0.42
3:C:35:ILE:HD11	3:C:52:VAL:HG13	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:4:MET:HE3	2:L:23:CYS:SG	2.60	0.41
2:B:143:GLU:HB3	6:B:466:HOH:O	2.20	0.41
2:L:94:THR:HA	2:L:95:PRO:C	2.40	0.41
1:H:164:HIS:CD2	2:L:137:ASN:HD21	2.39	0.41
2:L:4:MET:CE	2:L:23:CYS:SG	3.09	0.41
3:V:27:HIS:HB2	3:V:28:PRO:HD2	2.02	0.40
1:A:103:TRP:CE3	2:B:44:PRO:HD2	2.56	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	219/236 (93%)	213 (97%)	5 (2%)	1 (0%)	29	35
1	H	211/236 (89%)	205 (97%)	4 (2%)	2 (1%)	17	19
2	B	215/218 (99%)	211 (98%)	4 (2%)	0	100	100
2	L	214/218 (98%)	209 (98%)	4 (2%)	1 (0%)	29	35
3	C	93/116 (80%)	90 (97%)	2 (2%)	1 (1%)	14	15
3	V	93/116 (80%)	89 (96%)	2 (2%)	2 (2%)	6	5
All	All	1045/1140 (92%)	1017 (97%)	21 (2%)	7 (1%)	22	26

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	127	SER
2	L	211	ARG
3	V	63	ASP
1	A	129	LYS
3	V	26	CYS

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Mol	Chain	Res	Type
3	C	26	CYS
1	H	126	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	183/196 (93%)	169 (92%)	14 (8%)	13	16
1	H	178/196 (91%)	168 (94%)	10 (6%)	21	29
2	B	191/192 (100%)	181 (95%)	10 (5%)	23	32
2	L	190/192 (99%)	177 (93%)	13 (7%)	16	20
3	C	90/106 (85%)	82 (91%)	8 (9%)	9	11
3	V	90/106 (85%)	87 (97%)	3 (3%)	38	52
All	All	922/988 (93%)	864 (94%)	58 (6%)	18	24

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	25	SER
1	H	50	ARG
1	H	97	SER
1	H	115	SER
1	H	117	LYS
1	H	138	LEU
1	H	151	THR
1	H	189	LEU
1	H	196	CYS
1	H	209	LYS
2	L	1	ASP
2	L	9	SER
2	L	56	SER
2	L	94	THR
2	L	100	GLN
2	L	105	GLU

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Mol	Chain	Res	Type
2	L	114	SER
2	L	143	GLU
2	L	145	LYS
2	L	147	GLN
2	L	185	ASP
2	L	199	GLN
2	L	202	SER
3	V	24	SER
3	V	60	CYS
3	V	95	SER
1	A	25	SER
1	A	32	THR
1	A	48	VAL
1	A	82(B)	SER
1	A	94	ARG
1	A	97	SER
1	A	117	LYS
1	A	128	SER
1	A	129	LYS
1	A	130	SER
1	A	189	LEU
1	A	196	CYS
1	A	209	LYS
1	A	214	LYS
2	B	1	ASP
2	B	9	SER
2	B	22	THR
2	B	56	SER
2	B	105	GLU
2	B	129	THR
2	B	143	GLU
2	B	145	LYS
2	B	147	GLN
2	B	199	GLN
3	C	24	SER
3	C	60	CYS
3	C	63	ASP
3	C	64	GLU
3	C	95	SER
3	C	97	LEU
3	C	104	CYS
3	C	105	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	L	100	GLN
2	L	137	ASN
3	V	86	HIS
1	A	200	HIS
2	B	137	ASN
3	C	62	ASN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	EDO	L	301	-	3,3,3	0.85	0	2,2,2	0.23	0
4	EDO	B	301	-	3,3,3	0.47	0	2,2,2	0.99	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	L	301	-	-	0/1/1/1	-
4	EDO	B	301	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	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	L	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	A	221/236 (93%)	-0.32	2 (0%) 84 88	26, 41, 68, 112	0
1	H	215/236 (91%)	-0.28	3 (1%) 75 80	27, 43, 69, 107	0
2	B	216/218 (99%)	-0.09	1 (0%) 91 94	21, 38, 69, 88	0
2	L	216/218 (99%)	-0.02	1 (0%) 91 94	22, 42, 74, 85	0
3	C	95/116 (81%)	0.31	6 (6%) 20 26	36, 59, 99, 118	0
3	V	95/116 (81%)	0.19	1 (1%) 80 85	40, 57, 92, 105	0
All	All	1058/1140 (92%)	-0.10	14 (1%) 77 81	21, 44, 78, 118	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	99	TYR	5.3
3	C	103	GLU	3.7
3	C	65	GLY	3.3
3	C	62	ASN	3.2
3	C	104	CYS	3.1
1	H	214	LYS	2.8
1	A	127	SER	2.7
3	C	64	GLU	2.6
3	C	66	LEU	2.5
2	B	151	ASP	2.4
3	V	43	ILE	2.3
1	A	98	PHE	2.3
1	H	98	PHE	2.2
2	L	184	ALA	2.1

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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( $\text{\AA}^2$ )	Q<0.9
4	EDO	B	301	4/4	0.95	0.12	44,46,46,48	0
4	EDO	L	301	4/4	0.96	0.12	40,41,42,44	0
5	CL	A	301	1/1	0.97	0.09	57,57,57,57	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.