



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2022 – 04:45 pm BST

PDB ID : 7ZP0
Title : Crystal structure of CusS histidine kinase catalytic core from Escherichia coli
Authors : Cociurovscaia, A.; Bujacz, G.; Pietrzyk-Brzezinka, A.
Deposited on : 2022-04-26
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

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>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.29
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.29

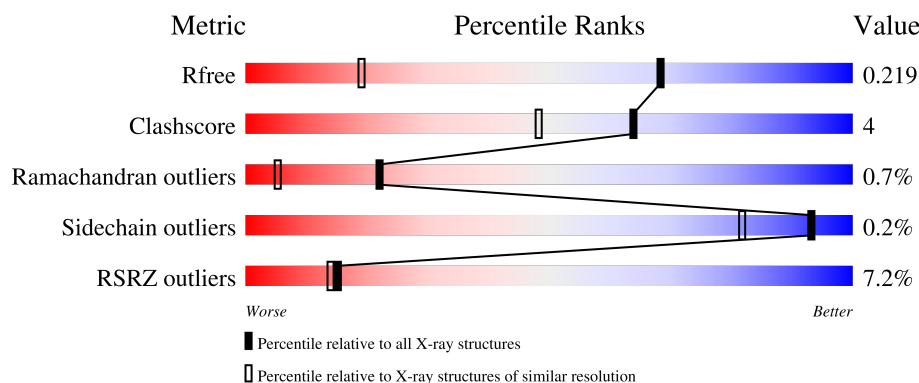
1 Overall quality at a glance

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 ≥ 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	217	<div> <div>5%</div> <div>93%</div> <div>7%</div> </div>
1	B	217	<div> <div>7%</div> <div>88%</div> <div>12%</div> </div>
1	C	217	<div> <div>7%</div> <div>91%</div> <div>9%</div> </div>
1	D	217	<div> <div>6%</div> <div>92%</div> <div>7%</div> </div>
1	E	217	<div> <div>10%</div> <div>89%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	217	<div><div></div><div>8%</div><div>88%</div><div>11%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11462 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 Sensor protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	4	0
			1711	1070	308	325	8			
1	B	217	Total	C	N	O	S	0	3	0
			1706	1068	309	321	8			
1	C	217	Total	C	N	O	S	0	0	0
			1679	1053	301	317	8			
1	D	217	Total	C	N	O	S	0	0	0
			1679	1053	301	317	8			
1	E	216	Total	C	N	O	S	0	1	0
			1681	1054	301	318	8			
1	F	216	Total	C	N	O	S	0	3	0
			1696	1062	303	323	8			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	264	GLY	-	expression tag	UNP A0A2J1D710
A	265	ALA	-	expression tag	UNP A0A2J1D710
A	266	MET	-	expression tag	UNP A0A2J1D710
A	435	ALA	ASP	variant	UNP A0A2J1D710
B	264	GLY	-	expression tag	UNP A0A2J1D710
B	265	ALA	-	expression tag	UNP A0A2J1D710
B	266	MET	-	expression tag	UNP A0A2J1D710
B	435	ALA	ASP	variant	UNP A0A2J1D710
C	264	GLY	-	expression tag	UNP A0A2J1D710
C	265	ALA	-	expression tag	UNP A0A2J1D710
C	266	MET	-	expression tag	UNP A0A2J1D710
C	435	ALA	ASP	variant	UNP A0A2J1D710
D	264	GLY	-	expression tag	UNP A0A2J1D710
D	265	ALA	-	expression tag	UNP A0A2J1D710
D	266	MET	-	expression tag	UNP A0A2J1D710
D	435	ALA	ASP	variant	UNP A0A2J1D710
E	264	GLY	-	expression tag	UNP A0A2J1D710

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Chain	Residue	Modelled	Actual	Comment	Reference
E	265	ALA	-	expression tag	UNP A0A2J1D710
E	266	MET	-	expression tag	UNP A0A2J1D710
E	435	ALA	ASP	variant	UNP A0A2J1D710
F	264	GLY	-	expression tag	UNP A0A2J1D710
F	265	ALA	-	expression tag	UNP A0A2J1D710
F	266	MET	-	expression tag	UNP A0A2J1D710
F	435	ALA	ASP	variant	UNP A0A2J1D710

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	236	Total O 236 236	0	0
3	B	215	Total O 215 215	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	184	Total 184	O 184	0	0
3	D	228	Total 228	O 228	0	0
3	E	191	Total 191	O 191	0	0
3	F	240	Total 240	O 240	0	0

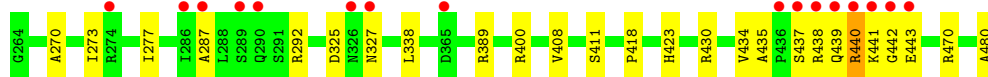
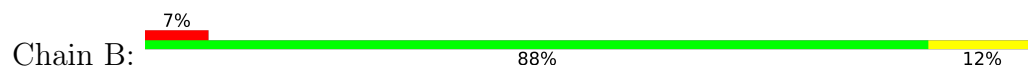
3 Residue-property plots [i](#)

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: Sensor protein



- Molecule 1: Sensor protein



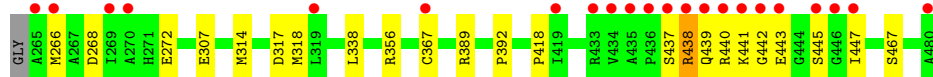
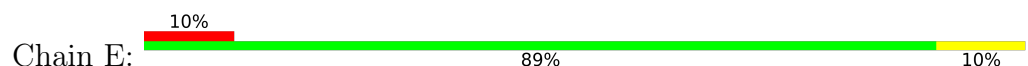
- Molecule 1: Sensor protein



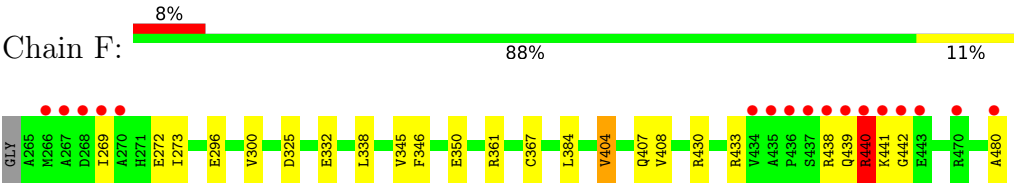
- Molecule 1: Sensor protein



- Molecule 1: Sensor protein



- Molecule 1: Sensor protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.76Å 129.09Å 69.83Å 90.00° 92.09° 90.00°	Depositor
Resolution (Å)	36.63 – 1.40 47.39 – 1.40	Depositor EDS
% Data completeness (in resolution range)	98.9 (36.63-1.40) 98.7 (47.39-1.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 1.40Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.177 , 0.219 0.178 , 0.219	Depositor DCC
R_{free} test set	2522 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.025 for l,k,-h 0.043 for h,-k,-l 0.119 for l,-k,h	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	11462	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.36% 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: 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	0.35	0/1736	0.51	0/2348
1	B	0.32	0/1732	0.50	0/2343
1	C	0.30	0/1704	0.47	0/2306
1	D	0.36	0/1704	0.52	0/2306
1	E	0.32	0/1706	0.52	0/2309
1	F	0.34	0/1721	0.52	0/2329
All	All	0.33	0/10303	0.51	0/13941

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	1711	0	1738	11	0
1	B	1706	0	1735	18	0
1	C	1679	0	1713	16	0
1	D	1679	0	1713	11	0
1	E	1681	0	1714	19	0
1	F	1696	0	1723	19	0
2	D	4	0	6	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	12	0	18	3	0
3	A	236	0	0	3	0
3	B	215	0	0	1	0
3	C	184	0	0	3	0
3	D	228	0	0	1	0
3	E	191	0	0	1	0
3	F	240	0	0	5	0
All	All	11462	0	10360	87	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 4.

All (87) 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:E:266:MET:HB3	1:F:269:ILE:HD13	1.78	0.64
1:C:270:ALA:HB2	1:D:318:MET:HE2	1.79	0.64
1:B:440:ARG:O	1:B:442:GLY:N	2.31	0.64
1:E:317:ASP:HB3	1:E:447:ILE:HG21	1.80	0.63
1:F:272:GLU:OE1	1:F:433:ARG:NH2	2.31	0.63
1:C:325:ASP:OD2	1:C:430:ARG:NH2	2.23	0.62
1:F:361:ARG:NH1	3:F:505:HOH:O	2.33	0.61
1:A:437:SER:OG	1:A:438:ARG:N	2.34	0.60
1:F:272:GLU:HB2	3:F:510:HOH:O	2.02	0.59
1:D:435:ALA:O	1:D:437:SER:N	2.38	0.57
1:D:345:VAL:HG12	1:D:384:LEU:HD22	1.85	0.57
1:F:346:PHE:O	1:F:350[B]:GLU:HG2	2.04	0.56
1:A:287:ALA:O	1:A:292:ARG:NH1	2.38	0.56
1:F:338:LEU:HB2	1:F:367:CYS:SG	2.46	0.56
1:F:433:ARG:NH1	3:F:508:HOH:O	2.39	0.56
1:C:314:MET:O	1:C:318:MET:HG3	2.07	0.54
1:F:440:ARG:O	1:F:442:GLY:N	2.41	0.54
1:A:427:LEU:HD12	1:A:465:VAL:HG11	1.90	0.54
1:F:408:VAL:HG23	1:F:480:ALA:HB2	1.88	0.54
1:C:324:ALA:HA	1:C:329:LEU:HG	1.89	0.54
1:C:313:LYS:NZ	3:C:505:HOH:O	2.41	0.53
1:A:318:MET:HE2	1:B:270:ALA:HB2	1.90	0.52
1:A:290:GLN:NE2	3:A:508:HOH:O	2.42	0.52
1:B:389:ARG:HD2	1:B:443:GLU:OE1	2.11	0.50
1:D:392:PRO:HB2	1:D:395:GLU:HG3	1.93	0.50
1:B:470:ARG:NH1	1:D:406:HIS:HE1	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:433:ARG:NH1	3:A:510:HOH:O	2.44	0.49
1:C:315:VAL:HA	1:C:318:MET:CE	2.43	0.49
1:E:437:SER:O	1:E:438:ARG:NE	2.46	0.49
1:E:439:GLN:HG3	1:E:442:GLY:H	1.77	0.49
1:E:272:GLU:HG2	1:E:314:MET:SD	2.53	0.48
1:F:439:GLN:O	1:F:441:LYS:N	2.46	0.48
1:A:290:GLN:H	1:A:292:ARG:HH12	1.60	0.48
1:D:386:ASN:O	1:D:389:ARG:HG2	2.12	0.48
1:C:283:GLN:OE1	1:C:304:ASN:ND2	2.45	0.48
1:E:392:PRO:HG3	2:E:503:EDO:H21	1.96	0.48
1:F:404:VAL:HG23	1:F:407:GLN:HB2	1.96	0.47
1:B:435:ALA:O	1:B:437:SER:N	2.42	0.47
1:E:389:ARG:HH11	1:E:443:GLU:HB2	1.79	0.47
1:B:418:PRO:HG2	1:F:332:GLU:HG2	1.96	0.46
1:E:440:ARG:HE	1:E:441:LYS:NZ	2.13	0.46
1:C:437:SER:HB3	1:C:443:GLU:OE1	2.14	0.46
1:E:356:ARG:HE	2:E:502:EDO:C2	2.28	0.46
1:B:325:ASP:OD1	1:B:430:ARG:NH2	2.46	0.46
1:B:437:SER:O	1:B:439:GLN:N	2.48	0.46
1:C:378:ARG:NH2	3:C:516:HOH:O	2.48	0.46
1:E:389:ARG:HD2	1:E:443:GLU:HB3	1.98	0.46
1:A:440:ARG:N	1:A:443:GLU:OE2	2.50	0.45
1:E:418:PRO:HB3	1:E:467:SER:HB2	1.98	0.45
1:E:445:SER:HB2	1:E:447:ILE:HG22	1.97	0.45
1:E:268:ASP:O	1:E:318:MET:HE1	2.17	0.45
1:E:266:MET:CB	1:F:269:ILE:HD13	2.44	0.45
1:B:400:ARG:HB3	1:B:411:SER:OG	2.17	0.45
1:A:332[B]:GLU:OE1	1:C:460:LYS:NZ	2.33	0.44
1:C:315:VAL:HA	1:C:318:MET:HE3	1.99	0.44
1:B:325:ASP:CG	1:B:430:ARG:HH22	2.21	0.44
1:D:332:GLU:HG2	2:D:501:EDO:H21	2.00	0.44
1:F:273:ILE:HG13	3:F:510:HOH:O	2.17	0.44
1:B:408:VAL:HG23	1:B:480:ALA:HB2	1.98	0.44
1:D:440:ARG:O	1:D:441:LYS:HB2	2.18	0.44
1:C:325:ASP:C	1:C:327:ASN:H	2.21	0.44
1:B:423:HIS:CD2	1:B:434:VAL:HG13	2.53	0.43
1:C:325:ASP:CG	1:C:430:ARG:HH22	2.13	0.43
1:E:389:ARG:NH1	1:E:443:GLU:HB2	2.33	0.43
1:C:466:THR:HG22	3:C:629:HOH:O	2.17	0.43
1:C:338:LEU:HA	1:C:338:LEU:HD12	1.79	0.43
1:B:287:ALA:HA	1:B:292:ARG:HE	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:327:ASN:HB3	3:D:777:HOH:O	2.19	0.43
1:B:273:ILE:HG22	1:B:277:ILE:HG12	1.99	0.43
1:B:338:LEU:HA	1:B:338:LEU:HD23	1.73	0.42
1:E:307:GLU:N	1:E:441:LYS:HE3	2.34	0.42
2:E:502:EDO:H11	3:E:744:HOH:O	2.18	0.42
1:B:443:GLU:HG3	3:B:528:HOH:O	2.18	0.42
1:A:347:ASP:OD2	3:A:501:HOH:O	2.22	0.42
1:B:325:ASP:C	1:B:327:ASN:H	2.22	0.42
1:B:400:ARG:HD2	1:D:405:ASN:OD1	2.19	0.42
1:F:325:ASP:CG	1:F:430:ARG:HH12	2.22	0.42
1:F:440:ARG:HA	1:F:440:ARG:HD2	1.76	0.42
1:D:366:LYS:H	1:D:366:LYS:HG2	1.49	0.42
1:F:345:VAL:HG12	1:F:384:LEU:HD12	2.02	0.42
1:E:389:ARG:HD2	1:E:443:GLU:CB	2.50	0.42
1:C:321:LEU:HD23	1:C:321:LEU:HA	1.83	0.41
1:F:269:ILE:HG13	3:F:510:HOH:O	2.18	0.41
1:A:400:ARG:HB3	1:A:411:SER:OG	2.21	0.41
1:E:438:ARG:HD3	1:E:438:ARG:HA	1.90	0.41
1:F:296:GLU:O	1:F:300:VAL:HG23	2.21	0.40
1:E:338:LEU:HD12	1:E:338:LEU:HA	1.89	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	219/217 (101%)	215 (98%)	4 (2%)	0	100	100
1	B	218/217 (100%)	211 (97%)	4 (2%)	3 (1%)	11	1
1	C	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	D	215/217 (99%)	207 (96%)	6 (3%)	2 (1%)	17	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	215/217 (99%)	205 (95%)	8 (4%)	2 (1%)	17	3
1	F	217/217 (100%)	210 (97%)	5 (2%)	2 (1%)	17	3
All	All	1299/1302 (100%)	1258 (97%)	32 (2%)	9 (1%)	22	5

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	441	LYS
1	D	441	LYS
1	E	438	ARG
1	F	440	ARG
1	B	438	ARG
1	B	440	ARG
1	D	436	PRO
1	E	367	CYS
1	F	404	VAL

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	188/184 (102%)	188 (100%)	0	100	100
1	B	187/184 (102%)	187 (100%)	0	100	100
1	C	184/184 (100%)	184 (100%)	0	100	100
1	D	184/184 (100%)	184 (100%)	0	100	100
1	E	185/184 (100%)	185 (100%)	0	100	100
1	F	187/184 (102%)	185 (99%)	2 (1%)	73	50
All	All	1115/1104 (101%)	1113 (100%)	2 (0%)	93	82

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	438	ARG

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Mol	Chain	Res	Type
1	F	440	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	326	ASN
1	D	406	HIS

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](#)

4 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	$\# Z > 2$
2	EDO	E	503	-	3,3,3	0.47	0	2,2,2	0.35	0
2	EDO	E	502	-	3,3,3	0.45	0	2,2,2	0.18	0
2	EDO	D	501	-	3,3,3	0.36	0	2,2,2	0.52	0
2	EDO	E	501	-	3,3,3	0.46	0	2,2,2	0.31	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	EDO	E	503	-	-	1/1/1/1	-
2	EDO	E	502	-	-	0/1/1/1	-
2	EDO	D	501	-	-	0/1/1/1	-
2	EDO	E	501	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	503	EDO	O1-C1-C2-O2
2	E	501	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	503	EDO	1	0
2	E	502	EDO	2	0
2	D	501	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, 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	217/217 (100%)	0.10	10 (4%)	32 32	15, 27, 66, 130	0
1	B	217/217 (100%)	0.17	16 (7%)	14 13	16, 28, 66, 100	0
1	C	217/217 (100%)	0.14	15 (6%)	16 15	22, 34, 76, 135	0
1	D	217/217 (100%)	0.03	13 (5%)	21 20	15, 29, 66, 138	0
1	E	216/217 (99%)	0.41	22 (10%)	6 6	18, 32, 96, 133	0
1	F	216/217 (99%)	0.14	17 (7%)	12 12	14, 28, 89, 116	0
All	All	1300/1302 (99%)	0.16	93 (7%)	15 14	14, 30, 82, 138	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	480	ALA	11.3
1	C	437	SER	10.4
1	E	438	ARG	9.5
1	E	440	ARG	9.2
1	E	269	ILE	9.1
1	A	440	ARG	8.9
1	A	442	GLY	8.8
1	E	443	GLU	8.4
1	C	329	LEU	8.2
1	D	438	ARG	8.0
1	F	440	ARG	7.8
1	B	436	PRO	7.5
1	A	441	LYS	7.5
1	E	434	VAL	7.2
1	F	437	SER	6.9
1	E	439	GLN	6.9
1	E	435	ALA	6.8
1	B	442	GLY	6.8
1	F	442	GLY	6.8

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Mol	Chain	Res	Type	RSRZ
1	D	437	SER	6.2
1	E	265	ALA	6.0
1	E	441	LYS	6.0
1	F	438	ARG	5.9
1	B	326	ASN	5.9
1	B	440	ARG	5.8
1	E	442	GLY	5.7
1	B	438	ARG	5.6
1	D	440	ARG	5.5
1	A	439	GLN	5.5
1	D	439	GLN	5.4
1	F	439	GLN	5.0
1	F	269	ILE	4.9
1	D	436	PRO	4.9
1	F	266	MET	4.7
1	B	439	GLN	4.4
1	C	330	ILE	4.4
1	F	435	ALA	4.4
1	B	441	LYS	4.3
1	A	438	ARG	4.3
1	C	438	ARG	4.2
1	E	436	PRO	4.1
1	E	367	CYS	4.0
1	D	470	ARG	4.0
1	D	442	GLY	3.8
1	E	266	MET	3.8
1	C	440	ARG	3.7
1	C	324	ALA	3.7
1	E	319	LEU	3.6
1	D	434	VAL	3.6
1	D	444	GLY	3.6
1	A	436	PRO	3.5
1	A	308	LEU	3.5
1	F	270	ALA	3.5
1	F	434	VAL	3.4
1	F	267	ALA	3.4
1	B	290	GLN	3.3
1	F	436	PRO	3.2
1	E	437	SER	3.2
1	D	441	LYS	3.1
1	F	480	ALA	3.0
1	F	441	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	268	ASP	2.8
1	E	433	ARG	2.8
1	D	265	ALA	2.7
1	C	326	ASN	2.7
1	B	287	ALA	2.6
1	D	443	GLU	2.6
1	B	437	SER	2.6
1	C	366	LYS	2.6
1	C	441	LYS	2.6
1	E	446	GLY	2.6
1	A	287	ALA	2.6
1	C	439	GLN	2.6
1	C	327	ASN	2.6
1	C	365	ASP	2.5
1	A	443	GLU	2.5
1	E	445	SER	2.4
1	B	286	ILE	2.4
1	B	289	SER	2.4
1	C	436	PRO	2.4
1	E	447	ILE	2.3
1	F	443	GLU	2.2
1	E	270	ALA	2.2
1	E	419	ILE	2.2
1	B	443	GLU	2.2
1	F	470	ARG	2.2
1	D	405	ASN	2.2
1	E	480	ALA	2.1
1	C	302	TYR	2.1
1	B	365	ASP	2.1
1	A	311	MET	2.0
1	B	274	ARG	2.0
1	B	327	ASN	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(\AA^2)	Q<0.9
2	EDO	E	501	4/4	0.83	0.16	60,60,61,61	0
2	EDO	E	503	4/4	0.87	0.12	30,53,59,106	0
2	EDO	E	502	4/4	0.90	0.10	26,49,59,62	0
2	EDO	D	501	4/4	0.94	0.14	31,38,38,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.