



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 11:29 PM GMT

PDB ID : 2XWG
Title : CRYSTAL STRUCTURE OF SORTASE C-1 FROM ACTINOMYCES ORIS
(FORMERLY ACTINOMYCES NAESLUNDII)
Authors : Persson, K.
Deposited on : 2010-11-02
Resolution : 2.40 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

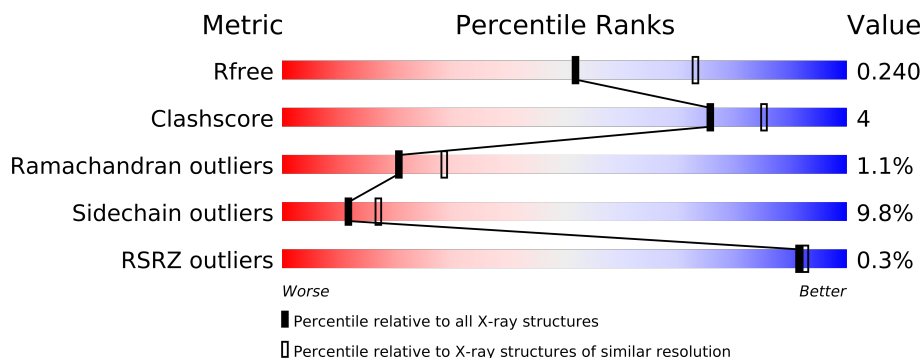
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	235	
1	B	235	
1	C	235	
1	D	235	
1	E	235	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	CA	A	1287	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7181 atoms, of which 0 are hydrogen and 0 are deuterium.

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 SORTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	0	0	0
			1399	881	238	275	5			
1	B	185	Total	C	N	O	S	0	0	0
			1423	895	242	281	5			
1	C	176	Total	C	N	O	S	0	0	0
			1357	857	229	266	5			
1	D	184	Total	C	N	O	S	0	0	0
			1414	889	241	279	5			
1	E	177	Total	C	N	O	S	0	0	0
			1364	861	230	268	5			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	MET	-	EXPRESSION TAG	UNP Q0Z952
A	55	LYS	-	EXPRESSION TAG	UNP Q0Z952
A	56	HIS	-	EXPRESSION TAG	UNP Q0Z952
A	57	HIS	-	EXPRESSION TAG	UNP Q0Z952
A	58	HIS	-	EXPRESSION TAG	UNP Q0Z952
A	59	HIS	-	EXPRESSION TAG	UNP Q0Z952
A	60	HIS	-	EXPRESSION TAG	UNP Q0Z952
A	61	HIS	-	EXPRESSION TAG	UNP Q0Z952
A	62	PRO	-	EXPRESSION TAG	UNP Q0Z952
A	63	MET	-	EXPRESSION TAG	UNP Q0Z952
A	64	SER	-	EXPRESSION TAG	UNP Q0Z952
A	65	ASP	-	EXPRESSION TAG	UNP Q0Z952
A	66	TYR	-	EXPRESSION TAG	UNP Q0Z952
A	67	ASP	-	EXPRESSION TAG	UNP Q0Z952
A	68	ILE	-	EXPRESSION TAG	UNP Q0Z952
A	69	PRO	-	EXPRESSION TAG	UNP Q0Z952
A	70	THR	-	EXPRESSION TAG	UNP Q0Z952
A	71	THR	-	EXPRESSION TAG	UNP Q0Z952
A	72	GLU	-	EXPRESSION TAG	UNP Q0Z952

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Chain	Residue	Modelled	Actual	Comment	Reference
A	73	ASN	-	EXPRESSION TAG	UNP Q0Z952
A	74	LEU	-	EXPRESSION TAG	UNP Q0Z952
A	75	TYR	-	EXPRESSION TAG	UNP Q0Z952
A	76	PHE	-	EXPRESSION TAG	UNP Q0Z952
A	77	GLN	-	EXPRESSION TAG	UNP Q0Z952
B	54	MET	-	EXPRESSION TAG	UNP Q0Z952
B	55	LYS	-	EXPRESSION TAG	UNP Q0Z952
B	56	HIS	-	EXPRESSION TAG	UNP Q0Z952
B	57	HIS	-	EXPRESSION TAG	UNP Q0Z952
B	58	HIS	-	EXPRESSION TAG	UNP Q0Z952
B	59	HIS	-	EXPRESSION TAG	UNP Q0Z952
B	60	HIS	-	EXPRESSION TAG	UNP Q0Z952
B	61	HIS	-	EXPRESSION TAG	UNP Q0Z952
B	62	PRO	-	EXPRESSION TAG	UNP Q0Z952
B	63	MET	-	EXPRESSION TAG	UNP Q0Z952
B	64	SER	-	EXPRESSION TAG	UNP Q0Z952
B	65	ASP	-	EXPRESSION TAG	UNP Q0Z952
B	66	TYR	-	EXPRESSION TAG	UNP Q0Z952
B	67	ASP	-	EXPRESSION TAG	UNP Q0Z952
B	68	ILE	-	EXPRESSION TAG	UNP Q0Z952
B	69	PRO	-	EXPRESSION TAG	UNP Q0Z952
B	70	THR	-	EXPRESSION TAG	UNP Q0Z952
B	71	THR	-	EXPRESSION TAG	UNP Q0Z952
B	72	GLU	-	EXPRESSION TAG	UNP Q0Z952
B	73	ASN	-	EXPRESSION TAG	UNP Q0Z952
B	74	LEU	-	EXPRESSION TAG	UNP Q0Z952
B	75	TYR	-	EXPRESSION TAG	UNP Q0Z952
B	76	PHE	-	EXPRESSION TAG	UNP Q0Z952
B	77	GLN	-	EXPRESSION TAG	UNP Q0Z952
C	54	MET	-	EXPRESSION TAG	UNP Q0Z952
C	55	LYS	-	EXPRESSION TAG	UNP Q0Z952
C	56	HIS	-	EXPRESSION TAG	UNP Q0Z952
C	57	HIS	-	EXPRESSION TAG	UNP Q0Z952
C	58	HIS	-	EXPRESSION TAG	UNP Q0Z952
C	59	HIS	-	EXPRESSION TAG	UNP Q0Z952
C	60	HIS	-	EXPRESSION TAG	UNP Q0Z952
C	61	HIS	-	EXPRESSION TAG	UNP Q0Z952
C	62	PRO	-	EXPRESSION TAG	UNP Q0Z952
C	63	MET	-	EXPRESSION TAG	UNP Q0Z952
C	64	SER	-	EXPRESSION TAG	UNP Q0Z952
C	65	ASP	-	EXPRESSION TAG	UNP Q0Z952
C	66	TYR	-	EXPRESSION TAG	UNP Q0Z952

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Chain	Residue	Modelled	Actual	Comment	Reference
C	67	ASP	-	EXPRESSION TAG	UNP Q0Z952
C	68	ILE	-	EXPRESSION TAG	UNP Q0Z952
C	69	PRO	-	EXPRESSION TAG	UNP Q0Z952
C	70	THR	-	EXPRESSION TAG	UNP Q0Z952
C	71	THR	-	EXPRESSION TAG	UNP Q0Z952
C	72	GLU	-	EXPRESSION TAG	UNP Q0Z952
C	73	ASN	-	EXPRESSION TAG	UNP Q0Z952
C	74	LEU	-	EXPRESSION TAG	UNP Q0Z952
C	75	TYR	-	EXPRESSION TAG	UNP Q0Z952
C	76	PHE	-	EXPRESSION TAG	UNP Q0Z952
C	77	GLN	-	EXPRESSION TAG	UNP Q0Z952
D	54	MET	-	EXPRESSION TAG	UNP Q0Z952
D	55	LYS	-	EXPRESSION TAG	UNP Q0Z952
D	56	HIS	-	EXPRESSION TAG	UNP Q0Z952
D	57	HIS	-	EXPRESSION TAG	UNP Q0Z952
D	58	HIS	-	EXPRESSION TAG	UNP Q0Z952
D	59	HIS	-	EXPRESSION TAG	UNP Q0Z952
D	60	HIS	-	EXPRESSION TAG	UNP Q0Z952
D	61	HIS	-	EXPRESSION TAG	UNP Q0Z952
D	62	PRO	-	EXPRESSION TAG	UNP Q0Z952
D	63	MET	-	EXPRESSION TAG	UNP Q0Z952
D	64	SER	-	EXPRESSION TAG	UNP Q0Z952
D	65	ASP	-	EXPRESSION TAG	UNP Q0Z952
D	66	TYR	-	EXPRESSION TAG	UNP Q0Z952
D	67	ASP	-	EXPRESSION TAG	UNP Q0Z952
D	68	ILE	-	EXPRESSION TAG	UNP Q0Z952
D	69	PRO	-	EXPRESSION TAG	UNP Q0Z952
D	70	THR	-	EXPRESSION TAG	UNP Q0Z952
D	71	THR	-	EXPRESSION TAG	UNP Q0Z952
D	72	GLU	-	EXPRESSION TAG	UNP Q0Z952
D	73	ASN	-	EXPRESSION TAG	UNP Q0Z952
D	74	LEU	-	EXPRESSION TAG	UNP Q0Z952
D	75	TYR	-	EXPRESSION TAG	UNP Q0Z952
D	76	PHE	-	EXPRESSION TAG	UNP Q0Z952
D	77	GLN	-	EXPRESSION TAG	UNP Q0Z952
E	54	MET	-	EXPRESSION TAG	UNP Q0Z952
E	55	LYS	-	EXPRESSION TAG	UNP Q0Z952
E	56	HIS	-	EXPRESSION TAG	UNP Q0Z952
E	57	HIS	-	EXPRESSION TAG	UNP Q0Z952
E	58	HIS	-	EXPRESSION TAG	UNP Q0Z952
E	59	HIS	-	EXPRESSION TAG	UNP Q0Z952
E	60	HIS	-	EXPRESSION TAG	UNP Q0Z952

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Chain	Residue	Modelled	Actual	Comment	Reference
E	61	HIS	-	EXPRESSION TAG	UNP Q0Z952
E	62	PRO	-	EXPRESSION TAG	UNP Q0Z952
E	63	MET	-	EXPRESSION TAG	UNP Q0Z952
E	64	SER	-	EXPRESSION TAG	UNP Q0Z952
E	65	ASP	-	EXPRESSION TAG	UNP Q0Z952
E	66	TYR	-	EXPRESSION TAG	UNP Q0Z952
E	67	ASP	-	EXPRESSION TAG	UNP Q0Z952
E	68	ILE	-	EXPRESSION TAG	UNP Q0Z952
E	69	PRO	-	EXPRESSION TAG	UNP Q0Z952
E	70	THR	-	EXPRESSION TAG	UNP Q0Z952
E	71	THR	-	EXPRESSION TAG	UNP Q0Z952
E	72	GLU	-	EXPRESSION TAG	UNP Q0Z952
E	73	ASN	-	EXPRESSION TAG	UNP Q0Z952
E	74	LEU	-	EXPRESSION TAG	UNP Q0Z952
E	75	TYR	-	EXPRESSION TAG	UNP Q0Z952
E	76	PHE	-	EXPRESSION TAG	UNP Q0Z952
E	77	GLN	-	EXPRESSION TAG	UNP Q0Z952

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 3 is water.

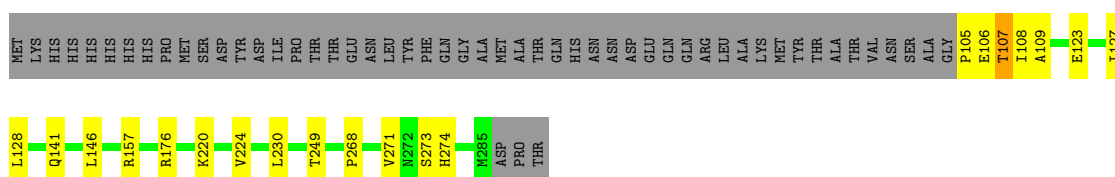
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	43	Total O 43 43	0	0
3	B	69	Total O 69 69	0	0
3	C	48	Total O 48 48	0	0
3	D	44	Total O 44 44	0	0
3	E	16	Total O 16 16	0	0

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.

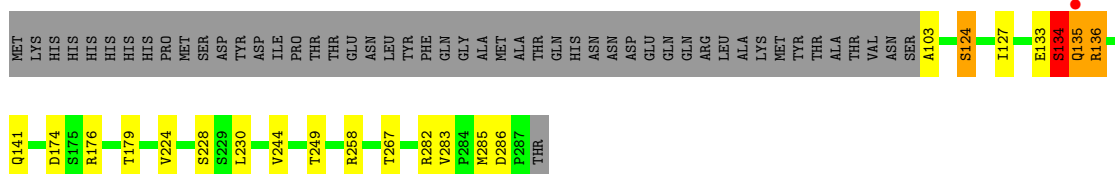
- Molecule 1: SORTASE

Chain A:



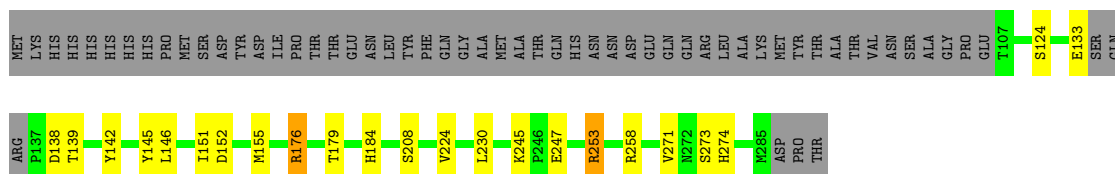
- Molecule 1: SORTASE

Chain B:



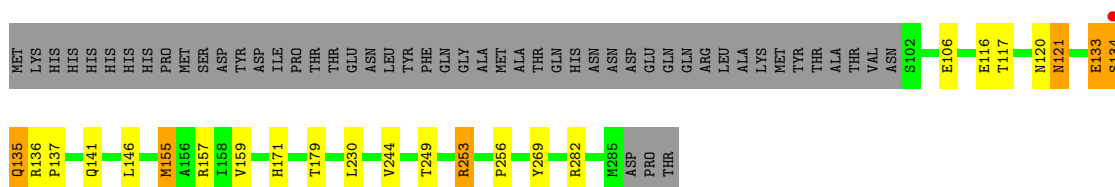
- Molecule 1: SORTASE

Chain C:



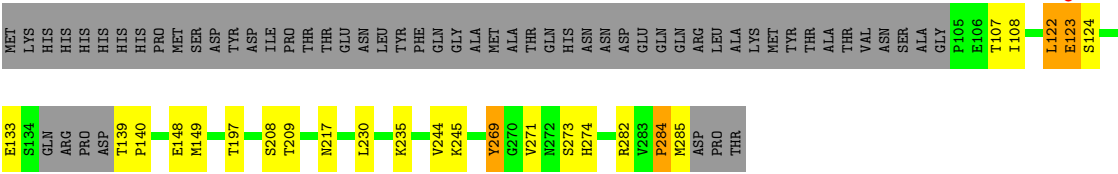
- Molecule 1: SORTASE

Chain D:



- Molecule 1: SORTASE

Chain E: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.07Å 108.23Å 143.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.67 – 2.40 44.57 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.6 (43.67-2.40) 91.4 (44.57-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.73 (at 2.39Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.205 , 0.244 0.196 , 0.240	Depositor DCC
R_{free} test set	3057 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.679	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 27.7	EDS
Estimated twinning fraction	0.029 for k,h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	1 of 58366 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7181	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.52	0/1431	0.65	0/1955
1	B	0.54	0/1456	0.74	0/1991
1	C	0.53	0/1387	0.69	0/1894
1	D	0.52	0/1446	0.74	1/1976 (0.1%)
1	E	0.46	0/1394	0.62	0/1903
All	All	0.51	0/7114	0.69	1/9719 (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	D	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	120	ASN	N-CA-C	5.62	126.19	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	135	GLN	Peptide

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1399	0	0	4	0
1	B	1423	0	0	5	0
1	C	1357	0	0	5	0
1	D	1414	0	0	6	0
1	E	1364	0	0	8	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	43	0	0	1	0
3	B	69	0	0	1	0
3	C	48	0	0	1	0
3	D	44	0	0	1	0
3	E	16	0	0	1	0
All	All	7181	0	0	27	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (27) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:122:LEU:CA	1:E:123:GLU:CB	2.69	0.70
1:D:133:GLU:O	1:D:134:SER:O	2.14	0.66
1:B:136:ARG:N	1:B:136:ARG:CD	2.66	0.59
1:D:157:ARG:NH1	3:D:2012:HOH:O	2.38	0.57
1:B:103:ALA:N	3:B:2001:HOH:O	2.38	0.57
1:D:253:ARG:NH1	1:D:253:ARG:CG	2.69	0.55
1:E:139:THR:N	1:E:140:PRO:CD	2.70	0.55
1:A:106:GLU:CG	1:A:109:ALA:CB	2.87	0.52
1:A:157:ARG:NE	3:A:2007:HOH:O	2.43	0.52
1:B:133:GLU:O	1:B:134:SER:C	2.49	0.51
1:D:155:MET:CE	1:D:171:HIS:CG	2.95	0.50
1:D:269:TYR:O	1:E:217:ASN:ND2	2.46	0.49
1:E:148:GLU:O	1:E:149:MET:C	2.52	0.48
1:C:139:THR:CG2	1:C:142:TYR:N	2.77	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:284:PRO:O	1:E:285:MET:CB	2.62	0.47
1:B:135:GLN:CB	1:B:136:ARG:CB	2.93	0.47
1:C:176:ARG:NH2	3:C:2023:HOH:O	2.49	0.45
1:E:273:SER:OG	1:E:274:HIS:ND1	2.50	0.45
1:A:273:SER:OG	1:A:274:HIS:ND1	2.50	0.44
1:B:135:GLN:CB	1:B:136:ARG:CG	2.95	0.44
1:D:117:THR:O	1:D:121:ASN:CB	2.67	0.43
1:E:282:ARG:NE	3:E:2016:HOH:O	2.52	0.42
1:A:105:PRO:N	1:A:107:THR:CG2	2.83	0.41
1:C:253:ARG:NH1	1:C:253:ARG:CG	2.83	0.41
1:C:273:SER:OG	1:C:274:HIS:ND1	2.53	0.41
1:C:145:TYR:OH	1:C:184:HIS:ND1	2.54	0.41
1:E:269:TYR:CD1	1:E:269:TYR:C	2.94	0.41

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	179/235 (76%)	167 (93%)	12 (7%)	0	100	100
1	B	183/235 (78%)	173 (94%)	8 (4%)	2 (1%)	21	29
1	C	172/235 (73%)	163 (95%)	8 (5%)	1 (1%)	33	47
1	D	182/235 (77%)	173 (95%)	5 (3%)	4 (2%)	10	11
1	E	173/235 (74%)	163 (94%)	7 (4%)	3 (2%)	14	17
All	All	889/1175 (76%)	839 (94%)	40 (4%)	10 (1%)	21	29

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	124	SER
1	D	121	ASN
1	D	134	SER

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Mol	Chain	Res	Type
1	D	137	PRO
1	E	123	GLU
1	E	133	GLU
1	B	124	SER
1	B	134	SER
1	D	256	PRO
1	E	284	PRO

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	161/208 (77%)	147 (91%)	14 (9%)	15	22
1	B	163/208 (78%)	143 (88%)	20 (12%)	7	8
1	C	156/208 (75%)	140 (90%)	16 (10%)	10	15
1	D	162/208 (78%)	147 (91%)	15 (9%)	13	19
1	E	157/208 (76%)	144 (92%)	13 (8%)	16	24
All	All	799/1040 (77%)	721 (90%)	78 (10%)	12	17

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	THR
1	A	108	ILE
1	A	123	GLU
1	A	127	ILE
1	A	128	LEU
1	A	141	GLN
1	A	146	LEU
1	A	176	ARG
1	A	220	LYS
1	A	224	VAL
1	A	230	LEU
1	A	249	THR
1	A	268	PRO
1	A	271	VAL

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Mol	Chain	Res	Type
1	B	124	SER
1	B	127	ILE
1	B	134	SER
1	B	135	GLN
1	B	136	ARG
1	B	141	GLN
1	B	174	ASP
1	B	176	ARG
1	B	179	THR
1	B	224	VAL
1	B	228	SER
1	B	230	LEU
1	B	244	VAL
1	B	249	THR
1	B	258	ARG
1	B	267	THR
1	B	282	ARG
1	B	283	VAL
1	B	285	MET
1	B	286	ASP
1	C	133	GLU
1	C	138	ASP
1	C	146	LEU
1	C	151	ILE
1	C	152	ASP
1	C	155	MET
1	C	176	ARG
1	C	179	THR
1	C	208	SER
1	C	224	VAL
1	C	230	LEU
1	C	245	LYS
1	C	247	GLU
1	C	253	ARG
1	C	258	ARG
1	C	271	VAL
1	D	106	GLU
1	D	116	GLU
1	D	133	GLU
1	D	135	GLN
1	D	136	ARG
1	D	141	GLN

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Mol	Chain	Res	Type
1	D	146	LEU
1	D	155	MET
1	D	159	VAL
1	D	179	THR
1	D	230	LEU
1	D	244	VAL
1	D	249	THR
1	D	253	ARG
1	D	282	ARG
1	E	107	THR
1	E	108	ILE
1	E	122	LEU
1	E	124	SER
1	E	197	THR
1	E	208	SER
1	E	209	THR
1	E	230	LEU
1	E	235	LYS
1	E	244	VAL
1	E	245	LYS
1	E	269	TYR
1	E	271	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	181/235 (77%)	-0.24	0 100 100	22, 39, 72, 99	0
1	B	185/235 (78%)	-0.45	1 (0%) 88 88	19, 32, 65, 106	0
1	C	176/235 (74%)	-0.27	0 100 100	25, 39, 73, 99	0
1	D	184/235 (78%)	-0.33	1 (0%) 88 88	23, 39, 70, 86	0
1	E	177/235 (75%)	-0.19	1 (0%) 86 86	32, 52, 86, 114	0
All	All	903/1175 (76%)	-0.30	3 (0%) 91 92	19, 40, 76, 114	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	135	GLN	2.4
1	E	123	GLU	2.2
1	D	134	SER	2.1

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CA	A	1287	1/1	0.20	2.63	72,72,72,72	0
2	CA	B	1288	1/1	0.11	0.30	71,71,71,71	0
2	CA	C	1286	1/1	0.06	-1.62	66,66,66,66	0
2	CA	A	1286	1/1	0.05	-5.56	44,44,44,44	0

6.5 Other polymers ⓘ

There are no such residues in this entry.