



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 13, 2020 – 05:55 PM BST

PDB ID : 2IHU
Title : Carboxyethylarginine synthase from Streptomyces clavuligerus: putative reaction intermediate complex
Authors : Caines, M.E.; Schofield, C.J.
Deposited on : 2006-09-27
Resolution : 2.05 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	FAILED
Xtriage (Phenix)	:	1.13
EDS	:	2.14.4.dev1
buster-report	:	FAILED
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)	:	2.14.4.dev1

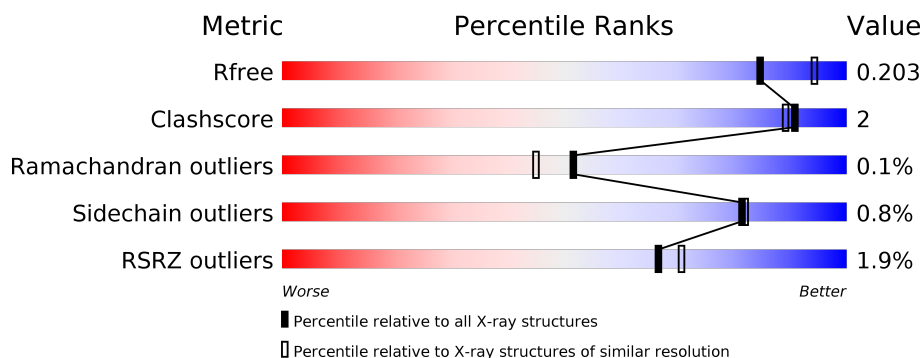
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	573	<div> <div>2%</div> <div> <div></div> <div>93%</div> <div></div> </div> <div>• •</div> </div>
1	B	573	<div> <div>%</div> <div> <div></div> <div>92%</div> <div></div> </div> <div>• •</div> </div>
1	C	573	<div> <div>2%</div> <div> <div></div> <div>94%</div> <div></div> </div> <div>• •</div> </div>
1	D	573	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div></div> </div> <div>• • •</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	TP8	C	600[A]	X	-	-	-
5	TAR	A	603	X	-	-	-
5	TAR	D	603	X	-	-	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 18287 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 Carboxyethylarginine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	562	Total	C	N	O	S	39	1	0
			4223	2679	728	802	14			
1	B	552	Total	C	N	O	S	37	3	0
			4168	2642	720	792	14			
1	C	551	Total	C	N	O	S	32	3	0
			4158	2636	719	790	13			
1	D	551	Total	C	N	O	S	53	3	0
			4162	2639	722	787	14			

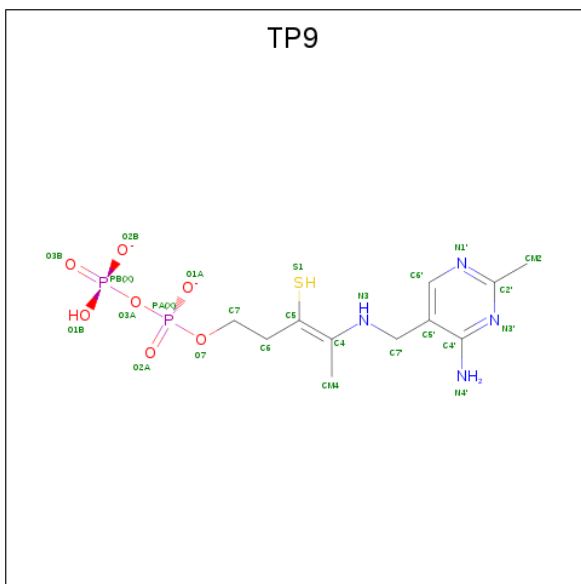
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

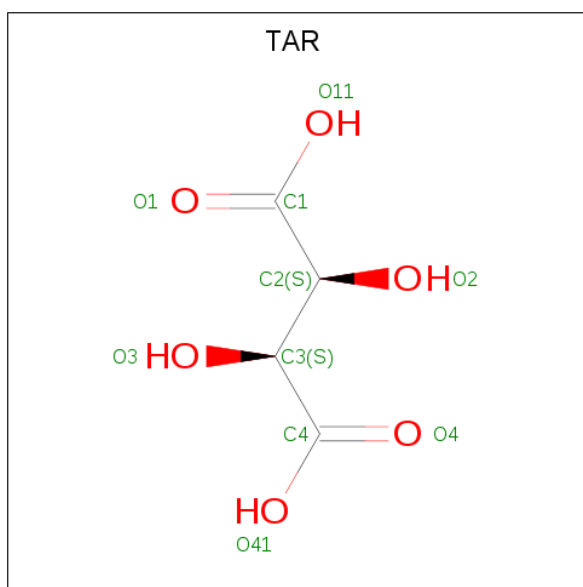
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	K	0	0
			1	1		
3	A	2	Total	K	0	0
			2	2		
3	D	1	Total	K	0	0
			1	1		
3	C	2	Total	K	0	0
			2	2		

- Molecule 4 is (3Z)-4-[[[(4-AMINO-2-METHYLPYRIMIDIN-5-YL)METHYL]AMINO}-3-MERCAPTOPENT-3-EN-1-YL TRIHYDROGEN DIPHOSPHATE (three-letter code: TP9) (formula: $C_{11}H_{18}N_4O_7P_2S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 25	C 11	N 4	O 7	P 2	S 1	0	0
4	B	1	Total 25	C 11	N 4	O 7	P 2	S 1	0	0
4	C	1	Total 25	C 11	N 4	O 7	P 2	S 1	0	1
4	D	1	Total 25	C 11	N 4	O 7	P 2	S 1	0	0

- Molecule 5 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: $\text{C}_4\text{H}_6\text{O}_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	4	6		
5	D	1	Total	C	O	0	0
			10	4	6		

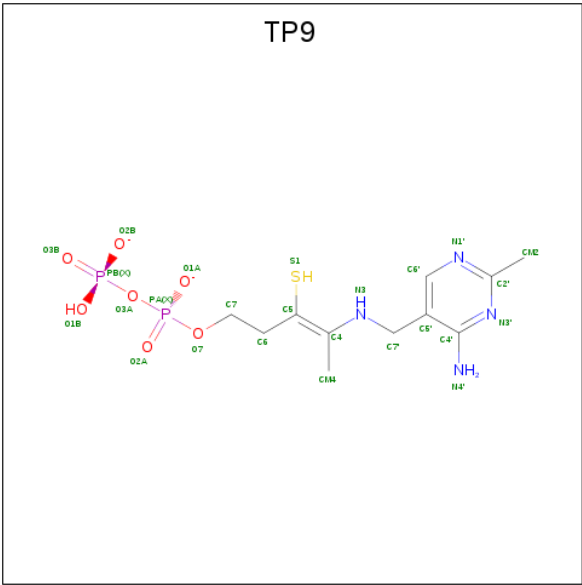
- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is 5-(2-{[HYDROXY(PHOSPHONOOXY)PHOSPHORYL]OXY}ETHYL)-2-

[(1Z)-1-HYDROXY-3-(PHOSPHONOOXY)PROP-1-EN-1-YL]-3-{[(4Z)-4-IMINO-2-METHYL-4,5-DIHYDROPYRIMIDIN-5-YL]METHYL}-4-METHYL-1,3-THIAZOL-3-IUM (three-letter code: TP9) (formula: C₁₁H₁₈N₄O₇P₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
7	C	1	35	15	4	12	3	1	0	1

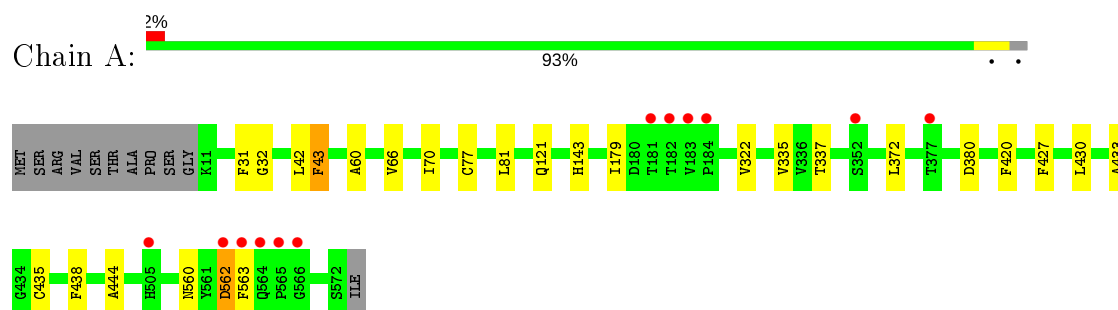
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	358	Total	O	0	0
			358	358		
8	B	377	Total	O	0	0
			377	377		
8	C	344	Total	O	0	0
			344	344		
8	D	326	Total	O	0	0
			326	326		

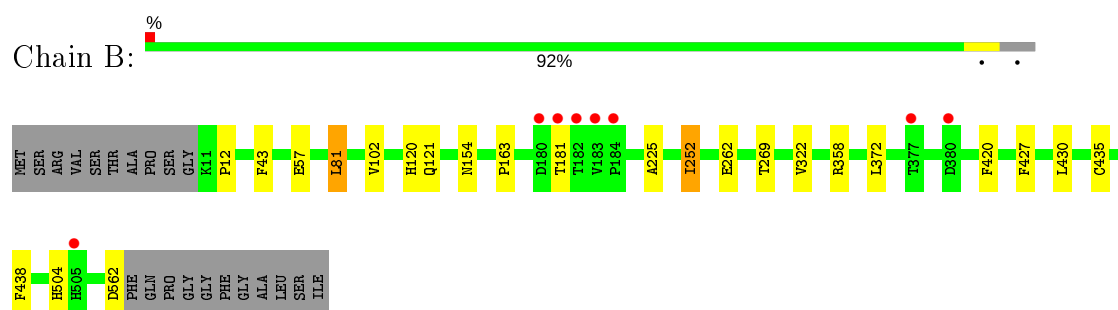
3 Residue-property plots [i](#)

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.

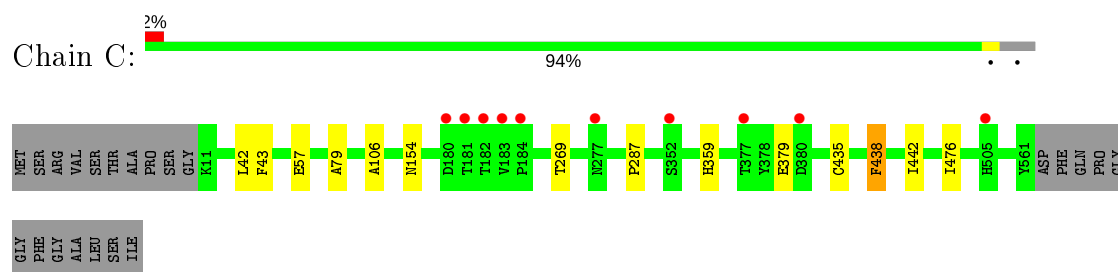
- Molecule 1: Carboxyethylarginine synthase



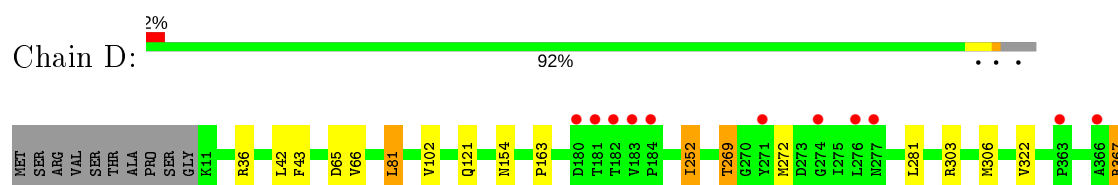
- Molecule 1: Carboxyethylarginine synthase

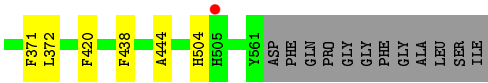


- Molecule 1: Carboxyethylarginine synthase



- Molecule 1: Carboxyethylarginine synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	119.69Å 127.86Å 197.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.13 – 2.05 27.95 – 2.05	Depositor EDS
% Data completeness (in resolution range)	97.0 (28.13-2.05) 97.0 (27.95-2.05)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.04Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.171 , 0.201 0.175 , 0.203	Depositor DCC
R_{free} test set	8830 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.581	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 51.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18287	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, MG, TAR, K, TP9, TP8

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	0.45	0/4322	0.56	0/5902
1	B	0.56	1/4270 (0.0%)	0.62	3/5832 (0.1%)
1	C	0.46	1/4260 (0.0%)	0.55	0/5819
1	D	0.48	1/4264 (0.0%)	0.57	0/5823
All	All	0.49	3/17116 (0.0%)	0.58	3/23376 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	562	ASP	CB-CG	22.08	1.98	1.51
1	D	367	ARG	CB-CG	-9.12	1.27	1.52
1	C	379	GLU	CB-CG	6.07	1.63	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	562	ASP	CA-CB-CG	-13.03	84.72	113.40
1	B	562	ASP	CB-CG-OD2	-10.70	108.67	118.30
1	B	562	ASP	CB-CG-OD1	10.06	127.36	118.30

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	A	4223	0	4177	17	0
1	B	4168	0	4133	18	0
1	C	4158	0	4125	9	0
1	D	4162	0	4136	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	A	25	0	17	1	0
4	B	25	0	17	0	0
4	C	25	0	34	4	0
4	D	25	0	17	1	0
5	A	10	0	4	0	0
5	D	10	0	4	0	0
6	B	6	0	8	0	0
7	C	35	0	0	0	0
8	A	358	0	0	0	0
8	B	377	0	0	0	0
8	C	344	0	0	0	0
8	D	326	0	0	1	0
All	All	18287	0	16672	55	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 2.

The worst 5 of 55 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:D:303[A]:ARG:HB2	1:D:306[A]:MET:HE3	1.66	0.78
1:D:372:LEU:HD21	1:D:420:PHE:HB3	1.70	0.73
1:B:12:PRO:HG2	1:B:181:THR:HG21	1.75	0.69
1:B:262[B]:GLU:CG	1:B:358:ARG:NH1	2.65	0.59
1:A:372:LEU:HD21	1:A:420:PHE:HB3	1.85	0.58

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	561/573 (98%)	548 (98%)	11 (2%)	2 (0%)	34	24
1	B	553/573 (96%)	539 (98%)	13 (2%)	1 (0%)	47	39
1	C	552/573 (96%)	538 (98%)	14 (2%)	0	100	100
1	D	552/573 (96%)	540 (98%)	12 (2%)	0	100	100
All	All	2218/2292 (97%)	2165 (98%)	50 (2%)	3 (0%)	51	45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	PHE
1	A	562	ASP
1	B	43	PHE

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	444/452 (98%)	441 (99%)	3 (1%)	84	84
1	B	440/452 (97%)	436 (99%)	4 (1%)	78	79
1	C	439/452 (97%)	437 (100%)	2 (0%)	88	89
1	D	439/452 (97%)	434 (99%)	5 (1%)	73	73
All	All	1762/1808 (98%)	1748 (99%)	14 (1%)	81	82

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	438	PHE
1	C	269	THR
1	D	252	ILE
1	B	269	THR
1	D	81	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	308	GLN
1	A	560	ASN
1	C	308	GLN
1	D	308	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

Mogul failed to run properly - this section is therefore empty.

5.5 Carbohydrates [i](#)

Mogul failed to run properly - this section is therefore empty.

5.6 Ligand geometry [i](#)

Mogul failed to run properly - this section is therefore empty.

5.7 Other polymers [i](#)

Mogul failed to run properly - this section is therefore empty.

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, 95th 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 ²)	Q<0.9
1	A	562/573 (98%)	-0.47	12 (2%) 63 67	11, 20, 32, 45	14 (2%)
1	B	552/573 (96%)	-0.48	8 (1%) 75 78	11, 19, 30, 45	11 (1%)
1	C	551/573 (96%)	-0.44	10 (1%) 68 71	11, 20, 30, 45	15 (2%)
1	D	551/573 (96%)	-0.40	12 (2%) 62 66	11, 20, 31, 45	19 (3%)
All	All	2216/2292 (96%)	-0.45	42 (1%) 66 71	11, 19, 31, 45	59 (2%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	VAL	7.2
1	C	182	THR	5.8
1	C	183	VAL	5.8
1	B	182	THR	5.2
1	D	182	THR	5.1

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, 95th 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(\AA^2)	Q<0.9
5	TAR	D	603	10/10	0.81	0.20	65,66,67,67	0
6	GOL	B	603	6/6	0.82	0.17	64,64,65,65	0
5	TAR	A	603	10/10	0.88	0.17	51,53,53,54	0
3	K	C	602	1/1	0.95	0.07	35,35,35,35	0
3	K	A	602	1/1	0.96	0.06	30,30,30,30	0
4	TP8	C	600[A]	35/35	0.96	0.12	13,17,31,31	35
3	K	D	602	1/1	0.96	0.08	32,32,32,32	0
4	TP9	D	600	25/25	0.97	0.08	15,25,29,33	0
4	TP9	C	600[B]	25/25	0.97	0.09	22,24,24,25	25
4	TP9	B	600	25/25	0.97	0.08	17,21,27,32	0
3	K	B	602	1/1	0.98	0.08	29,29,29,29	0
4	TP9	A	600	25/25	0.98	0.08	15,19,25,30	0
2	MG	B	601	1/1	0.99	0.10	11,11,11,11	0
3	K	C	1502	1/1	0.99	0.05	23,23,23,23	0
2	MG	D	601	1/1	0.99	0.06	12,12,12,12	0
2	MG	C	601	1/1	0.99	0.11	11,11,11,11	0
2	MG	A	601	1/1	0.99	0.09	8,8,8,8	0
3	K	A	1501	1/1	1.00	0.05	21,21,21,21	0

6.5 Other polymers ⓘ

There are no such residues in this entry.