



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 31, 2022 – 02:04 PM EDT

PDB ID : 7S2X
Title : Structure of SalC, a gamma-lactam-beta-lactone bicyclase for salinosporamide biosynthesis
Authors : Chen, P.Y.-T.; Trivella, D.B.B.; Bauman, K.D.; Moore, B.S.
Deposited on : 2021-09-04
Resolution : 2.85 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

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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
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)	:	2.27

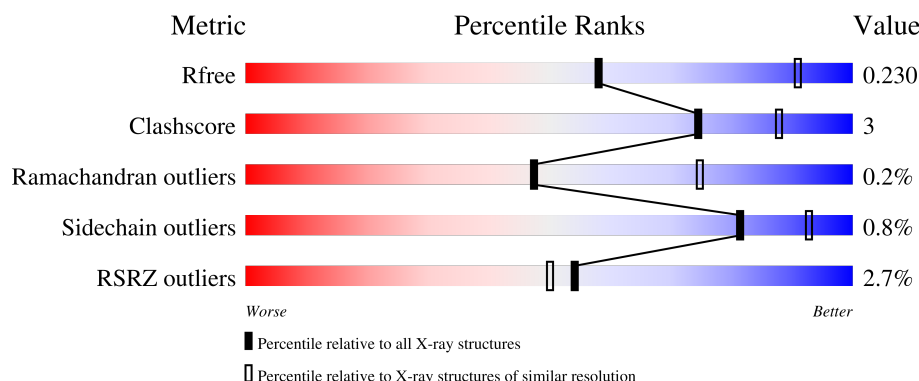
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 ≥ 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	597	
1	B	597	
1	C	597	
1	D	597	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17986 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.

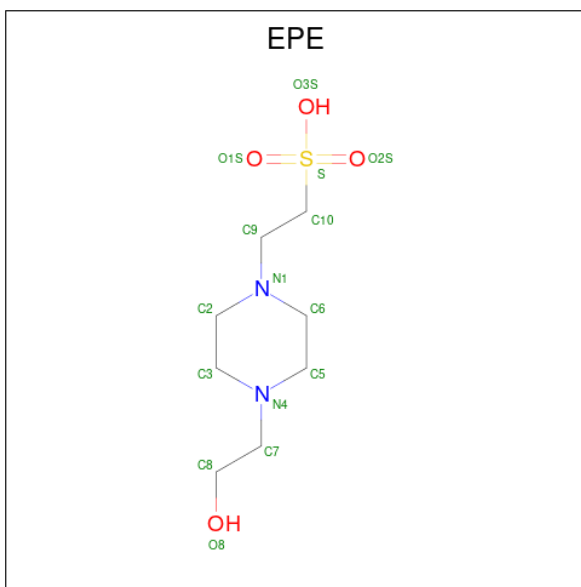
- Molecule 1 is a protein called SalC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	589	Total	C	N	O	S	0	0	0
			4502	2814	812	858	18			
1	B	587	Total	C	N	O	S	0	0	0
			4482	2801	810	853	18			
1	C	587	Total	C	N	O	S	0	0	0
			4482	2801	810	853	18			
1	D	587	Total	C	N	O	S	0	0	0
			4482	2801	810	853	18			

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

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

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

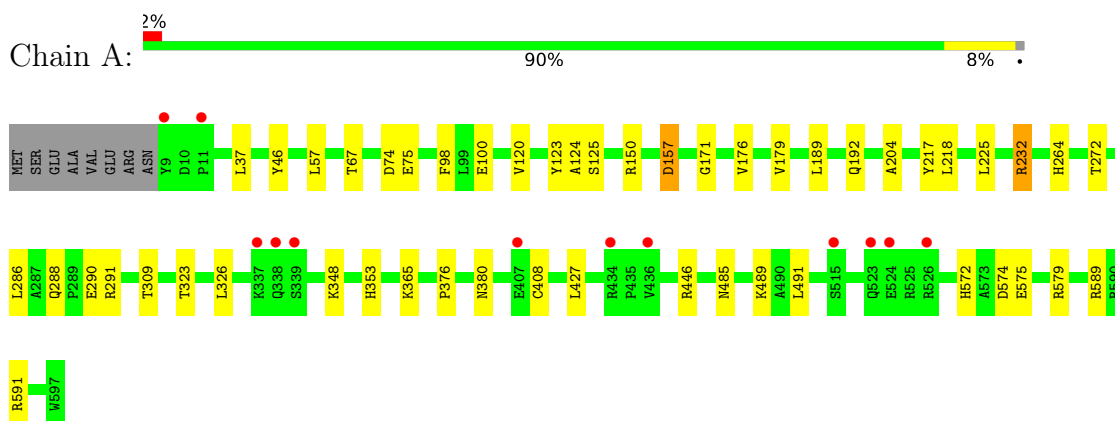
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total	O	0	0
			5	5		
4	B	5	Total	O	0	0
			5	5		
4	C	5	Total	O	0	0
			5	5		
4	D	4	Total	O	0	0
			4	4		

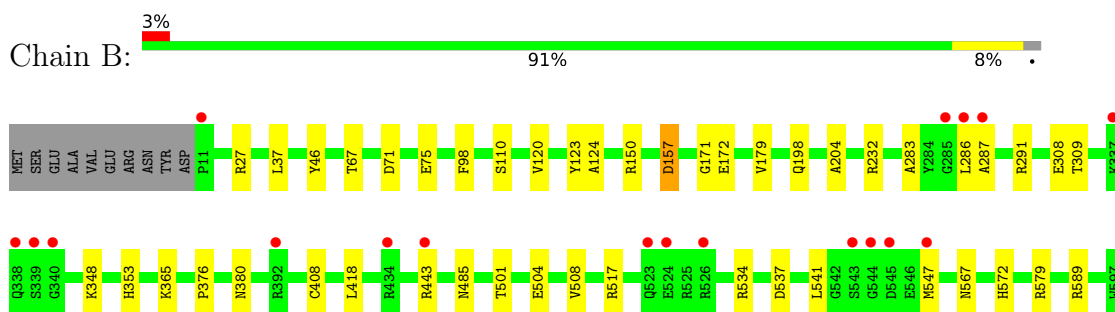
3 Residue-property plots [i](#)

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.

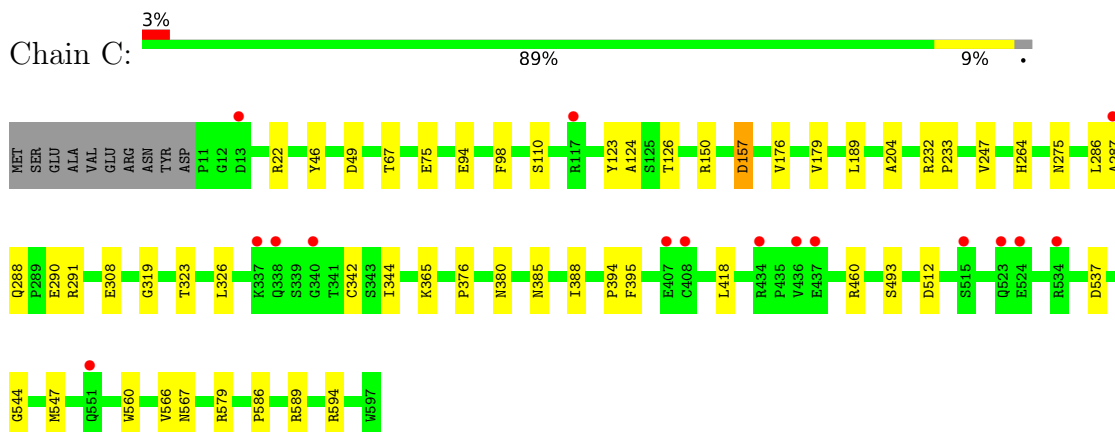
• Molecule 1: SalC



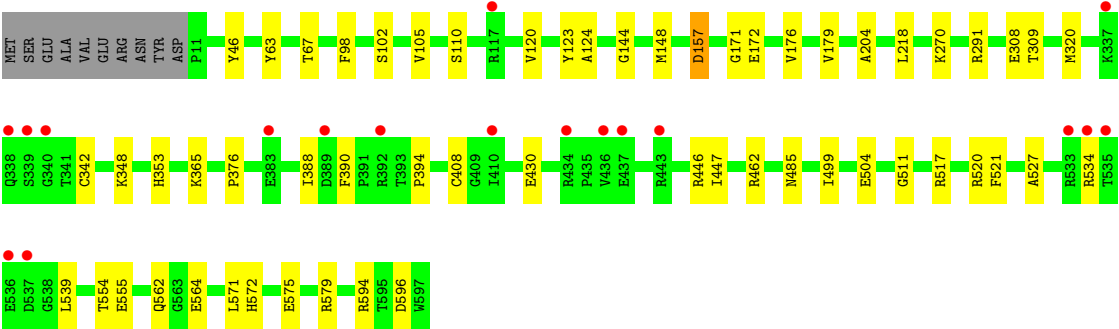
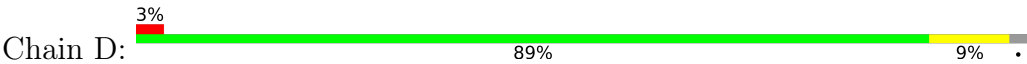
• Molecule 1: SalC



• Molecule 1: SalC



● Molecule 1: SalC



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.33Å 218.29Å 87.87Å 90.00° 111.01° 90.00°	Depositor
Resolution (Å)	44.85 – 2.85 44.85 – 2.85	Depositor EDS
% Data completeness (in resolution range)	97.0 (44.85-2.85) 91.6 (44.85-2.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.197 , 0.230 0.197 , 0.230	Depositor DCC
R_{free} test set	3314 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	46.9	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 24.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	17986	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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: EPE, K

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	0.27	0/4606	0.46	0/6267
1	B	0.27	0/4585	0.46	0/6237
1	C	0.26	0/4585	0.45	0/6237
1	D	0.27	0/4585	0.47	0/6237
All	All	0.27	0/18361	0.46	0/24978

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	A	4502	0	4360	30	0
1	B	4482	0	4348	25	0
1	C	4482	0	4348	31	0
1	D	4482	0	4348	31	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
3	D	15	0	17	0	0
4	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	4	0	0	0	0
All	All	17986	0	17421	114	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 (114) 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:A:75:GLU:HB3	1:A:589:ARG:HB3	1.69	0.73
1:B:75:GLU:HB3	1:B:589:ARG:HB3	1.74	0.68
1:A:192:GLN:NE2	1:B:198:GLN:OE1	2.28	0.67
1:A:74:ASP:OD2	1:A:591:ARG:NH1	2.28	0.66
1:B:157:ASP:N	1:B:157:ASP:OD1	2.28	0.66
1:C:75:GLU:HB3	1:C:589:ARG:HB3	1.77	0.66
1:C:365:LYS:HE3	1:C:376:PRO:HG2	1.77	0.66
1:B:365:LYS:HE3	1:B:376:PRO:HG2	1.77	0.66
1:D:527:ALA:H	1:D:562:GLN:HE22	1.41	0.66
1:C:110:SER:O	1:C:579:ARG:NH2	2.28	0.65
1:B:110:SER:O	1:B:579:ARG:NH2	2.30	0.65
1:C:157:ASP:N	1:C:157:ASP:OD1	2.29	0.65
1:A:286:LEU:HD23	1:A:323:THR:HG22	1.80	0.62
1:D:462:ARG:NH2	1:D:511:GLY:O	2.34	0.61
1:B:283:ALA:HB3	1:B:286:LEU:HD13	1.84	0.59
1:A:348:LYS:HE3	1:A:353:HIS:ND1	2.17	0.59
1:D:157:ASP:N	1:D:157:ASP:OD1	2.36	0.59
1:D:348:LYS:HE3	1:D:353:HIS:ND1	2.18	0.58
1:B:348:LYS:HE3	1:B:353:HIS:ND1	2.19	0.57
1:C:286:LEU:HD22	1:C:326:LEU:HD12	1.87	0.56
1:A:290:GLU:N	1:A:290:GLU:OE2	2.38	0.56
1:B:232:ARG:HG2	1:B:380:ASN:HB3	1.87	0.55
1:D:308:GLU:OE1	1:D:308:GLU:N	2.34	0.55
1:B:287:ALA:HB2	1:B:418:LEU:HD21	1.89	0.55
1:A:485:ASN:HD22	1:A:572:HIS:HE1	1.56	0.54
1:C:288:GLN:NE2	1:C:290:GLU:OE1	2.41	0.54
1:D:521:PHE:CZ	1:D:555:GLU:HG2	2.43	0.53
1:D:446:ARG:NH1	1:D:575:GLU:OE2	2.36	0.53
1:A:176:VAL:HG11	1:A:189:LEU:HD12	1.91	0.53
1:A:485:ASN:HD22	1:A:572:HIS:CE1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:ASP:N	1:C:49:ASP:OD1	2.43	0.52
1:C:232:ARG:HG2	1:C:380:ASN:HB3	1.91	0.52
1:B:485:ASN:HD22	1:B:572:HIS:CE1	2.28	0.51
1:C:290:GLU:OE1	1:C:290:GLU:N	2.42	0.51
1:D:447:ILE:HD12	1:D:571:LEU:HD21	1.92	0.51
1:B:308:GLU:OE1	1:B:308:GLU:N	2.34	0.51
1:C:176:VAL:HG12	1:D:176:VAL:HG12	1.91	0.51
1:A:365:LYS:HE3	1:A:376:PRO:HG2	1.93	0.50
1:D:46:TYR:HE2	1:D:67:THR:HG22	1.77	0.50
1:D:110:SER:HB2	1:D:579:ARG:HB3	1.94	0.50
1:D:539:LEU:HD11	1:D:564:GLU:HG2	1.93	0.49
1:C:22:ARG:HB2	1:C:247:VAL:HG12	1.93	0.49
1:C:233:PRO:HA	1:C:319:GLY:HA2	1.94	0.49
1:A:272:THR:HG22	1:A:427:LEU:HD12	1.94	0.49
1:A:446:ARG:NH1	1:A:575:GLU:OE1	2.29	0.49
1:C:308:GLU:OE1	1:C:308:GLU:N	2.37	0.49
1:C:460:ARG:HE	1:C:586:PRO:HB2	1.77	0.49
1:B:485:ASN:HD22	1:B:572:HIS:HE1	1.59	0.48
1:D:365:LYS:HE3	1:D:376:PRO:HG2	1.94	0.48
1:A:288:GLN:HG3	1:A:291:ARG:H	1.79	0.47
1:C:287:ALA:HB2	1:C:418:LEU:HD21	1.94	0.47
1:C:286:LEU:HD23	1:C:323:THR:HG22	1.96	0.47
1:B:46:TYR:HE2	1:B:67:THR:HG22	1.79	0.47
1:D:485:ASN:HD22	1:D:572:HIS:CE1	2.32	0.47
1:D:517:ARG:HD3	1:D:554:THR:OG1	2.15	0.47
1:A:286:LEU:HD22	1:A:326:LEU:HD12	1.96	0.47
1:A:157:ASP:OD1	1:A:157:ASP:N	2.46	0.46
1:D:63:TYR:HD1	1:D:218:LEU:HD13	1.80	0.46
1:C:94:GLU:OE1	1:C:126:THR:OG1	2.28	0.46
1:D:309:THR:HA	1:D:408:CYS:SG	2.55	0.46
1:C:275:ASN:HA	1:D:172:GLU:HB3	1.97	0.46
1:A:309:THR:HA	1:A:408:CYS:SG	2.56	0.45
1:C:123:TYR:O	1:C:204:ALA:HA	2.16	0.45
1:D:485:ASN:HD22	1:D:572:HIS:HE1	1.62	0.45
1:A:125:SER:HA	1:A:176:VAL:O	2.16	0.45
1:C:344:ILE:HB	1:C:395:PHE:HB3	1.99	0.45
1:A:232:ARG:HB3	1:A:380:ASN:O	2.16	0.45
1:B:443:ARG:NH1	1:B:501:THR:HG22	2.32	0.45
1:B:541:LEU:HD12	1:B:547:MET:HG2	1.99	0.45
1:C:176:VAL:HG11	1:C:189:LEU:HD12	1.99	0.45
1:A:120:VAL:O	1:A:171:GLY:HA3	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:THR:HA	1:B:408:CYS:SG	2.57	0.44
1:C:537:ASP:HB2	1:C:567:ASN:ND2	2.32	0.44
1:A:100:GLU:OE2	1:A:589:ARG:NH2	2.47	0.44
1:B:98:PHE:CZ	1:B:124:ALA:HB2	2.52	0.44
1:C:264:HIS:HB2	1:C:579:ARG:O	2.17	0.44
1:D:123:TYR:O	1:D:204:ALA:HA	2.17	0.44
1:D:499:ILE:HB	1:D:504:GLU:HG3	1.99	0.44
1:D:270:LYS:HE2	1:D:430:GLU:OE1	2.18	0.44
1:A:574:ASP:OD1	1:A:574:ASP:N	2.50	0.43
1:C:512:ASP:OD1	1:C:512:ASP:N	2.51	0.43
1:A:264:HIS:HB2	1:A:579:ARG:O	2.19	0.43
1:A:291:ARG:HA	1:A:291:ARG:HD2	1.82	0.43
1:C:291:ARG:HD2	1:C:291:ARG:HA	1.82	0.43
1:A:57:LEU:HD13	1:A:218:LEU:HD22	2.00	0.43
1:C:560:TRP:HB2	1:C:566:VAL:HG21	2.00	0.43
1:B:123:TYR:OH	1:B:172:GLU:OE2	2.36	0.43
1:D:388:ILE:O	1:D:390:PHE:N	2.52	0.43
1:D:98:PHE:CZ	1:D:124:ALA:HB2	2.54	0.42
1:B:291:ARG:HA	1:B:291:ARG:HD2	1.81	0.42
1:C:46:TYR:HE2	1:C:67:THR:HG22	1.84	0.42
1:A:98:PHE:CZ	1:A:124:ALA:HB2	2.55	0.42
1:B:37:LEU:HD12	1:B:37:LEU:HA	1.92	0.42
1:D:517:ARG:HA	1:D:520:ARG:NH1	2.35	0.42
1:A:37:LEU:HD12	1:A:37:LEU:HA	1.87	0.42
1:B:120:VAL:O	1:B:171:GLY:HA3	2.20	0.42
1:A:123:TYR:O	1:A:204:ALA:HA	2.20	0.41
1:C:342:CYS:N	1:C:394:PRO:O	2.50	0.41
1:C:385:ASN:ND2	1:C:388:ILE:HG13	2.36	0.41
1:C:544:GLY:HA2	1:C:547:MET:HE2	2.02	0.41
1:B:27:ARG:NH2	1:B:71:ASP:HB3	2.34	0.41
1:C:98:PHE:CZ	1:C:124:ALA:HB2	2.56	0.41
1:D:102:SER:O	1:D:105:VAL:HG12	2.20	0.41
1:A:489:LYS:HD3	1:A:491:LEU:HD21	2.02	0.41
1:A:217:TYR:CE2	1:A:225:LEU:HB3	2.56	0.41
1:B:504:GLU:O	1:B:508:VAL:HG22	2.21	0.41
1:D:291:ARG:HA	1:D:291:ARG:HD2	1.82	0.41
1:D:342:CYS:N	1:D:394:PRO:O	2.53	0.41
1:D:594:ARG:NH2	1:D:596:ASP:O	2.54	0.41
1:D:120:VAL:O	1:D:171:GLY:HA3	2.21	0.40
1:B:123:TYR:O	1:B:204:ALA:HA	2.21	0.40
1:D:144:GLY:O	1:D:148:MET:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:537:ASP:HB2	1:B:567:ASN:ND2	2.37	0.40
1:A:46:TYR:HE2	1:A:67:THR:HG22	1.85	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	587/597 (98%)	579 (99%)	7 (1%)	1 (0%)	47	75
1	B	585/597 (98%)	577 (99%)	7 (1%)	1 (0%)	47	75
1	C	585/597 (98%)	578 (99%)	6 (1%)	1 (0%)	47	75
1	D	585/597 (98%)	577 (99%)	7 (1%)	1 (0%)	47	75
All	All	2342/2388 (98%)	2311 (99%)	27 (1%)	4 (0%)	47	75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	179	VAL
1	C	179	VAL
1	A	179	VAL
1	D	179	VAL

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	460/467 (98%)	457 (99%)	3 (1%)	84	94
1	B	458/467 (98%)	454 (99%)	4 (1%)	78	92
1	C	458/467 (98%)	454 (99%)	4 (1%)	78	92
1	D	458/467 (98%)	455 (99%)	3 (1%)	84	94
All	All	1834/1868 (98%)	1820 (99%)	14 (1%)	81	93

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	150	ARG
1	A	157	ASP
1	A	232	ARG
1	B	150	ARG
1	B	157	ASP
1	B	517	ARG
1	B	534	ARG
1	C	150	ARG
1	C	157	ASP
1	C	493	SER
1	C	594	ARG
1	D	157	ASP
1	D	320	MET
1	D	534	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	GLN
1	A	572	HIS
1	B	31	GLN
1	B	198	GLN
1	B	572	HIS
1	C	31	GLN
1	C	184	HIS
1	C	192	GLN
1	C	198	GLN
1	C	572	HIS
1	D	192	GLN
1	D	198	GLN
1	D	562	GLN
1	D	572	HIS

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z > 2$
3	EPE	D	601	-	15,15,15	0.84	1 (6%)	18,20,20	1.71	5 (27%)

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
3	EPE	D	601	-	-	6/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	601	EPE	C10-S	2.71	1.81	1.77

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	601	EPE	C5-N4-C3	3.91	117.64	108.83
3	D	601	EPE	C7-N4-C3	3.25	119.54	111.23
3	D	601	EPE	C7-N4-C5	2.87	118.58	111.23
3	D	601	EPE	O1S-S-C10	2.17	109.53	106.92
3	D	601	EPE	O2S-S-C10	2.07	109.41	106.92

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	601	EPE	C8-C7-N4-C3
3	D	601	EPE	C9-C10-S-O3S
3	D	601	EPE	C10-C9-N1-C2
3	D	601	EPE	C9-C10-S-O1S
3	D	601	EPE	C10-C9-N1-C6
3	D	601	EPE	C9-C10-S-O2S

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	589/597 (98%)	0.04	12 (2%) 65 62	29, 45, 81, 109	0
1	B	587/597 (98%)	0.09	18 (3%) 49 44	27, 43, 81, 120	0
1	C	587/597 (98%)	0.17	16 (2%) 54 50	31, 50, 85, 123	0
1	D	587/597 (98%)	0.09	18 (3%) 49 44	30, 46, 76, 143	0
All	All	2350/2388 (98%)	0.10	64 (2%) 54 50	27, 46, 82, 143	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	338	GLN	5.6
1	A	338	GLN	5.1
1	D	340	GLY	5.0
1	A	434	ARG	4.7
1	C	117	ARG	4.4
1	C	407	GLU	4.1
1	B	287	ALA	3.9
1	B	524	GLU	3.8
1	C	524	GLU	3.6
1	A	9	TYR	3.6
1	D	339	SER	3.5
1	B	545	ASP	3.4
1	D	434	ARG	3.3
1	D	338	GLN	3.3
1	A	515	SER	3.3
1	A	524	GLU	3.2
1	D	436	VAL	3.2
1	D	443	ARG	3.2
1	B	338	GLN	3.1
1	B	340	GLY	3.1
1	A	436	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	339	SER	2.9
1	C	436	VAL	2.9
1	A	526	ARG	2.9
1	C	523	GLN	2.8
1	C	515	SER	2.8
1	B	286	LEU	2.8
1	B	523	GLN	2.8
1	C	434	ARG	2.8
1	D	534	ARG	2.8
1	B	547	MET	2.7
1	C	437	GLU	2.7
1	B	526	ARG	2.7
1	C	408	CYS	2.5
1	B	443	ARG	2.5
1	D	536	GLU	2.5
1	C	551	GLN	2.5
1	B	339	SER	2.5
1	B	434	ARG	2.5
1	B	285	GLY	2.4
1	A	407	GLU	2.4
1	C	337	LYS	2.4
1	D	537	ASP	2.4
1	C	534	ARG	2.4
1	D	535	THR	2.4
1	B	543	SER	2.4
1	D	389	ASP	2.3
1	A	523	GLN	2.3
1	D	437	GLU	2.3
1	D	533	ARG	2.3
1	A	337	LYS	2.3
1	C	287	ALA	2.3
1	D	392	ARG	2.2
1	B	11	PRO	2.2
1	D	410	ILE	2.2
1	C	13	ASP	2.1
1	B	544	GLY	2.1
1	C	340	GLY	2.1
1	D	337	LYS	2.1
1	B	337	LYS	2.1
1	D	117	ARG	2.0
1	B	392	ARG	2.0
1	A	11	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	383	GLU	2.0

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(Å ²)	Q<0.9
2	K	A	601	1/1	0.85	0.18	62,62,62,62	0
2	K	C	601	1/1	0.86	0.18	64,64,64,64	0
3	EPE	D	601	15/15	0.92	0.25	40,45,53,55	0
2	K	B	602	1/1	0.96	0.16	48,48,48,48	0
2	K	B	601	1/1	0.97	0.06	52,52,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.