



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 6, 2023 – 08:03 PM EST

PDB ID : 5VRK  
Title : Crystal structure of SsoPox AsA6 mutant (F46L-C258A-W263M-I280T) - open form  
Authors : Hiblot, J.; Gotthard, G.; Jacquet, P.; Daude, D.; Bergonzi, C.; Chabriere, E.; Elias, M.  
Deposited on : 2017-05-10  
Resolution : 1.40 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  
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

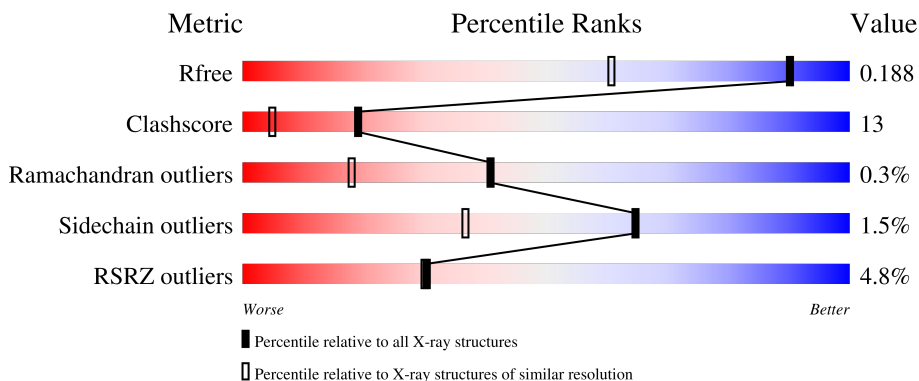
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.40 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	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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	A	314	
1	B	314	

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	GOL	A	405	-	-	X	-
4	GOL	B	405	-	-	X	-
4	GOL	B	406	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6002 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 Aryldialkylphosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	314	2638	1684	448	497	9	0	17	0
1	B	314	2658	1694	461	495	8	0	18	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	LEU	PHE	engineered mutation	UNP Q97VT7
A	258	ALA	CYS	engineered mutation	UNP Q97VT7
A	263	MET	TRP	engineered mutation	UNP Q97VT7
A	280	THR	ILE	engineered mutation	UNP Q97VT7
B	46	LEU	PHE	engineered mutation	UNP Q97VT7
B	258	ALA	CYS	engineered mutation	UNP Q97VT7
B	263	MET	TRP	engineered mutation	UNP Q97VT7
B	280	THR	ILE	engineered mutation	UNP Q97VT7

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		

- Molecule 3 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Co	0	0
			1	1		
3	B	1	Total	Co	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 12 6 6	0	1
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 8 4 4	0	1
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

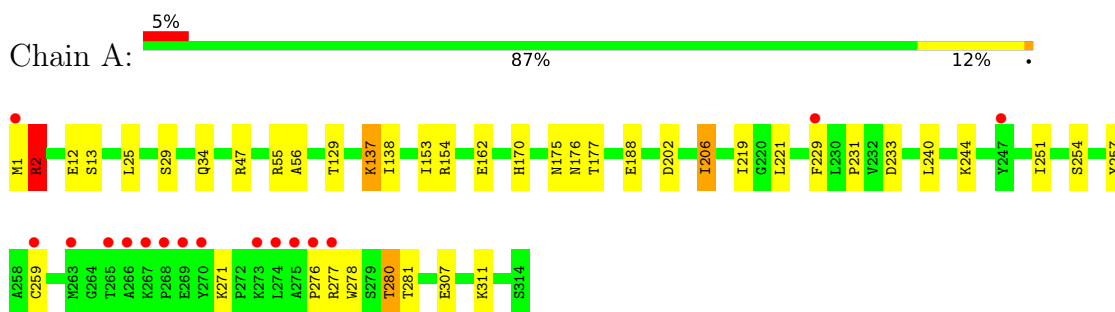
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	326	Total O 326 326	0	0
6	B	308	Total O 308 308	0	0

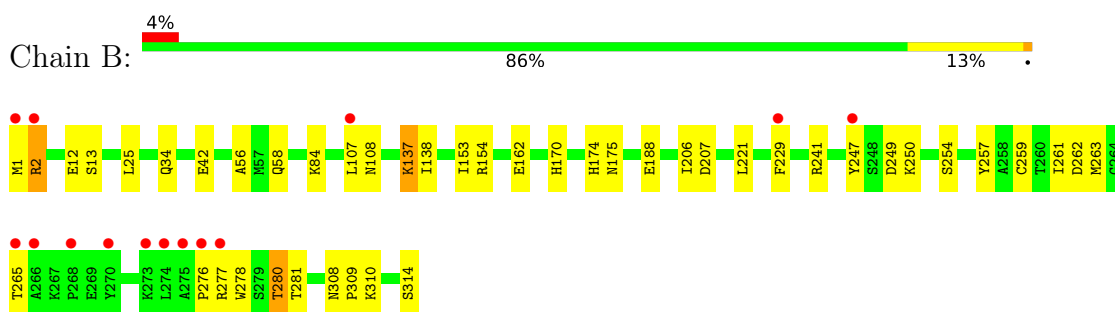
### 3 Residue-property plots [i](#)

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: Aryldialkylphosphatase



- Molecule 1: Aryldialkylphosphatase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.28Å 137.20Å 49.36Å 90.00° 98.70° 90.00°	Depositor
Resolution (Å)	45.97 – 1.40 45.97 – 1.40	Depositor EDS
% Data completeness (in resolution range)	96.1 (45.97-1.40) 95.7 (45.97-1.40)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.01 (at 1.40Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.139 , 0.175 0.162 , 0.188	Depositor DCC
$R_{free}$ test set	6096 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.1	Xtrriage
Anisotropy	0.043	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 39.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.457 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6002	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.01% 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: KCX, EDO, CO, FE2, GOL

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	0.60	0/2682	0.64	1/3617 (0.0%)
1	B	0.61	0/2702	0.66	1/3641 (0.0%)
All	All	0.60	0/5384	0.65	2/7258 (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	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	207	ASP	CB-CG-OD1	5.42	123.18	118.30
1	A	2	ARG	N-CA-CB	5.16	119.89	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	221	LEU	Peptide

### 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	A	2638	0	2670	65	0
1	B	2658	0	2699	79	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	24	0	32	7	0
4	B	24	0	32	12	0
5	A	12	0	18	1	0
5	B	8	0	12	1	0
6	A	326	0	0	13	0
6	B	308	0	0	21	0
All	All	6002	0	5463	141	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 13.

All (141) 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:B:263[A]:MET:CE	6:B:783:HOH:O	1.78	1.27
1:B:263[A]:MET:HE1	6:B:783:HOH:O	1.37	1.15
1:B:107[B]:LEU:HD12	1:B:108:ASN:ND2	1.74	1.02
1:A:47[B]:ARG:HB2	1:A:47[B]:ARG:NH2	1.76	1.00
1:A:34[B]:GLN:HG3	1:B:34[B]:GLN:NE2	1.78	0.97
1:A:34[B]:GLN:CD	1:B:34[B]:GLN:HE21	1.70	0.94
1:A:34[B]:GLN:OE1	1:B:34[B]:GLN:NE2	1.99	0.94
1:A:47[B]:ARG:NH1	6:A:501:HOH:O	2.07	0.85
1:B:247:TYR:CE2	4:B:406:GOL:H11	2.16	0.80
1:A:34[B]:GLN:CG	1:B:34[B]:GLN:NE2	2.45	0.79
1:B:2[A]:ARG:CZ	1:B:2[A]:ARG:HB2	2.12	0.78
1:B:263[A]:MET:HE3	6:B:783:HOH:O	1.54	0.77
1:A:206:ILE:HD13	1:A:206:ILE:H	1.49	0.77
1:A:47[B]:ARG:NH2	1:A:47[B]:ARG:CB	2.48	0.76
1:B:107[B]:LEU:HD13	1:B:108:ASN:N	2.01	0.76
1:B:262:ASP:HA	4:B:405:GOL:H12	1.66	0.76
1:A:34[B]:GLN:CG	1:B:34[B]:GLN:HE21	1.97	0.76
1:B:154[A]:ARG:NH1	1:B:188:GLU:OE2	2.18	0.76
4:B:405:GOL:H2	6:B:504:HOH:O	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:ASP:OD2	4:A:405:GOL:C3	2.35	0.75
1:A:2:ARG:HD2	1:A:13:SER:H	1.54	0.73
1:B:174:HIS:HE1	6:B:624:HOH:O	1.71	0.73
1:B:2[A]:ARG:CD	1:B:13:SER:H	2.02	0.72
1:A:34[B]:GLN:HG3	1:B:34[B]:GLN:HE22	1.54	0.72
1:A:47[B]:ARG:HH21	1:A:47[B]:ARG:CG	1.99	0.72
1:A:2:ARG:CD	1:A:13:SER:H	2.03	0.72
1:A:221[B]:LEU:HD23	1:A:251:ILE:HG23	1.71	0.72
1:A:129:THR:HG22	4:A:406:GOL:H11	1.72	0.71
1:A:154:ARG:NH2	1:A:188:GLU:OE2	2.23	0.71
1:A:202:ASP:OD2	4:A:405:GOL:H31	1.89	0.71
1:B:162[B]:GLU:HG2	6:B:568:HOH:O	1.90	0.70
1:B:249:ASP:OD1	4:B:406:GOL:H32	1.91	0.70
1:B:247:TYR:CD2	4:B:406:GOL:H11	2.28	0.69
1:A:47[B]:ARG:HH21	1:A:47[B]:ARG:HG3	1.58	0.69
1:A:221[B]:LEU:HD22	1:A:221[B]:LEU:N	2.08	0.68
1:B:107[B]:LEU:HD12	1:B:108:ASN:CG	2.12	0.68
1:A:162[B]:GLU:HG2	6:A:606:HOH:O	1.92	0.68
1:B:2[A]:ARG:HD2	1:B:13:SER:H	1.58	0.68
1:A:34[B]:GLN:OE1	1:B:34[B]:GLN:HG3	1.94	0.67
1:A:307[A]:GLU:OE2	6:A:502:HOH:O	2.13	0.67
1:B:261:ILE:HG12	1:B:263[B]:MET:HG2	1.77	0.66
1:B:107[B]:LEU:CD1	1:B:108:ASN:CG	2.63	0.66
1:A:34[B]:GLN:OE1	6:A:503:HOH:O	2.14	0.66
1:A:47[B]:ARG:HB2	1:A:47[B]:ARG:HH21	1.59	0.66
1:A:231:PRO:HG3	1:A:271:LYS:HZ3	1.61	0.65
1:A:240:LEU:HG	1:A:244:LYS:HE3	1.77	0.65
1:B:2[A]:ARG:HG2	1:B:2[A]:ARG:HH11	1.61	0.64
1:A:221[B]:LEU:HD22	1:A:221[B]:LEU:H	1.60	0.64
1:A:1[A]:MET:HG3	1:A:12:GLU:HG2	1.80	0.63
1:B:42[A]:GLU:OE1	6:B:501:HOH:O	2.13	0.63
1:A:206:ILE:HD13	1:A:206:ILE:N	2.13	0.63
1:B:310[B]:LYS:HB3	1:B:310[B]:LYS:NZ	2.14	0.63
1:B:249:ASP:OD1	4:B:406:GOL:C3	2.48	0.62
1:B:107[B]:LEU:CD1	1:B:108:ASN:ND2	2.58	0.61
1:B:1:MET:H2	1:B:12:GLU:HG2	1.65	0.61
1:B:265:THR:HG21	6:B:758:HOH:O	1.99	0.61
1:B:262:ASP:CA	4:B:405:GOL:H12	2.29	0.61
1:A:138[B]:ILE:HD13	6:A:539:HOH:O	2.01	0.61
1:B:138[A]:ILE:HD13	6:B:530:HOH:O	2.01	0.60
1:A:175[B]:ASN:O	1:A:175[B]:ASN:OD1	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:ILE:H	1:A:206:ILE:CD1	2.13	0.60
1:B:34[B]:GLN:NE2	6:B:505:HOH:O	2.35	0.60
1:B:175[B]:ASN:O	5:B:404:EDO:O2	2.20	0.59
1:B:58[A]:GLN:HG3	6:B:533:HOH:O	2.02	0.59
1:A:276:PRO:HA	6:A:609:HOH:O	2.03	0.58
1:B:2[A]:ARG:HH11	1:B:2[A]:ARG:CG	2.15	0.58
1:A:280[A]:THR:HG22	1:A:281:THR:HG23	1.86	0.57
1:B:2[B]:ARG:NH1	1:B:314:SER:OXT	2.37	0.57
1:A:280[A]:THR:O	1:A:280[A]:THR:HG23	2.04	0.57
1:A:47[B]:ARG:CB	1:A:47[B]:ARG:CZ	2.82	0.56
1:A:175[B]:ASN:O	1:A:175[B]:ASN:CG	2.40	0.56
1:B:56:ALA:HB2	1:B:280[A]:THR:CG2	2.36	0.56
1:B:280[A]:THR:HG22	1:B:281:THR:HG23	1.88	0.56
1:A:47[B]:ARG:CB	1:A:47[B]:ARG:HH21	2.12	0.56
1:B:276:PRO:HA	6:B:651:HOH:O	2.06	0.55
1:B:1:MET:N	1:B:12:GLU:HG2	2.21	0.55
1:A:175[B]:ASN:O	1:A:177:THR:N	2.40	0.55
1:A:56:ALA:HB2	1:A:280[A]:THR:CG2	2.37	0.54
1:A:25:LEU:O	1:A:259:CYS:HB2	2.08	0.54
1:B:310[A]:LYS:HE2	6:B:745:HOH:O	2.07	0.54
1:B:25:LEU:O	1:B:259:CYS:HB2	2.08	0.54
1:B:2[A]:ARG:HD2	1:B:13:SER:OG	2.07	0.53
1:B:250:LYS:HG3	4:B:406:GOL:H12	1.90	0.53
1:A:47[B]:ARG:HB2	1:A:47[B]:ARG:CZ	2.38	0.53
1:A:138[A]:ILE:HD12	1:A:153:ILE:HG12	1.89	0.53
1:B:138[B]:ILE:HD12	1:B:153:ILE:HG12	1.90	0.53
1:A:29[B]:SER:OG	6:A:504:HOH:O	2.17	0.52
1:A:229:PHE:HD1	4:A:405:GOL:H12	1.75	0.52
1:B:280[A]:THR:O	1:B:280[A]:THR:HG23	2.09	0.52
1:A:2:ARG:HG3	1:A:12:GLU:HA	1.90	0.52
1:B:2[A]:ARG:CD	1:B:13:SER:N	2.73	0.52
1:B:310[A]:LYS:CE	6:B:745:HOH:O	2.57	0.52
1:A:34[B]:GLN:OE1	1:B:34[B]:GLN:CG	2.57	0.52
4:B:403:GOL:H11	6:B:624:HOH:O	2.11	0.50
1:A:129:THR:CG2	4:A:406:GOL:H11	2.40	0.50
1:A:2:ARG:CD	1:A:13:SER:N	2.75	0.50
1:A:257:TYR:CE2	1:A:259:CYS:HA	2.46	0.49
1:B:2[A]:ARG:HD3	1:B:13:SER:N	2.28	0.49
1:B:2[A]:ARG:CG	1:B:2[A]:ARG:NH1	2.70	0.49
1:A:175[B]:ASN:OD1	1:A:175[B]:ASN:C	2.51	0.48
1:B:257:TYR:CE2	1:B:259:CYS:HA	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:310[B]:LYS:HB3	1:B:310[B]:LYS:HZ3	1.78	0.47
1:A:229:PHE:CD1	4:A:405:GOL:H12	2.49	0.47
1:B:262:ASP:CB	4:B:405:GOL:H12	2.44	0.47
1:A:56:ALA:HB2	1:A:280[A]:THR:HG21	1.96	0.47
1:B:2[A]:ARG:HG3	1:B:12:GLU:HA	1.95	0.47
1:B:2[B]:ARG:HB2	6:B:767:HOH:O	2.15	0.46
1:B:310[B]:LYS:NZ	1:B:310[B]:LYS:CB	2.79	0.46
1:A:231:PRO:HB2	1:A:233[A]:ASP:OD1	2.15	0.46
1:B:2[A]:ARG:CZ	1:B:2[A]:ARG:CB	2.82	0.46
4:B:405:GOL:C2	6:B:504:HOH:O	2.53	0.46
1:B:84:LYS:HD2	6:B:643:HOH:O	2.16	0.45
1:B:2[A]:ARG:HD2	1:B:13:SER:CB	2.46	0.45
1:B:206:ILE:CD1	1:B:241[B]:ARG:HG2	2.46	0.45
1:A:2:ARG:HD3	1:A:13:SER:N	2.31	0.45
1:B:56:ALA:HB2	1:B:280[A]:THR:HG21	1.98	0.45
1:A:307[A]:GLU:HG3	6:A:502:HOH:O	2.17	0.45
1:B:107[B]:LEU:HD13	1:B:107[B]:LEU:C	2.37	0.45
1:B:277[B]:ARG:NH1	1:B:278:TRP:O	2.50	0.44
1:B:257:TYR:HA	1:B:278:TRP:CZ2	2.53	0.44
1:B:84:LYS:HG3	6:B:606:HOH:O	2.17	0.43
1:B:137:KCX:OQ2	1:B:170:HIS:HB2	2.18	0.43
4:A:405:GOL:H32	6:A:544:HOH:O	2.17	0.43
1:A:206:ILE:HD13	6:A:685:HOH:O	2.17	0.43
1:A:221[B]:LEU:N	1:A:221[B]:LEU:CD2	2.79	0.43
1:A:138[B]:ILE:C	1:A:138[B]:ILE:HD12	2.39	0.42
1:A:137:KCX:OQ2	1:A:170:HIS:HB2	2.19	0.42
1:A:257:TYR:HA	1:A:278:TRP:CZ2	2.55	0.42
1:B:1:MET:H2	1:B:12:GLU:CG	2.29	0.42
1:B:229:PHE:CD1	4:B:403:GOL:H2	2.54	0.41
1:B:308:ASN:HB2	1:B:309:PRO:HD3	2.03	0.41
1:A:219:ILE:O	1:A:221[B]:LEU:HD22	2.19	0.41
1:B:138[A]:ILE:HD12	1:B:138[A]:ILE:C	2.41	0.41
1:B:277[A]:ARG:HD3	6:B:524:HOH:O	2.21	0.41
1:B:2[B]:ARG:NH2	1:B:13:SER:OG	2.54	0.41
1:A:55[C]:ARG:HG3	6:A:527:HOH:O	2.19	0.41
1:B:58[A]:GLN:CG	6:B:533:HOH:O	2.63	0.41
1:B:206:ILE:CD1	1:B:241[A]:ARG:CG	2.99	0.41
1:A:311:LYS:HG3	6:A:502:HOH:O	2.20	0.40
5:A:404[B]:EDO:H21	6:A:754:HOH:O	2.20	0.40
1:B:206:ILE:CD1	1:B:241[A]:ARG:HG2	2.50	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	327/314 (104%)	316 (97%)	9 (3%)	2 (1%)	25	7
1	B	329/314 (105%)	321 (98%)	8 (2%)	0	100	100
All	All	656/628 (104%)	637 (97%)	17 (3%)	2 (0%)	41	18

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	ASN
1	A	2	ARG

### 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	288/271 (106%)	282 (98%)	6 (2%)	53	21
1	B	289/271 (107%)	284 (98%)	5 (2%)	60	31
All	All	577/542 (106%)	566 (98%)	11 (2%)	65	25

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	206	ILE
1	A	254	SER
1	A	277	ARG

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Mol	Chain	Res	Type
1	A	280[A]	THR
1	A	280[B]	THR
1	B	2[A]	ARG
1	B	2[B]	ARG
1	B	254	SER
1	B	280[A]	THR
1	B	280[B]	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	108	ASN
1	B	174	HIS
1	B	294	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](#)

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	KCX	B	137	3,2,1	9,11,12	0.99	1 (11%)	5,12,14	0.65	0
1	KCX	A	137	3,2,1	9,11,12	2.08	2 (22%)	5,12,14	1.63	1 (20%)

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	KCX	B	137	3,2,1	-	0/9/10/12	-
1	KCX	A	137	3,2,1	-	0/9/10/12	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	137	KCX	OQ1-CX	5.46	1.31	1.21
1	A	137	KCX	CX-NZ	-2.70	1.30	1.35
1	B	137	KCX	CX-NZ	-2.50	1.30	1.35

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	KCX	OQ1-CX-NZ	-3.61	119.36	124.96

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
1	B	137	KCX	1	0
1	A	137	KCX	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 4 are monoatomic - leaving 13 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	GOL	B	403	-	5,5,5	0.38	0	5,5,5	0.26	0
4	GOL	B	407	-	5,5,5	0.49	0	5,5,5	0.47	0
4	GOL	A	403[B]	-	5,5,5	0.41	0	5,5,5	0.26	0
5	EDO	B	404	-	3,3,3	0.54	0	2,2,2	0.20	0
5	EDO	B	408	3	3,3,3	0.60	0	2,2,2	0.50	0
5	EDO	A	404[B]	-	3,3,3	0.45	0	2,2,2	0.33	0
5	EDO	A	404[A]	-	3,3,3	0.54	0	2,2,2	0.23	0
4	GOL	A	405	-	5,5,5	0.21	0	5,5,5	0.46	0
5	EDO	A	407	3	3,3,3	0.47	0	2,2,2	0.75	0
4	GOL	A	403[A]	-	5,5,5	0.47	0	5,5,5	0.26	0
4	GOL	B	406	-	5,5,5	0.27	0	5,5,5	0.45	0
4	GOL	B	405	-	5,5,5	0.31	0	5,5,5	0.72	0
4	GOL	A	406	-	5,5,5	0.36	0	5,5,5	0.53	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	GOL	B	403	-	-	0/4/4/4	-
4	GOL	B	407	-	-	0/4/4/4	-
4	GOL	A	403[B]	-	-	0/4/4/4	-
5	EDO	B	404	-	-	1/1/1/1	-
5	EDO	B	408	3	-	0/1/1/1	-
5	EDO	A	404[B]	-	-	1/1/1/1	-
5	EDO	A	404[A]	-	-	0/1/1/1	-
4	GOL	A	405	-	-	2/4/4/4	-
5	EDO	A	407	3	-	1/1/1/1	-
4	GOL	A	403[A]	-	-	2/4/4/4	-
4	GOL	B	406	-	-	2/4/4/4	-
4	GOL	B	405	-	-	4/4/4/4	-
4	GOL	A	406	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	405	GOL	C1-C2-C3-O3
4	A	406	GOL	C1-C2-C3-O3
4	B	405	GOL	C1-C2-C3-O3
4	B	406	GOL	O1-C1-C2-C3
4	A	403[A]	GOL	O1-C1-C2-C3
4	B	405	GOL	O1-C1-C2-C3
4	A	405	GOL	O2-C2-C3-O3
4	B	405	GOL	O2-C2-C3-O3
4	B	406	GOL	O1-C1-C2-O2
5	A	407	EDO	O1-C1-C2-O2
4	A	406	GOL	O2-C2-C3-O3
5	B	404	EDO	O1-C1-C2-O2
5	A	404[B]	EDO	O1-C1-C2-O2
4	B	405	GOL	O1-C1-C2-O2
4	A	403[A]	GOL	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	403	GOL	2	0
5	B	404	EDO	1	0
5	A	404[B]	EDO	1	0
4	A	405	GOL	5	0
4	B	406	GOL	5	0
4	B	405	GOL	5	0
4	A	406	GOL	2	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	313/314 (99%)	-0.10	16 (5%) 28 27	9, 17, 42, 72	0
1	B	313/314 (99%)	-0.08	14 (4%) 33 33	9, 16, 40, 87	0
All	All	626/628 (99%)	-0.09	30 (4%) 30 30	9, 17, 40, 87	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	275	ALA	5.6
1	A	274	LEU	5.5
1	B	266	ALA	5.5
1	B	1	MET	5.4
1	A	275	ALA	5.0
1	A	266	ALA	4.6
1	A	259	CYS	4.4
1	A	268	PRO	4.3
1	B	273	LYS	3.7
1	A	265	THR	3.5
1	A	276	PRO	3.5
1	A	229	PHE	3.5
1	A	267	LYS	3.4
1	A	273	LYS	3.4
1	B	276	PRO	3.3
1	B	229	PHE	3.3
1	B	268	PRO	2.9
1	A	1[A]	MET	2.9
1	A	269	GLU	2.8
1	A	270	TYR	2.6
1	B	277[A]	ARG	2.4
1	B	270	TYR	2.4
1	B	107[A]	LEU	2.4
1	B	274	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	2[A]	ARG	2.3
1	A	277	ARG	2.2
1	A	263[A]	MET	2.2
1	B	247	TYR	2.2
1	A	247	TYR	2.1
1	B	265	THR	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	KCX	B	137	12/13	0.97	0.07	9,11,12,13	0
1	KCX	A	137	12/13	0.98	0.06	10,10,13,13	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
5	EDO	A	404[A]	4/4	0.68	0.15	37,53,55,69	4
5	EDO	A	404[B]	4/4	0.68	0.15	32,47,48,54	4
4	GOL	B	405	6/6	0.80	0.25	27,28,31,37	6
5	EDO	B	404	4/4	0.81	0.11	26,36,44,46	0
4	GOL	B	406	6/6	0.86	0.12	36,37,47,64	0
4	GOL	B	403	6/6	0.90	0.16	19,35,51,52	0
5	EDO	A	407	4/4	0.91	0.11	21,23,29,31	0
4	GOL	A	406	6/6	0.91	0.14	25,43,45,50	0
5	EDO	B	408	4/4	0.91	0.12	23,24,28,29	0
4	GOL	B	407	6/6	0.93	0.09	17,20,27,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	A	403[A]	6/6	0.95	0.09	18,20,25,32	6
4	GOL	A	403[B]	6/6	0.95	0.09	17,20,20,23	6
4	GOL	A	405	6/6	0.96	0.12	22,46,49,54	0
3	CO	A	402	1/1	0.99	0.05	13,13,13,13	0
3	CO	B	402	1/1	0.99	0.05	13,13,13,13	0
2	FE2	A	401	1/1	0.99	0.06	10,10,10,10	0
2	FE2	B	401	1/1	1.00	0.06	10,10,10,10	0

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

There are no such residues in this entry.