



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3K42  
Title : Crystal structure of sCD-MPR mutant E19Q/K137M pH 7.0  
Authors : Olson, L.J.; Sun, G.; Bohnsack, R.N.; Peterson, F.C.; Dahms, N.M.; Kim, J.J.P.  
Deposited on : 2009-10-05  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

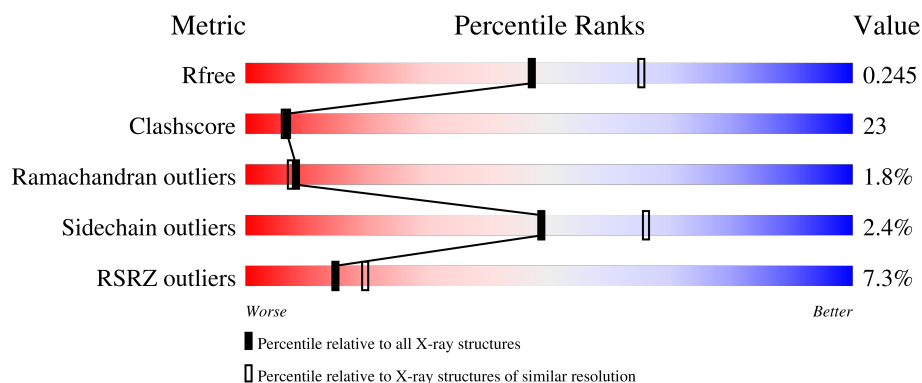
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	154	<div> <div>7%</div> <div> <div></div> <div>62%</div> <div>26%</div> <div>•• 8%</div> </div> </div>
1	B	154	<div> <div>6%</div> <div> <div></div> <div>58%</div> <div>28%</div> <div>8% • 5%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2536 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 Cation-dependent mannose-6-phosphate receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1115	693	195	217	10			
1	B	146	Total	C	N	O	S	0	0	0
			1153	714	203	225	11			

There are 12 discrepancies between the modelled and reference sequences:

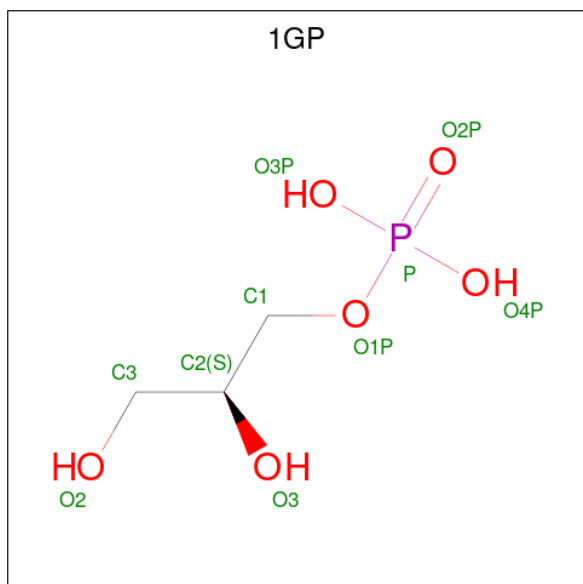
Chain	Residue	Modelled	Actual	Comment	Reference
A	19	GLN	GLU	engineered mutation	UNP P11456
A	31	GLN	ASN	engineered mutation	UNP P11456
A	57	GLN	ASN	engineered mutation	UNP P11456
A	68	GLN	ASN	engineered mutation	UNP P11456
A	87	GLN	ASN	engineered mutation	UNP P11456
A	137	MET	LYS	engineered mutation	UNP P11456
B	19	GLN	GLU	engineered mutation	UNP P11456
B	31	GLN	ASN	engineered mutation	UNP P11456
B	57	GLN	ASN	engineered mutation	UNP P11456
B	68	GLN	ASN	engineered mutation	UNP P11456
B	87	GLN	ASN	engineered mutation	UNP P11456
B	137	MET	LYS	engineered mutation	UNP P11456

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is SN-GLYCEROL-1-PHOSPHATE (three-letter code: 1GP) (formula:  $C_3H_9O_6P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			10	3	6	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

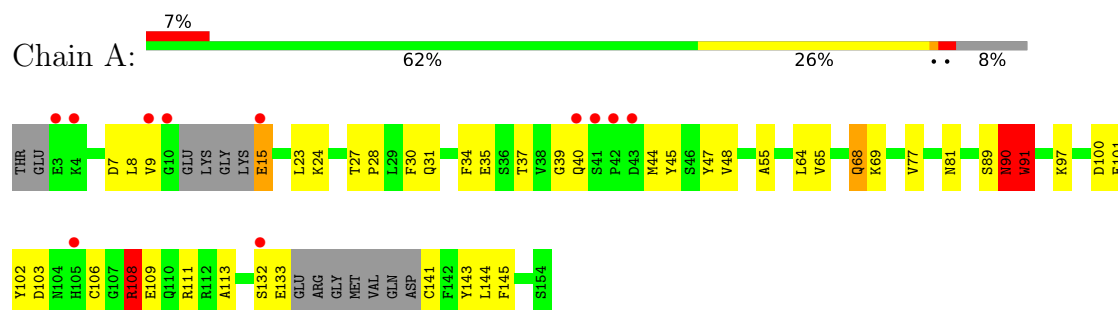
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	91	Total 91	O 91	0	0
5	B	89	Total 89	O 89	0	0

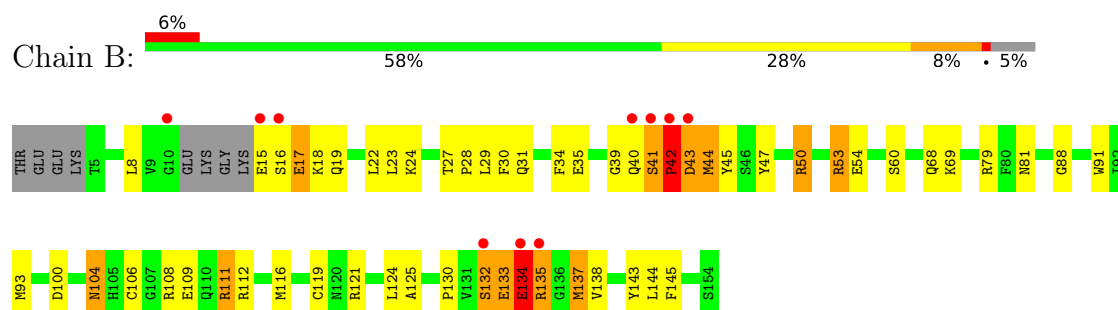
### 3 Residue-property plots [i](#)

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: Cation-dependent mannose-6-phosphate receptor



- Molecule 1: Cation-dependent mannose-6-phosphate receptor



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.58Å 102.58Å 100.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.27 – 2.30 36.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.3 (36.27-2.30) 96.5 (36.27-2.30)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.60 (at 2.29Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.228 , 0.249 0.222 , 0.245	Depositor DCC
$R_{free}$ test set	1530 reflections (6.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.1	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.003 for l,-k,h 0.016 for -l,-k,-h 0.020 for -h,-l,-k 0.004 for -h,l,k 0.048 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	2536	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, SO4, 1GP

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	0.46	0/1133	0.68	0/1518
1	B	0.97	7/1172 (0.6%)	1.07	13/1572 (0.8%)
All	All	0.77	7/2305 (0.3%)	0.90	13/3090 (0.4%)

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	0	3
1	B	0	3
All	All	0	6

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	41	SER	CB-OG	-8.94	1.30	1.42
1	B	133	GLU	C-N	8.25	1.53	1.34
1	B	39	GLY	C-N	6.31	1.48	1.34
1	B	41	SER	CA-CB	-6.23	1.43	1.52
1	B	42	PRO	CA-C	-6.21	1.40	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	135	ARG	NE-CZ-NH2	7.34	123.97	120.30
1	B	121	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	B	79	ARG	NE-CZ-NH2	6.33	123.47	120.30
1	B	108	ARG	NE-CZ-NH2	6.13	123.37	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	53	ARG	NE-CZ-NH2	6.05	123.33	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	ARG	Sidechain
1	A	15	GLU	Peptide
1	A	91	TRP	Mainchain
1	B	132	SER	Peptide
1	B	41	SER	Peptide,Mainchain

## 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	1115	0	1066	53	5
1	B	1153	0	1099	56	5
2	A	14	0	13	3	0
2	B	14	0	13	0	0
3	A	10	0	7	1	0
3	B	10	0	7	1	0
4	A	20	0	0	0	0
4	B	20	0	0	0	0
5	A	91	0	0	2	0
5	B	89	0	0	8	0
All	All	2536	0	2205	106	5

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 23.

The worst 5 of 106 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:40:GLN:O	1:B:43:ASP:O	1.64	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:16:SER:O	1:B:18:LYS:N	1.87	1.07
1:B:132:SER:HB2	1:B:133:GLU:O	1.73	0.88
1:B:27:THR:HG22	1:B:30:PHE:CE2	2.09	0.87
1:A:81:ASN:HD21	2:A:3001:NAG:C1	1.90	0.85

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:LYS:NZ	1:B:31:GLN:NE2[4_555]	0.94	1.26
1:A:24:LYS:NZ	1:B:31:GLN:CD[4_555]	1.53	0.67
1:A:24:LYS:CE	1:B:31:GLN:NE2[4_555]	1.77	0.43
1:A:24:LYS:NZ	1:B:31:GLN:OE1[4_555]	2.06	0.14
1:A:27:THR:OG1	1:B:27:THR:OG1[4_555]	2.06	0.14

## 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	135/154 (88%)	128 (95%)	5 (4%)	2 (2%)	10	10
1	B	142/154 (92%)	125 (88%)	14 (10%)	3 (2%)	7	5
All	All	277/308 (90%)	253 (91%)	19 (7%)	5 (2%)	8	7

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	43	ASP
1	A	91	TRP
1	B	17	GLU
1	B	42	PRO
1	A	90	ASN

### 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	124/135 (92%)	121 (98%)	3 (2%)	49	66
1	B	128/135 (95%)	125 (98%)	3 (2%)	50	67
All	All	252/270 (93%)	246 (98%)	6 (2%)	49	66

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	104	ASN
1	B	119	CYS
1	B	134	GLU
1	A	90	ASN
1	A	68	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	HIS
1	B	40	GLN
1	B	139	GLN
1	B	104	ASN
1	A	90	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

12 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
3	1GP	A	7000	-	9,9,9	0.84	0	11,12,12	1.10	1 (9%)
4	SO4	A	6000	-	4,4,4	0.25	0	6,6,6	0.07	0
4	SO4	A	6007	-	4,4,4	0.27	0	6,6,6	0.12	0
2	NAG	B	4001	1	14,14,15	0.49	0	17,19,21	0.80	1 (5%)
4	SO4	B	6006	-	4,4,4	0.30	0	6,6,6	0.09	0
4	SO4	B	6001	-	4,4,4	0.27	0	6,6,6	0.06	0
4	SO4	B	6005	-	4,4,4	0.26	0	6,6,6	0.04	0
3	1GP	B	7001	-	9,9,9	1.16	0	11,12,12	1.18	1 (9%)
4	SO4	A	6002	-	4,4,4	0.27	0	6,6,6	0.09	0
2	NAG	A	3001	-	14,14,15	0.49	0	17,19,21	0.70	0
4	SO4	B	6004	-	4,4,4	0.31	0	6,6,6	0.11	0
4	SO4	A	6003	-	4,4,4	0.24	0	6,6,6	0.17	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
2	NAG	B	4001	1	-	2/6/23/26	0/1/1/1
3	1GP	A	7000	-	-	0/8/8/8	-
2	NAG	A	3001	-	-	2/6/23/26	0/1/1/1
3	1GP	B	7001	-	-	0/8/8/8	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	7001	1GP	P-O1P-C1	-2.99	110.06	118.30
3	A	7000	1GP	P-O1P-C1	-2.77	110.66	118.30
2	B	4001	NAG	C2-N2-C7	-2.51	119.33	122.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3001	NAG	C8-C7-N2-C2
2	A	3001	NAG	O7-C7-N2-C2
2	B	4001	NAG	C8-C7-N2-C2
2	B	4001	NAG	O7-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	7000	1GP	1	0
3	B	7001	1GP	1	0
2	A	3001	NAG	3	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	141/154 (91%)	0.30	11 (7%) 13 17	14, 28, 54, 67	0
1	B	146/154 (94%)	0.32	10 (6%) 17 22	14, 25, 60, 80	0
All	All	287/308 (93%)	0.31	21 (7%) 15 20	14, 26, 60, 80	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	135	ARG	8.6
1	B	10	GLY	6.1
1	B	15	GLU	5.7
1	A	42	PRO	5.5
1	B	42	PRO	5.5

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

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

### 6.3 Carbohydrates [i](#)

There are no 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
2	NAG	A	3001	14/15	0.81	0.27	51,52,53,54	0
3	1GP	B	7001	10/10	0.82	0.21	49,52,53,53	0
4	SO4	A	6002	5/5	0.83	0.19	85,86,86,86	0
2	NAG	B	4001	14/15	0.89	0.27	42,43,44,45	0
4	SO4	B	6004	5/5	0.92	0.15	58,59,60,61	0
3	1GP	A	7000	10/10	0.93	0.18	38,41,43,44	0
4	SO4	B	6005	5/5	0.95	0.19	54,55,55,56	0
4	SO4	B	6001	5/5	0.97	0.14	47,48,48,48	0
4	SO4	A	6003	5/5	0.97	0.14	48,49,50,50	0
4	SO4	A	6007	5/5	0.97	0.22	66,67,68,68	0
4	SO4	A	6000	5/5	0.98	0.11	50,50,51,51	0
4	SO4	B	6006	5/5	0.98	0.19	54,55,56,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.