



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:40 PM GMT

PDB ID : 4A2L
Title : Structure of the periplasmic domain of the heparin and heparan sulphate sensing hybrid two component system BT4663 in apo and ligand bound forms
Authors : Lowe, E.C.; Basle, A.; Czjzek, M.; Firbank, S.J.; Bolam, D.N.
Deposited on : 2011-09-27
Resolution : 2.60 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

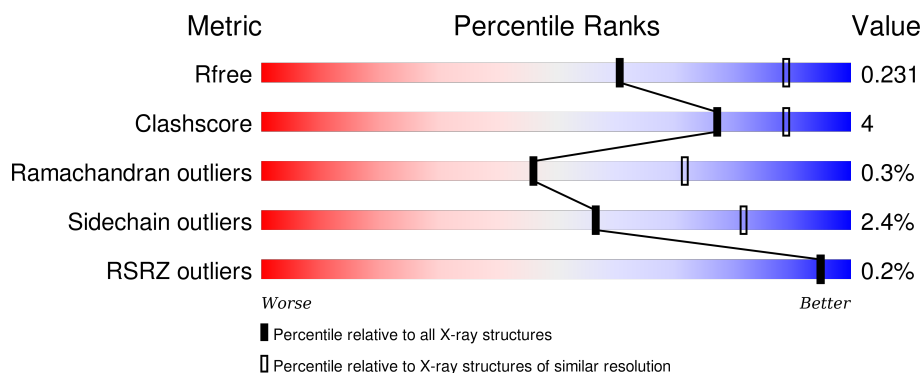
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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. 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	795	 84% 9% • 6%
1	B	795	 83% 10% 6%
1	C	795	 84% 10% • 6%
1	D	795	 85% 9% 6%
1	E	795	 84% 9% • 6%

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Mol	Chain	Length	Quality of chain
1	F	795	

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
2	PGE	A	1785	-	-	-	X
2	PGE	A	1786	-	-	-	X
2	PGE	E	1785	-	-	-	X
3	EDO	A	1787	-	-	-	X
4	PEG	B	1784	-	-	-	X
4	PEG	C	1785	-	-	-	X
4	PEG	C	1787	-	-	-	X
4	PEG	D	1784	-	-	-	X
4	PEG	D	1786	-	-	-	X
6	MES	B	1789	-	-	-	X
6	MES	E	1787	-	-	-	X
7	OAA	C	1788	-	-	-	X
7	OAA	E	1786	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 35839 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 TWO-COMPONENT SYSTEM SENSOR HISTIDINE KINASE/RESPONSE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	747	Total	C	N	O	S	0	0	0
			5869	3734	980	1143	12			
1	B	744	Total	C	N	O	S	0	0	0
			5873	3739	977	1145	12			
1	C	749	Total	C	N	O	S	0	0	0
			5910	3757	988	1153	12			
1	D	745	Total	C	N	O	S	0	0	0
			5880	3739	977	1152	12			
1	E	744	Total	C	N	O	S	0	0	0
			5893	3748	980	1153	12			
1	F	749	Total	C	N	O	S	0	0	0
			5889	3745	983	1149	12			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	788	LEU	-	EXPRESSION TAG	UNP Q89YR8
A	789	GLU	-	EXPRESSION TAG	UNP Q89YR8
A	790	HIS	-	EXPRESSION TAG	UNP Q89YR8
A	791	HIS	-	EXPRESSION TAG	UNP Q89YR8
A	792	HIS	-	EXPRESSION TAG	UNP Q89YR8
A	793	HIS	-	EXPRESSION TAG	UNP Q89YR8
A	794	HIS	-	EXPRESSION TAG	UNP Q89YR8
A	795	HIS	-	EXPRESSION TAG	UNP Q89YR8
B	788	LEU	-	EXPRESSION TAG	UNP Q89YR8
B	789	GLU	-	EXPRESSION TAG	UNP Q89YR8
B	790	HIS	-	EXPRESSION TAG	UNP Q89YR8
B	791	HIS	-	EXPRESSION TAG	UNP Q89YR8
B	792	HIS	-	EXPRESSION TAG	UNP Q89YR8
B	793	HIS	-	EXPRESSION TAG	UNP Q89YR8
B	794	HIS	-	EXPRESSION TAG	UNP Q89YR8
B	795	HIS	-	EXPRESSION TAG	UNP Q89YR8

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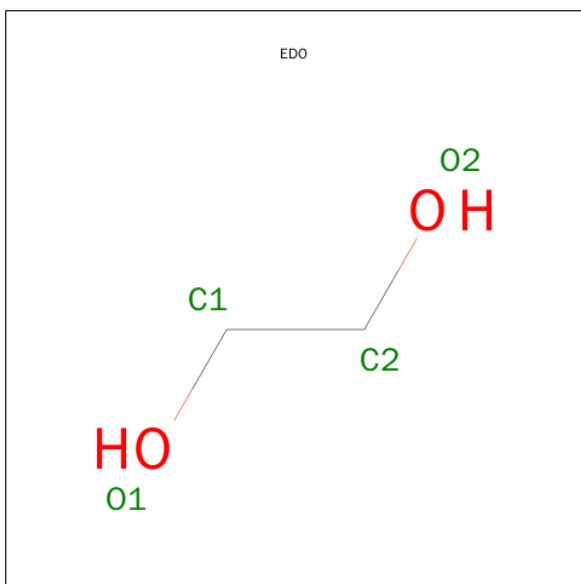
Chain	Residue	Modelled	Actual	Comment	Reference
C	788	LEU	-	EXPRESSION TAG	UNP Q89YR8
C	789	GLU	-	EXPRESSION TAG	UNP Q89YR8
C	790	HIS	-	EXPRESSION TAG	UNP Q89YR8
C	791	HIS	-	EXPRESSION TAG	UNP Q89YR8
C	792	HIS	-	EXPRESSION TAG	UNP Q89YR8
C	793	HIS	-	EXPRESSION TAG	UNP Q89YR8
C	794	HIS	-	EXPRESSION TAG	UNP Q89YR8
C	795	HIS	-	EXPRESSION TAG	UNP Q89YR8
D	788	LEU	-	EXPRESSION TAG	UNP Q89YR8
D	789	GLU	-	EXPRESSION TAG	UNP Q89YR8
D	790	HIS	-	EXPRESSION TAG	UNP Q89YR8
D	791	HIS	-	EXPRESSION TAG	UNP Q89YR8
D	792	HIS	-	EXPRESSION TAG	UNP Q89YR8
D	793	HIS	-	EXPRESSION TAG	UNP Q89YR8
D	794	HIS	-	EXPRESSION TAG	UNP Q89YR8
D	795	HIS	-	EXPRESSION TAG	UNP Q89YR8
E	788	LEU	-	EXPRESSION TAG	UNP Q89YR8
E	789	GLU	-	EXPRESSION TAG	UNP Q89YR8
E	790	HIS	-	EXPRESSION TAG	UNP Q89YR8
E	791	HIS	-	EXPRESSION TAG	UNP Q89YR8
E	792	HIS	-	EXPRESSION TAG	UNP Q89YR8
E	793	HIS	-	EXPRESSION TAG	UNP Q89YR8
E	794	HIS	-	EXPRESSION TAG	UNP Q89YR8
E	795	HIS	-	EXPRESSION TAG	UNP Q89YR8
F	788	LEU	-	EXPRESSION TAG	UNP Q89YR8
F	789	GLU	-	EXPRESSION TAG	UNP Q89YR8
F	790	HIS	-	EXPRESSION TAG	UNP Q89YR8
F	791	HIS	-	EXPRESSION TAG	UNP Q89YR8
F	792	HIS	-	EXPRESSION TAG	UNP Q89YR8
F	793	HIS	-	EXPRESSION TAG	UNP Q89YR8
F	794	HIS	-	EXPRESSION TAG	UNP Q89YR8
F	795	HIS	-	EXPRESSION TAG	UNP Q89YR8

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



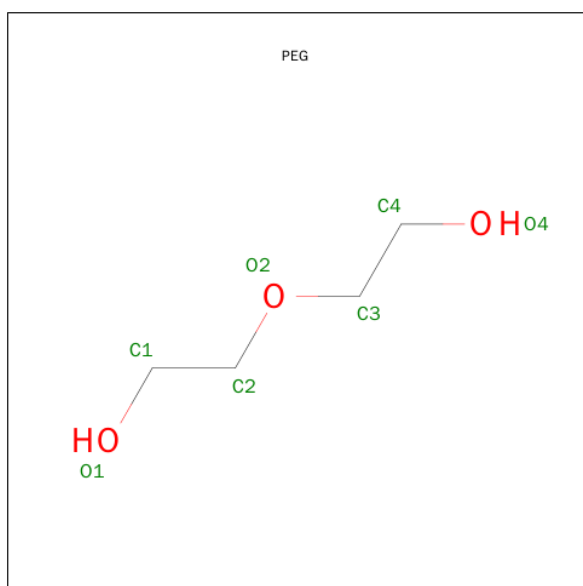
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	6	4		
2	A	1	Total	C	O	0	0
			10	6	4		
2	B	1	Total	C	O	0	0
			10	6	4		
2	E	1	Total	C	O	0	0
			7	4	3		
2	F	1	Total	C	O	0	0
			10	6	4		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



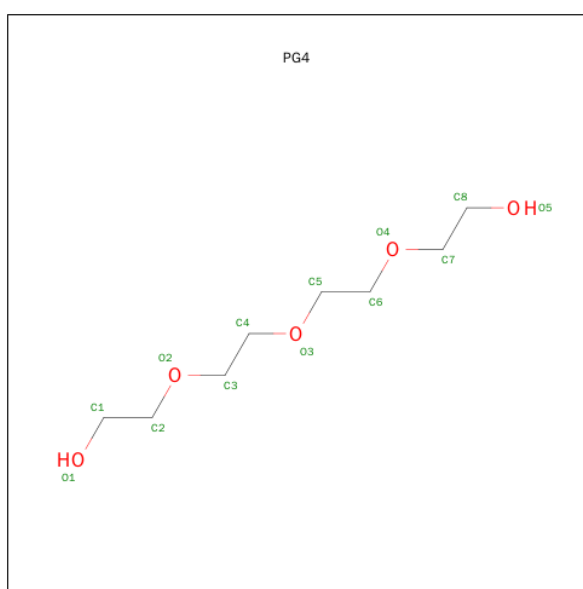
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 7 4 3	0	0
4	C	1	Total C O 7 4 3	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 7 4 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			7	4	3		
4	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



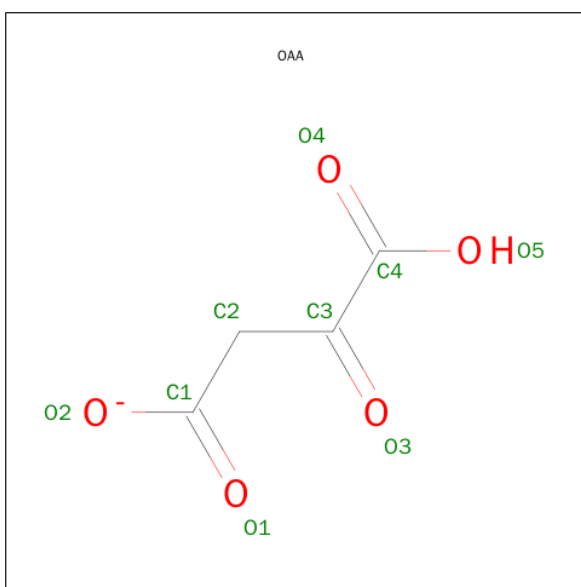
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	E	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 7 is OXALOACETATE ION (three-letter code: OAA) (formula: $C_4H_3O_5$).



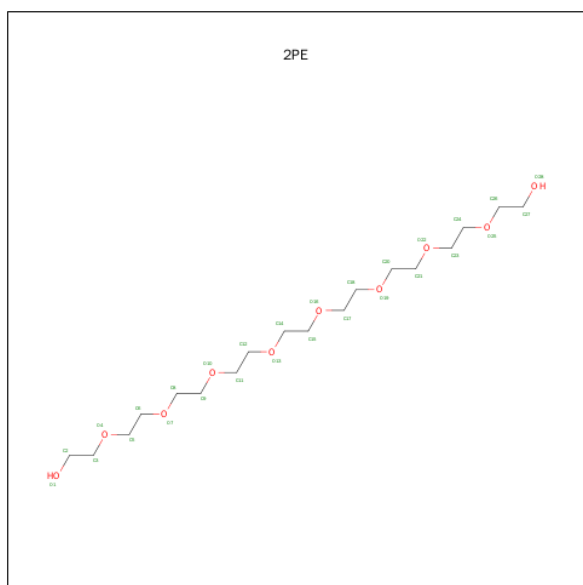
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			9	4	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			9	4	5		
7	E	1	Total	C	O	0	0
			9	4	5		

- Molecule 8 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: C₁₈H₃₈O₁₀).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total	C	O	0	0
			19	12	7		

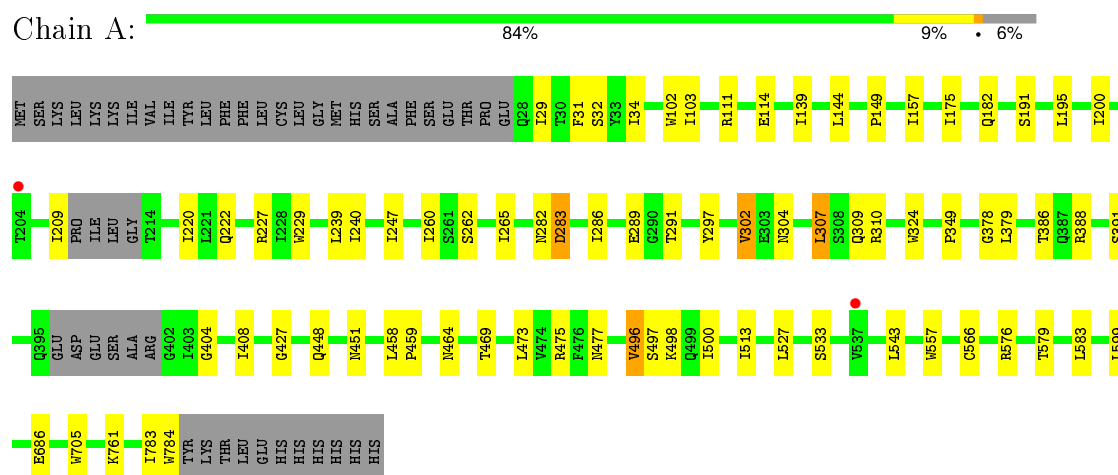
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	68	Total	O	0	0
			68	68		
9	B	36	Total	O	0	0
			36	36		
9	C	75	Total	O	0	0
			75	75		
9	D	37	Total	O	0	0
			37	37		
9	E	36	Total	O	0	0
			36	36		
9	F	49	Total	O	0	0
			49	49		

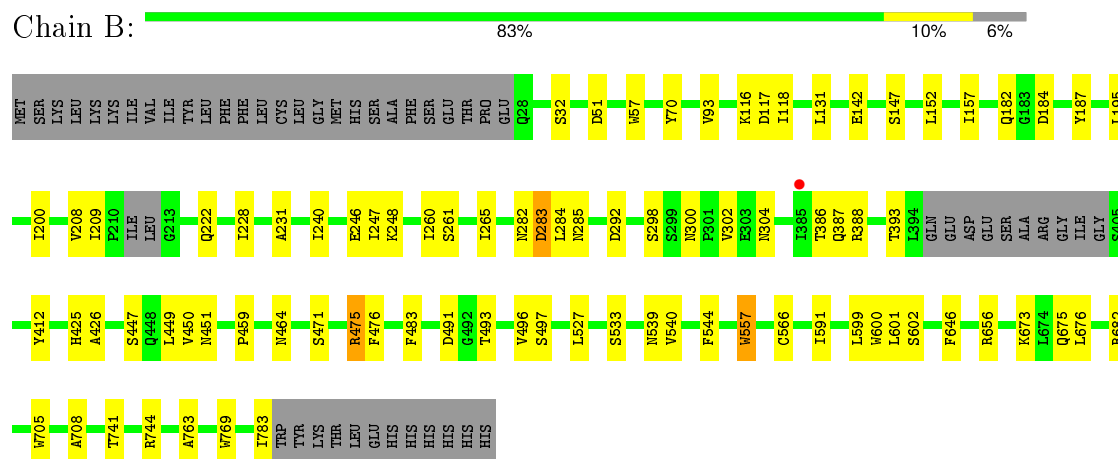
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

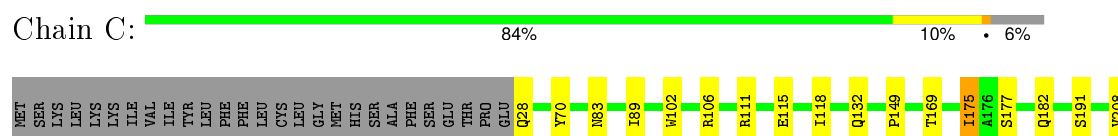
• Molecule 1: TWO-COMPONENT SYSTEM SENSOR HISTIDINE KINASE/RESPONSE

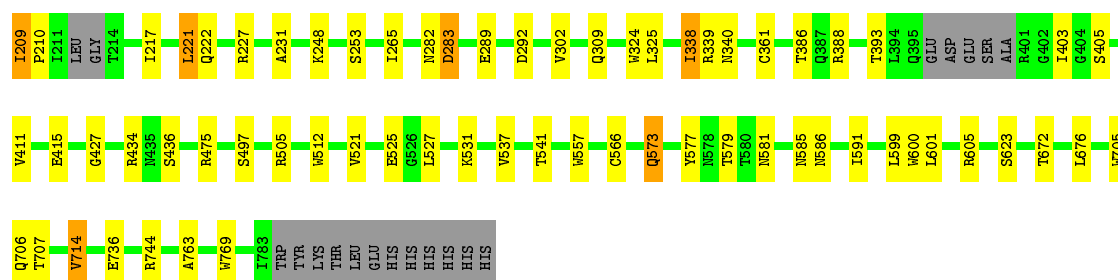


• Molecule 1: TWO-COMPONENT SYSTEM SENSOR HISTIDINE KINASE/RESPONSE




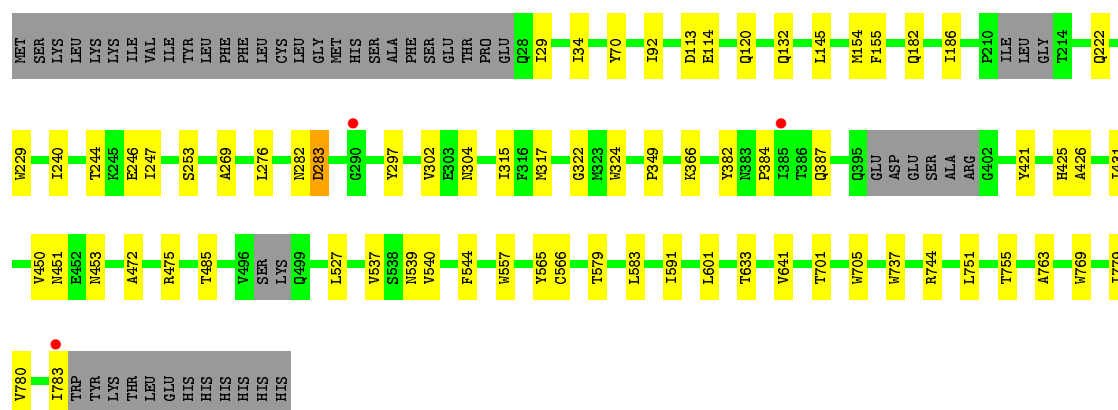
• Molecule 1: TWO-COMPONENT SYSTEM SENSOR HISTIDINE KINASE/RESPONSE



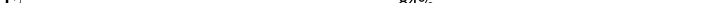


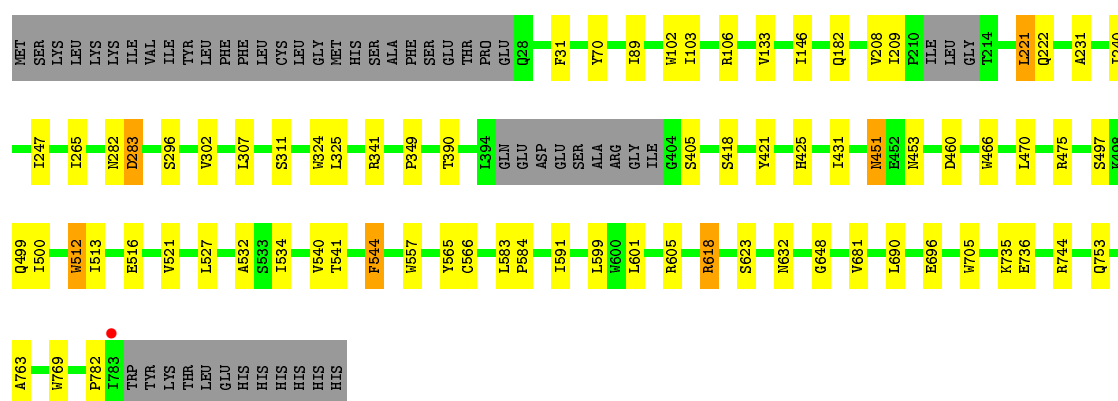
- Molecule 1: TWO-COMPONENT SYSTEM SENSOR HISTIDINE KINASE/RESPONSE

Chain D:  85% 9% 6%

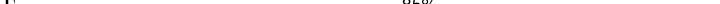


- Molecule 1: TWO-COMPONENT SYSTEM SENSOR HISTIDINE KINASE/RESPONSE

Chain E:  84% 9% • 6%



- Molecule 1: TWO-COMPONENT SYSTEM SENSOR HISTIDINE KINASE/RESPONSE

Chain F:  85% 9% 6%





4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	342.47Å 342.47Å 97.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	296.59 – 2.60 62.97 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.0 (296.59-2.60) 90.3 (62.97-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.186 , 0.231 0.188 , 0.231	Depositor DCC
R_{free} test set	9134 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.0	EDS
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 181421 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	35839	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PGE, OAA, EDO, PG4, 2PE, MES, PEG

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	0.59	2/6006 (0.0%)	0.69	0/8175
1	B	0.59	2/6009 (0.0%)	0.70	1/8172 (0.0%)
1	C	0.59	1/6046 (0.0%)	0.70	1/8222 (0.0%)
1	D	0.58	2/6015 (0.0%)	0.68	0/8183
1	E	0.58	3/6029 (0.0%)	0.68	1/8196 (0.0%)
1	F	0.59	0/6024	0.69	1/8194 (0.0%)
All	All	0.59	10/36129 (0.0%)	0.69	4/49142 (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	A	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	784	TRP	CD2-CE2	6.03	1.48	1.41
1	E	512	TRP	CD2-CE2	5.64	1.48	1.41
1	D	705	TRP	CD2-CE2	5.52	1.48	1.41
1	E	466	TRP	CD2-CE2	5.49	1.48	1.41
1	D	737	TRP	CD2-CE2	5.25	1.47	1.41
1	B	557	TRP	CD2-CE2	5.25	1.47	1.41
1	C	705	TRP	CD2-CE2	5.22	1.47	1.41
1	A	705	TRP	CD2-CE2	5.18	1.47	1.41
1	B	705	TRP	CD2-CE2	5.12	1.47	1.41
1	E	705	TRP	CD2-CE2	5.11	1.47	1.41

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	475	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	E	618	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	F	618	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	C	434	ARG	NE-CZ-NH2	-5.12	117.74	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	404	GLY	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	5869	0	5549	38	0
1	B	5873	0	5582	50	0
1	C	5910	0	5615	48	0
1	D	5880	0	5556	37	0
1	E	5893	0	5609	51	0
1	F	5889	0	5568	41	0
2	A	20	0	28	0	0
2	B	10	0	14	0	0
2	E	7	0	9	0	0
2	F	10	0	14	0	0
3	A	4	0	6	0	0
3	B	8	0	12	0	0
3	C	4	0	6	0	0
3	D	4	0	6	0	0
4	A	7	0	10	0	0
4	B	4	0	5	0	0
4	C	18	0	25	1	0
4	D	19	0	25	1	0
4	E	7	0	10	0	0
4	F	7	0	10	0	0
5	B	13	0	18	0	0
6	B	12	0	12	0	0
6	D	12	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	12	0	12	2	0
7	C	18	0	4	0	0
7	E	9	0	2	0	0
8	D	19	0	25	0	0
9	A	68	0	0	0	0
9	B	36	0	0	1	0
9	C	75	0	0	0	0
9	D	37	0	0	0	0
9	E	36	0	0	1	0
9	F	49	0	0	0	0
All	All	35839	0	33744	259	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 (259) 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:755:THR:HG22	1:D:779:ILE:HG23	1.45	0.96
1:B:208:VAL:HG12	1:B:209:ILE:HD13	1.59	0.82
1:E:425:HIS:O	1:E:453:ASN:ND2	2.14	0.80
1:C:393:THR:C	1:C:403:ILE:HG22	2.06	0.77
1:F:105:THR:HG22	1:F:107:ASP:H	1.48	0.75
1:E:208:VAL:HG12	1:E:209:ILE:HD12	1.68	0.75
1:E:302:VAL:HG13	1:E:349:PRO:HD2	1.68	0.74
1:F:240:ILE:HG12	1:F:247:ILE:HG22	1.69	0.74
1:D:579:THR:HG22	1:D:583:LEU:O	1.88	0.73
1:F:521:VAL:HG13	1:F:532:ALA:HB3	1.71	0.71
1:E:540:VAL:HG13	1:E:565:TYR:CZ	2.26	0.71
1:E:540:VAL:HG13	1:E:565:TYR:CE1	2.26	0.70
1:E:500:ILE:HD12	1:E:513:ILE:CG2	2.23	0.69
1:D:591:ILE:HG12	1:D:601:LEU:HD22	1.76	0.68
1:C:209:ILE:HG22	1:C:210:PRO:HD2	1.75	0.67
1:C:282:ASN:O	1:C:283:ASP:HB2	1.94	0.67
1:D:557:TRP:CE3	1:D:566:CYS:HB3	2.31	0.66
1:F:641:VAL:O	1:F:656:ARG:NH2	2.28	0.66
1:B:450:VAL:HG23	1:B:451:ASN:N	2.12	0.65
1:C:361:CYS:SG	1:C:411:VAL:HG23	2.37	0.64
1:E:282:ASN:O	1:E:283:ASP:HB2	1.97	0.64
1:F:282:ASN:O	1:F:283:ASP:HB2	1.97	0.64
1:E:182:GLN:HG2	1:E:222:GLN:OE1	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:763:ALA:HB2	1:F:769:TRP:CD2	2.34	0.63
1:A:282:ASN:O	1:A:283:ASP:HB2	1.99	0.63
1:E:231:ALA:HB1	1:E:265:ILE:HG22	1.81	0.62
1:B:557:TRP:CZ3	1:B:566:CYS:HB3	2.34	0.62
1:E:540:VAL:CG1	1:E:565:TYR:CZ	2.82	0.62
1:E:500:ILE:HD12	1:E:513:ILE:HG23	1.81	0.62
1:E:763:ALA:HB2	1:E:769:TRP:CD2	2.35	0.62
1:A:182:GLN:HG2	1:A:222:GLN:OE1	2.00	0.62
1:E:451:ASN:HD22	1:E:453:ASN:H	1.47	0.61
1:E:500:ILE:CD1	1:E:513:ILE:CG2	2.78	0.61
1:B:261:SER:HB2	1:B:285:ASN:HD21	1.63	0.61
1:F:29:ILE:HD12	1:F:297:TYR:CZ	2.35	0.61
1:D:240:ILE:HG12	1:D:247:ILE:HG22	1.83	0.61
1:C:386:THR:HG21	1:C:388:ARG:HD3	1.82	0.61
1:F:408:ILE:HD13	1:F:424:THR:HG22	1.84	0.60
1:D:425:HIS:O	1:D:453:ASN:ND2	2.33	0.60
1:B:284:LEU:C	1:B:285:ASN:HD22	2.06	0.58
1:B:763:ALA:HB2	1:B:769:TRP:CD2	2.38	0.58
1:F:460:ASP:OD2	1:F:475:ARG:NH1	2.36	0.58
1:F:149:PRO:O	1:F:175:ILE:HD12	2.03	0.58
1:A:557:TRP:CZ3	1:A:566:CYS:HB3	2.39	0.58
1:A:543:LEU:HD11	1:A:576:ARG:HH11	1.68	0.58
1:B:673:LYS:HE3	1:B:675:GLN:HE21	1.70	0.57
1:C:227:ARG:NH1	1:C:289:GLU:OE2	2.36	0.57
1:F:105:THR:HG22	1:F:107:ASP:N	2.19	0.57
1:D:450:VAL:HG23	1:D:451:ASN:N	2.20	0.56
1:B:282:ASN:O	1:B:283:ASP:HB2	2.05	0.56
1:F:92:ILE:HG22	1:F:104:GLY:HA3	1.87	0.56
1:B:591:ILE:HG12	1:B:601:LEU:HD22	1.87	0.56
1:F:557:TRP:CE2	1:F:599:LEU:HD11	2.40	0.56
1:C:338:ILE:HG22	1:C:339:ARG:N	2.20	0.56
1:B:142:GLU:HA	1:B:157:ILE:HD12	1.85	0.56
1:E:696:GLU:HB2	9:E:2003:HOH:O	2.05	0.56
1:B:240:ILE:HG12	1:B:247:ILE:HG22	1.88	0.56
1:A:473:LEU:HD22	1:A:513:ILE:HD11	1.87	0.56
1:E:221:LEU:HD12	1:E:222:GLN:N	2.21	0.56
1:A:29:ILE:HD12	1:A:297:TYR:CZ	2.41	0.55
1:F:602:SER:HB3	1:F:646:PHE:CD1	2.42	0.55
1:F:501:THR:HG23	1:F:515:GLY:HA2	1.88	0.55
1:D:426:ALA:HA	1:D:453:ASN:HD22	1.72	0.55
1:C:221:LEU:C	1:C:221:LEU:HD12	2.26	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:LEU:HD11	1:A:220:ILE:HD13	1.89	0.55
1:B:300:ASN:OD1	1:B:302:VAL:HG22	2.06	0.55
1:C:557:TRP:CZ3	1:C:566:CYS:HB3	2.42	0.55
1:B:676:LEU:HD12	1:B:708:ALA:O	2.06	0.54
1:B:602:SER:HB3	1:B:646:PHE:CD1	2.42	0.54
1:F:444:GLN:HG3	1:F:452:GLU:HG3	1.88	0.54
1:B:282:ASN:O	1:B:283:ASP:CB	2.54	0.54
1:D:557:TRP:CZ3	1:D:566:CYS:HB3	2.43	0.54
1:E:557:TRP:CZ3	1:E:566:CYS:HB3	2.44	0.53
1:C:28:GLN:O	1:C:340:ASN:ND2	2.41	0.53
1:D:302:VAL:O	1:D:302:VAL:CG1	2.57	0.53
1:A:139:ILE:O	1:A:200:ILE:HD13	2.09	0.53
1:B:260:ILE:HD11	1:B:265:ILE:CD1	2.39	0.53
1:E:324:TRP:C	1:E:325:LEU:HD12	2.28	0.53
1:E:302:VAL:HG22	1:F:302:VAL:HG12	1.90	0.52
1:E:591:ILE:HG12	1:E:601:LEU:HD22	1.91	0.52
1:F:282:ASN:O	1:F:283:ASP:CB	2.57	0.52
1:A:579:THR:HG22	1:A:583:LEU:O	2.09	0.52
1:C:282:ASN:O	1:C:283:ASP:CB	2.57	0.52
1:C:302:VAL:CG1	1:D:302:VAL:HG22	2.39	0.52
1:A:458:LEU:HD12	1:A:459:PRO:HD2	1.90	0.52
1:A:302:VAL:CG1	1:B:302:VAL:HG12	2.40	0.52
1:E:753:GLN:OE1	1:E:782:PRO:HB3	2.09	0.52
1:E:311:SER:CB	6:E:1787:MES:O3S	2.58	0.52
1:E:475:ARG:NH2	1:E:527:LEU:O	2.43	0.52
1:B:763:ALA:HB2	1:B:769:TRP:CE2	2.45	0.52
1:A:31:PHE:CE2	1:A:307:LEU:HD13	2.45	0.52
1:E:302:VAL:HG22	1:F:302:VAL:CG1	2.40	0.51
1:F:521:VAL:HG11	1:F:534:ILE:HG12	1.92	0.51
1:F:93:VAL:HG23	1:F:103:ILE:HD13	1.93	0.51
1:D:763:ALA:HB2	1:D:769:TRP:CD2	2.45	0.51
1:B:450:VAL:CG2	1:B:451:ASN:N	2.73	0.51
1:D:426:ALA:HA	1:D:453:ASN:ND2	2.26	0.51
1:A:282:ASN:O	1:A:283:ASP:CB	2.59	0.51
1:B:557:TRP:CE2	1:B:599:LEU:HD11	2.46	0.51
1:C:600:TRP:C	1:C:601:LEU:HD23	2.32	0.51
1:C:132:GLN:O	1:C:149:PRO:HD3	2.11	0.51
1:E:681:VAL:HG12	1:E:690:LEU:HD12	1.93	0.50
1:B:260:ILE:HD11	1:B:265:ILE:HD13	1.93	0.50
1:C:763:ALA:HB2	1:C:769:TRP:CD2	2.47	0.50
1:E:583:LEU:HD12	1:E:584:PRO:HD2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:282:ASN:O	1:E:283:ASP:CB	2.60	0.50
1:A:229:TRP:CE2	1:A:239:LEU:HD13	2.46	0.50
1:C:89:ILE:HD12	1:C:106:ARG:HD2	1.93	0.50
1:B:557:TRP:CE3	1:B:566:CYS:HB3	2.47	0.50
1:D:475:ARG:NH2	1:D:527:LEU:O	2.45	0.50
1:B:187:TYR:OH	1:B:228:ILE:HD11	2.12	0.50
1:A:473:LEU:HD22	1:A:513:ILE:CD1	2.40	0.49
1:E:70:TYR:CD2	1:E:744:ARG:HD2	2.47	0.49
1:A:149:PRO:O	1:A:175:ILE:HD12	2.12	0.49
1:C:393:THR:O	1:C:403:ILE:HG22	2.11	0.49
1:B:475:ARG:NH2	1:B:527:LEU:O	2.45	0.49
1:A:302:VAL:HG11	1:B:302:VAL:HG12	1.95	0.49
1:B:51:ASP:HB2	9:B:2004:HOH:O	2.12	0.49
1:D:366:LYS:HA	4:D:1785:PEG:H22	1.94	0.49
1:A:475:ARG:NH2	1:A:527:LEU:O	2.45	0.49
1:F:241:ASN:ND2	1:F:244:THR:H	2.09	0.49
1:C:324:TRP:C	1:C:325:LEU:HD12	2.33	0.49
1:C:325:LEU:HD12	1:C:325:LEU:N	2.28	0.49
1:B:412:TYR:CZ	1:B:459:PRO:HG3	2.47	0.49
1:C:672:THR:CG2	1:C:714:VAL:HG22	2.42	0.49
1:F:105:THR:CG2	1:F:106:ARG:N	2.75	0.49
1:D:282:ASN:O	1:D:283:ASP:HB2	2.13	0.49
1:E:31:PHE:CE2	1:E:307:LEU:HD13	2.46	0.49
1:C:579:THR:HG23	1:C:586:ASN:OD1	2.13	0.49
1:B:261:SER:CB	1:B:285:ASN:HD21	2.24	0.48
1:C:175:ILE:CD1	1:C:175:ILE:N	2.76	0.48
1:C:302:VAL:HG11	1:D:302:VAL:HG22	1.94	0.48
1:C:475:ARG:NH2	1:C:527:LEU:O	2.46	0.48
1:C:386:THR:HG21	1:C:388:ARG:CD	2.44	0.48
1:F:475:ARG:NH2	1:F:527:LEU:O	2.47	0.48
1:C:339:ARG:NH2	1:C:623:SER:O	2.46	0.48
1:F:31:PHE:CE2	1:F:307:LEU:HD13	2.49	0.48
1:B:208:VAL:HG12	1:B:209:ILE:CD1	2.38	0.47
1:E:557:TRP:CE2	1:E:599:LEU:HD11	2.49	0.47
1:A:260:ILE:HD12	1:A:265:ILE:HD11	1.96	0.47
1:F:763:ALA:HB2	1:F:769:TRP:CE2	2.49	0.47
1:D:540:VAL:HB	1:D:565:TYR:CE2	2.49	0.47
1:A:543:LEU:HD11	1:A:576:ARG:NH1	2.29	0.47
1:D:384:PRO:O	1:D:387:GLN:NE2	2.47	0.47
1:F:105:THR:CG2	1:F:107:ASP:H	2.21	0.47
1:F:635:SER:OG	1:F:647:GLY:HA3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:600:TRP:C	1:B:601:LEU:HD23	2.35	0.47
1:F:300:ASN:OD1	1:F:302:VAL:HG22	2.14	0.47
1:E:231:ALA:CB	1:E:265:ILE:HG22	2.45	0.46
1:D:244:THR:OG1	1:D:246:GLU:HG2	2.15	0.46
1:A:102:TRP:O	1:A:103:ILE:HD13	2.14	0.46
1:F:271:ASP:OD1	1:F:271:ASP:C	2.54	0.46
1:C:386:THR:HG22	1:C:388:ARG:HG3	1.98	0.46
1:A:464:ASN:OD1	1:A:477:ASN:ND2	2.42	0.46
1:D:34:ILE:HD12	1:D:324:TRP:CZ3	2.50	0.46
1:C:248:LYS:NZ	1:C:292:ASP:OD2	2.48	0.46
1:C:208:VAL:HG12	1:C:209:ILE:HG13	1.97	0.46
1:D:751:LEU:O	1:D:780:VAL:HG11	2.15	0.46
1:F:241:ASN:ND2	1:F:244:THR:HG23	2.31	0.46
1:E:209:ILE:HD13	1:E:240:ILE:HD13	1.97	0.46
1:C:577:TYR:HA	1:C:581:ASN:OD1	2.16	0.46
1:A:302:VAL:HG11	1:A:349:PRO:HB2	1.99	0.45
1:F:133:VAL:HG13	1:F:146:ILE:HG23	1.97	0.45
1:F:318:ASP:OD1	1:F:318:ASP:C	2.54	0.45
1:E:763:ALA:HB2	1:E:769:TRP:CE2	2.52	0.45
1:D:302:VAL:HG13	1:D:349:PRO:HD2	1.98	0.45
1:C:70:TYR:CD2	1:C:744:ARG:HD2	2.51	0.45
1:A:29:ILE:CD1	1:A:286:ILE:HD12	2.47	0.45
1:B:248:LYS:NZ	1:B:292:ASP:OD2	2.49	0.45
1:C:714:VAL:HG13	1:C:744:ARG:NH2	2.32	0.45
1:B:142:GLU:C	1:B:157:ILE:HD12	2.38	0.45
1:D:317:MET:HA	1:D:322:GLY:O	2.17	0.45
1:D:154:MET:HG2	1:D:155:PHE:N	2.32	0.45
1:B:142:GLU:CA	1:B:157:ILE:HD12	2.47	0.45
1:A:386:THR:HG22	1:A:388:ARG:HB2	1.99	0.45
1:F:142:GLU:HA	1:F:157:ILE:HD12	1.98	0.45
1:F:472:ALA:HB1	1:F:485:THR:HG23	1.99	0.45
1:D:113:ASP:HB2	1:D:120:GLN:NE2	2.32	0.45
1:C:505:ARG:NE	4:C:1787:PEG:H22	2.32	0.44
1:C:672:THR:HG23	1:C:714:VAL:HG22	2.00	0.44
1:A:34:ILE:HD12	1:A:324:TRP:CZ3	2.52	0.44
1:B:783:ILE:HD12	1:B:783:ILE:N	2.33	0.44
1:E:500:ILE:CD1	1:E:513:ILE:HG21	2.48	0.44
1:B:187:TYR:HB3	1:B:195:LEU:HD11	1.99	0.44
1:A:378:GLY:C	1:A:408:ILE:HD13	2.38	0.44
1:D:29:ILE:HB	1:D:297:TYR:CE1	2.53	0.44
1:F:105:THR:HG23	1:F:106:ARG:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:382:TYR:CD1	1:D:382:TYR:C	2.91	0.43
1:E:541:THR:O	1:E:541:THR:HG22	2.17	0.43
1:C:512:TRP:CD2	1:C:521:VAL:HG22	2.53	0.43
1:B:182:GLN:HG2	1:B:222:GLN:OE1	2.17	0.43
1:F:496:VAL:O	1:F:496:VAL:HG23	2.17	0.43
1:E:102:TRP:O	1:E:103:ILE:HD13	2.18	0.43
1:D:282:ASN:O	1:D:283:ASP:CB	2.67	0.43
1:E:512:TRP:CE3	1:E:521:VAL:HG22	2.53	0.43
1:E:557:TRP:CE3	1:E:566:CYS:HB3	2.54	0.43
1:F:51:ASP:OD1	1:F:51:ASP:C	2.57	0.43
1:C:591:ILE:HG12	1:C:601:LEU:HD22	2.00	0.43
1:A:557:TRP:CE2	1:A:599:LEU:HD11	2.53	0.43
1:A:500:ILE:HD12	1:A:513:ILE:HG22	2.00	0.43
1:A:500:ILE:HD12	1:A:513:ILE:CG2	2.49	0.43
1:B:260:ILE:CD1	1:B:265:ILE:HD11	2.49	0.43
1:A:451:ASN:HB3	1:A:469:THR:HB	2.00	0.43
1:F:287:TYR:OH	1:F:292:ASP:OD1	2.29	0.43
1:B:57:TRP:HB3	1:B:93:VAL:HG21	2.00	0.43
1:A:240:ILE:HG12	1:A:247:ILE:HG22	2.01	0.43
1:A:144:LEU:HG	1:A:157:ILE:HD11	2.00	0.43
1:D:70:TYR:CD2	1:D:744:ARG:HD2	2.54	0.43
1:C:83:ASN:HB3	1:C:118:ILE:HB	2.01	0.42
1:B:231:ALA:HB1	1:B:265:ILE:HB	2.01	0.42
1:C:585:ASN:HB2	1:C:605:ARG:HB2	2.01	0.42
1:C:537:VAL:CG1	1:C:537:VAL:O	2.67	0.42
1:E:89:ILE:HD12	1:E:106:ARG:HD2	2.00	0.42
1:E:231:ALA:HB1	1:E:265:ILE:CG2	2.49	0.42
1:E:311:SER:OG	6:E:1787:MES:O3S	2.34	0.42
1:B:70:TYR:CD2	1:B:744:ARG:HD2	2.55	0.42
1:B:449:LEU:HD13	1:B:483:PHE:CD2	2.54	0.42
1:B:184:ASP:O	1:B:200:ILE:HD12	2.20	0.42
1:E:632:ASN:HB2	1:E:648:GLY:HA2	2.02	0.42
1:E:460:ASP:OD2	1:E:475:ARG:NH1	2.53	0.42
1:E:470:LEU:O	1:E:499:GLN:HA	2.20	0.42
1:C:102:TRP:CZ3	1:C:111:ARG:HB2	2.55	0.42
1:C:676:LEU:HD21	1:C:706:GLN:HG2	2.01	0.42
1:C:557:TRP:CE2	1:C:599:LEU:HD11	2.55	0.42
1:D:182:GLN:HG2	1:D:222:GLN:OE1	2.20	0.42
1:F:324:TRP:C	1:F:325:LEU:HD12	2.40	0.42
1:E:208:VAL:HG12	1:E:209:ILE:CD1	2.44	0.42
1:E:240:ILE:HG12	1:E:247:ILE:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:302:VAL:HG11	1:D:349:PRO:HB2	2.01	0.42
1:E:133:VAL:HG13	1:E:146:ILE:HG23	2.02	0.42
1:E:421:TYR:CD1	1:E:431:ILE:HG12	2.55	0.41
1:A:783:ILE:N	1:A:783:ILE:HD12	2.35	0.41
1:A:227:ARG:NH2	1:A:289:GLU:OE2	2.51	0.41
1:A:379:LEU:O	1:A:391:SER:HA	2.20	0.41
1:C:231:ALA:HB1	1:C:265:ILE:HG22	2.02	0.41
1:E:516:GLU:HG2	1:E:544:PHE:CZ	2.56	0.41
1:B:491:ASP:HB2	1:B:493:THR:H	1.85	0.41
1:D:472:ALA:HB1	1:D:485:THR:HG23	2.01	0.41
1:E:735:LYS:C	1:E:736:GLU:HG3	2.40	0.41
1:A:34:ILE:HD12	1:A:324:TRP:HZ3	1.85	0.41
1:D:145:LEU:HD23	1:D:186:ILE:HG21	2.02	0.41
1:B:425:HIS:O	1:B:426:ALA:HB3	2.20	0.41
1:B:386:THR:HB	1:B:388:ARG:HG3	2.03	0.41
1:B:147:SER:HA	1:B:152:LEU:HD23	2.03	0.41
1:B:450:VAL:CG2	1:B:451:ASN:H	2.33	0.41
1:D:229:TRP:CE2	1:D:276:LEU:HD22	2.55	0.41
1:C:557:TRP:CE3	1:C:566:CYS:HB3	2.56	0.41
1:D:269:ALA:HB3	1:D:315:ILE:CG2	2.51	0.41
1:D:421:TYR:CD1	1:D:431:ILE:HG12	2.56	0.41
1:A:496:VAL:O	1:A:498:LYS:N	2.54	0.40
1:F:512:TRP:CZ2	1:F:556:ILE:HD12	2.56	0.40
1:E:532:ALA:HB1	1:E:534:ILE:HG23	2.02	0.40
1:C:221:LEU:HD12	1:C:222:GLN:N	2.36	0.40
1:C:573:GLN:HE21	1:C:573:GLN:HB3	1.69	0.40
1:C:182:GLN:HG2	1:C:222:GLN:OE1	2.21	0.40
1:B:464:ASN:HB3	1:B:476:PHE:O	2.21	0.40
1:B:116:LYS:HB2	1:B:118:ILE:HG12	2.04	0.40
1:B:117:ASP:O	1:B:682:ARG:NH2	2.55	0.40
1:C:177:SER:OG	1:C:217:ILE:O	2.22	0.40

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	741/795 (93%)	713 (96%)	25 (3%)	3 (0%)	39	65
1	B	738/795 (93%)	709 (96%)	27 (4%)	2 (0%)	46	72
1	C	743/795 (94%)	721 (97%)	19 (3%)	3 (0%)	39	65
1	D	737/795 (93%)	720 (98%)	16 (2%)	1 (0%)	56	81
1	E	738/795 (93%)	716 (97%)	20 (3%)	2 (0%)	46	72
1	F	743/795 (94%)	710 (96%)	30 (4%)	3 (0%)	39	65
All	All	4440/4770 (93%)	4289 (97%)	137 (3%)	14 (0%)	46	72

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	497	SER
1	B	283	ASP
1	E	497	SER
1	A	283	ASP
1	C	283	ASP
1	D	283	ASP
1	E	283	ASP
1	F	427	GLY
1	F	497	SER
1	A	427	GLY
1	C	427	GLY
1	F	283	ASP
1	B	497	SER
1	C	497	SER

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	632/712 (89%)	615 (97%)	17 (3%)	52	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	635/712 (89%)	619 (98%)	16 (2%)	55	81
1	C	640/712 (90%)	621 (97%)	19 (3%)	48	76
1	D	634/712 (89%)	622 (98%)	12 (2%)	65	86
1	E	641/712 (90%)	630 (98%)	11 (2%)	68	88
1	F	631/712 (89%)	616 (98%)	15 (2%)	57	82
All	All	3813/4272 (89%)	3723 (98%)	90 (2%)	57	82

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	SER
1	A	111	ARG
1	A	114	GLU
1	A	191	SER
1	A	209	ILE
1	A	262	SER
1	A	291	THR
1	A	302	VAL
1	A	304	ASN
1	A	307	LEU
1	A	309	GLN
1	A	310	ARG
1	A	448	GLN
1	A	496	VAL
1	A	533	SER
1	A	686	GLU
1	A	761	LYS
1	B	32	SER
1	B	131	LEU
1	B	246	GLU
1	B	298	SER
1	B	304	ASN
1	B	387	GLN
1	B	393	THR
1	B	447	SER
1	B	471	SER
1	B	496	VAL
1	B	533	SER
1	B	539	ASN
1	B	540	VAL

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Mol	Chain	Res	Type
1	B	544	PHE
1	B	656	ARG
1	B	741	THR
1	C	115	GLU
1	C	169	THR
1	C	175	ILE
1	C	191	SER
1	C	209	ILE
1	C	221	LEU
1	C	253	SER
1	C	309	GLN
1	C	338	ILE
1	C	405	SER
1	C	415	GLU
1	C	436	SER
1	C	525	GLU
1	C	531	LYS
1	C	541	THR
1	C	573	GLN
1	C	707	THR
1	C	714	VAL
1	C	736	GLU
1	D	92	ILE
1	D	114	GLU
1	D	132	GLN
1	D	253	SER
1	D	304	ASN
1	D	537	VAL
1	D	539	ASN
1	D	544	PHE
1	D	633	THR
1	D	641	VAL
1	D	701	THR
1	D	783	ILE
1	E	221	LEU
1	E	296	SER
1	E	341	ARG
1	E	390	THR
1	E	405	SER
1	E	418	SER
1	E	451	ASN
1	E	544	PHE

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Mol	Chain	Res	Type
1	E	605	ARG
1	E	618	ARG
1	E	623	SER
1	F	28	GLN
1	F	32	SER
1	F	105	THR
1	F	309	GLN
1	F	376	ASP
1	F	390	THR
1	F	418	SER
1	F	467	LEU
1	F	487	GLU
1	F	520	SER
1	F	530	GLN
1	F	544	PHE
1	F	618	ARG
1	F	745	THR
1	F	749	SER

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

Mol	Chain	Res	Type
1	B	98	GLN
1	B	675	GLN
1	C	448	GLN
1	C	573	GLN
1	C	675	GLN
1	C	722	GLN
1	D	120	GLN
1	E	304	ASN
1	E	441	ASN
1	F	28	GLN
1	F	222	GLN
1	F	241	ASN
1	F	675	GLN
1	F	757	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

29 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	PGE	A	1785	-	9,9,9	0.54	0	8,8,8	0.53	0
2	PGE	A	1786	-	9,9,9	0.65	0	8,8,8	0.38	0
3	EDO	A	1787	-	3,3,3	0.56	0	2,2,2	0.30	0
4	PEG	A	1788	-	6,6,6	0.57	0	5,5,5	0.44	0
4	PEG	B	1784	-	3,3,6	0.61	0	2,2,5	0.17	0
5	PG4	B	1785	-	12,12,12	0.58	0	11,11,11	0.35	0
2	PGE	B	1786	-	9,9,9	0.55	0	8,8,8	0.35	0
3	EDO	B	1787	-	3,3,3	0.54	0	2,2,2	0.39	0
3	EDO	B	1788	-	3,3,3	0.54	0	2,2,2	0.32	0
6	MES	B	1789	-	11,12,12	1.18	1 (9%)	14,16,16	7.62	10 (71%)
4	PEG	C	1784	-	3,3,6	0.41	0	2,2,5	0.42	0
4	PEG	C	1785	-	6,6,6	0.54	0	5,5,5	0.27	0
3	EDO	C	1786	-	3,3,3	0.53	0	2,2,2	0.36	0
4	PEG	C	1787	-	6,6,6	0.63	0	5,5,5	0.56	0
7	OAA	C	1788	-	2,8,8	8.77	2 (100%)	2,10,10	3.74	1 (50%)
7	OAA	C	1789	-	2,8,8	9.06	2 (100%)	2,10,10	4.81	1 (50%)
4	PEG	D	1784	-	3,3,6	0.60	0	2,2,5	0.12	0
4	PEG	D	1785	-	6,6,6	0.44	0	5,5,5	0.41	0
4	PEG	D	1786	-	3,3,6	0.50	0	2,2,5	0.28	0
3	EDO	D	1787	-	3,3,3	0.50	0	2,2,2	0.42	0
8	2PE	D	1788	-	18,18,27	0.58	0	17,17,26	0.41	0
4	PEG	D	1789	-	3,3,6	0.57	0	2,2,5	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	MES	D	1790	-	11,12,12	0.94	0	14,16,16	8.26	9 (64%)
4	PEG	E	1784	-	6,6,6	0.50	0	5,5,5	0.32	0
2	PGE	E	1785	-	6,6,9	0.58	0	5,5,8	0.31	0
7	OAA	E	1786	-	2,8,8	9.16	2 (100%)	2,10,10	2.49	1 (50%)
6	MES	E	1787	-	11,12,12	0.85	0	14,16,16	9.37	10 (71%)
2	PGE	F	1784	-	9,9,9	0.64	0	8,8,8	0.42	0
4	PEG	F	1785	-	6,6,6	0.51	0	5,5,5	0.20	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	PGE	A	1785	-	-	0/7/7/7	0/0/0/0
2	PGE	A	1786	-	-	0/7/7/7	0/0/0/0
3	EDO	A	1787	-	-	0/1/1/1	0/0/0/0
4	PEG	A	1788	-	-	0/4/4/4	0/0/0/0
4	PEG	B	1784	-	-	0/1/1/4	0/0/0/0
5	PG4	B	1785	-	-	0/10/10/10	0/0/0/0
2	PGE	B	1786	-	-	0/7/7/7	0/0/0/0
3	EDO	B	1787	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1788	-	-	0/1/1/1	0/0/0/0
6	MES	B	1789	-	-	0/6/14/14	0/1/1/1
4	PEG	C	1784	-	-	0/1/1/4	0/0/0/0
4	PEG	C	1785	-	-	0/4/4/4	0/0/0/0
3	EDO	C	1786	-	-	0/1/1/1	0/0/0/0
4	PEG	C	1787	-	-	0/4/4/4	0/0/0/0
7	OAA	C	1788	-	-	0/2/8/8	0/0/0/0
7	OAA	C	1789	-	-	0/2/8/8	0/0/0/0
4	PEG	D	1784	-	-	0/1/1/4	0/0/0/0
4	PEG	D	1785	-	-	0/4/4/4	0/0/0/0
4	PEG	D	1786	-	-	0/1/1/4	0/0/0/0
3	EDO	D	1787	-	-	0/1/1/1	0/0/0/0
8	2PE	D	1788	-	-	0/16/16/25	0/0/0/0
4	PEG	D	1789	-	-	0/1/1/4	0/0/0/0
6	MES	D	1790	-	-	0/6/14/14	0/1/1/1
4	PEG	E	1784	-	-	0/4/4/4	0/0/0/0
2	PGE	E	1785	-	-	0/4/4/7	0/0/0/0
7	OAA	E	1786	-	-	0/2/8/8	0/0/0/0
6	MES	E	1787	-	-	0/6/14/14	0/1/1/1
2	PGE	F	1784	-	-	0/7/7/7	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PEG	F	1785	-	-	0/4/4/4	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	1789	OAA	C2-C3	2.39	1.53	1.51
7	E	1786	OAA	C2-C3	2.40	1.53	1.51
7	C	1788	OAA	C2-C3	2.45	1.54	1.51
6	B	1789	MES	O3S-S	2.52	1.52	1.46
7	C	1788	OAA	O3-C3	12.16	1.43	1.22
7	C	1789	OAA	O3-C3	12.59	1.44	1.22
7	E	1786	OAA	O3-C3	12.73	1.44	1.22

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	1790	MES	O1S-S-C8	-24.28	86.19	106.91
6	E	1787	MES	O1S-S-C8	-19.58	90.20	106.91
6	B	1789	MES	O1S-S-C8	-16.45	92.87	106.91
6	D	1790	MES	O3S-S-O1S	-11.07	85.85	111.61
6	E	1787	MES	O2S-S-O1S	-9.17	80.06	113.48
6	B	1789	MES	O2S-S-O1S	-8.68	81.84	113.48
6	D	1790	MES	O2S-S-O1S	-7.97	84.45	113.48
6	B	1789	MES	O3S-S-O1S	-7.87	93.30	111.61
6	E	1787	MES	O3S-S-O1S	-7.66	93.78	111.61
7	C	1789	OAA	O3-C3-C2	-6.73	108.42	120.74
7	C	1788	OAA	O3-C3-C2	-5.08	111.43	120.74
7	E	1786	OAA	C1-C2-C3	-3.33	109.45	115.52
6	E	1787	MES	O1-C6-C5	-2.05	107.13	111.84
6	B	1789	MES	C7-C8-S	2.04	118.83	112.51
6	D	1790	MES	C6-O1-C2	2.15	117.13	109.89
6	E	1787	MES	C7-N4-C5	2.34	117.28	111.27
6	B	1789	MES	C6-C5-N4	2.60	114.06	110.12
6	E	1787	MES	C2-C3-N4	2.64	114.13	110.12
6	B	1789	MES	C7-N4-C5	2.79	118.42	111.27
6	D	1790	MES	C7-N4-C3	2.98	118.91	111.27
6	B	1789	MES	C7-N4-C3	3.85	121.13	111.27
6	D	1790	MES	O3S-S-O2S	3.87	120.61	111.61
6	E	1787	MES	C7-N4-C3	3.92	121.32	111.27
6	D	1790	MES	C7-N4-C5	4.02	121.58	111.27
6	B	1789	MES	O3S-S-O2S	4.43	121.91	111.61
6	D	1790	MES	C5-N4-C3	4.59	118.83	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1789	MES	C5-N4-C3	5.01	119.75	108.90
6	E	1787	MES	C5-N4-C3	5.77	121.39	108.90
6	E	1787	MES	O3S-S-O2S	6.09	125.78	111.61
6	D	1790	MES	O2S-S-C8	10.41	115.78	106.91
6	B	1789	MES	O2S-S-C8	17.96	122.23	106.91
6	E	1787	MES	O2S-S-C8	24.40	127.72	106.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1787	PEG	1	0
4	D	1785	PEG	1	0
6	E	1787	MES	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 ⓘ

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	747/795 (93%)	-0.45	2 (0%) 94 93	22, 41, 76, 95	0
1	B	744/795 (93%)	-0.46	1 (0%) 95 95	25, 42, 69, 97	0
1	C	749/795 (94%)	-0.50	0 100 100	23, 39, 67, 93	0
1	D	745/795 (93%)	-0.41	3 (0%) 93 91	26, 42, 70, 101	0
1	E	744/795 (93%)	-0.42	1 (0%) 95 95	26, 43, 66, 89	0
1	F	749/795 (94%)	-0.44	3 (0%) 93 91	23, 40, 71, 87	0
All	All	4478/4770 (93%)	-0.45	10 (0%) 95 95	22, 41, 70, 101	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	783	ILE	3.6
1	B	385	ILE	2.8
1	A	204	THR	2.5
1	A	537	VAL	2.5
1	F	400	ALA	2.4
1	F	169	THR	2.4
1	D	290	GLY	2.4
1	D	385	ILE	2.3
1	D	783	ILE	2.1
1	F	537	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	PEG	C	1787	7/7	0.86	0.30	12.52	54,56,58,60	0
7	OAA	C	1788	9/9	0.90	0.22	11.73	63,67,71,77	0
7	OAA	E	1786	9/9	0.87	0.24	5.29	74,75,78,79	0
4	PEG	D	1786	4/7	0.72	0.28	5.17	58,61,63,64	0
3	EDO	A	1787	4/4	0.81	0.19	4.82	47,48,51,51	0
2	PGE	A	1785	10/10	0.91	0.20	3.69	50,52,55,57	0
4	PEG	B	1784	4/7	0.93	0.19	3.40	49,49,50,50	0
6	MES	B	1789	12/12	0.93	0.18	3.10	71,75,95,99	0
6	MES	E	1787	12/12	0.92	0.20	3.08	60,63,75,84	0
2	PGE	E	1785	7/10	0.81	0.22	2.90	60,62,68,69	0
2	PGE	A	1786	10/10	0.92	0.18	2.86	49,55,58,59	0
4	PEG	C	1785	7/7	0.88	0.20	2.66	67,73,77,78	0
4	PEG	D	1784	4/7	0.91	0.23	2.44	49,52,55,59	0
8	2PE	D	1788	19/28	0.94	0.16	1.79	44,48,57,60	0
5	PG4	B	1785	13/13	0.88	0.19	1.12	47,49,51,52	0
6	MES	D	1790	12/12	0.93	0.17	0.76	66,70,74,78	0
3	EDO	C	1786	4/4	0.91	0.14	-0.00	60,60,60,61	0
2	PGE	F	1784	10/10	0.94	0.13	-0.08	43,47,49,52	0
3	EDO	D	1787	4/4	0.92	0.12	-0.12	54,56,57,60	0
2	PGE	B	1786	10/10	0.96	0.13	-0.23	43,49,51,53	0
4	PEG	D	1789	4/7	0.92	0.13	-0.58	50,51,54,54	0
4	PEG	C	1784	4/7	0.95	0.10	-1.38	51,51,52,53	0
3	EDO	B	1787	4/4	0.92	0.19	-	56,58,58,62	0
4	PEG	E	1784	7/7	0.90	0.24	-	60,62,65,66	0
7	OAA	C	1789	9/9	0.80	0.23	-	69,71,72,73	0
4	PEG	D	1785	7/7	0.82	0.33	-	69,70,79,80	0
4	PEG	F	1785	7/7	0.76	0.30	-	61,67,72,72	0
3	EDO	B	1788	4/4	0.76	0.14	-	65,69,70,70	0
4	PEG	A	1788	7/7	0.87	0.17	-	52,54,55,57	0

6.5 Other polymers

There are no such residues in this entry.