



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:23 PM GMT

PDB ID : 1TF5
Title : Crystal structure of SecA in an open conformation from Bacillus Subtilis
Authors : Osborne, A.R.; Clemons Jr., W.M.; Rapoport, T.A.
Deposited on : 2004-05-26
Resolution : 2.18 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

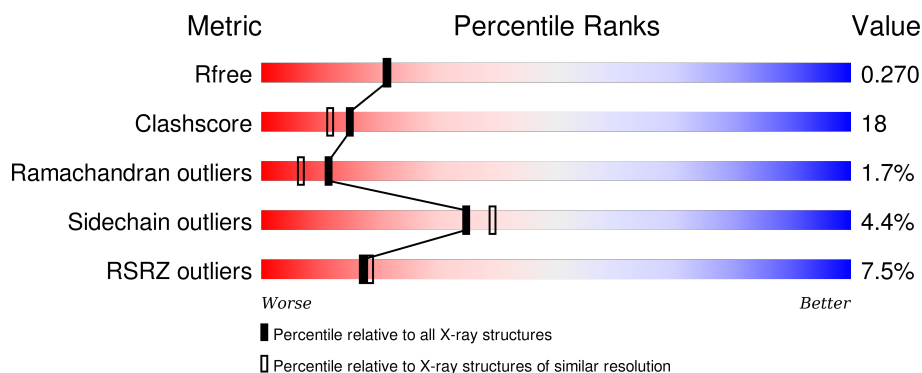
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 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	5130 (2.20-2.16)
Clashscore	102246	5965 (2.20-2.16)
Ramachandran outliers	100387	5863 (2.20-2.16)
Sidechain outliers	100360	5864 (2.20-2.16)
RSRZ outliers	91569	5142 (2.20-2.16)

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	844	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6316 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 Preprotein translocase secA subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	775	Total	C	N	O	S	0	0	0
			6187	3872	1080	1201	34			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	CLONING ARTIFACT	UNP P28366
A	-1	PRO	-	CLONING ARTIFACT	UNP P28366
A	0	HIS	-	CLONING ARTIFACT	UNP P28366

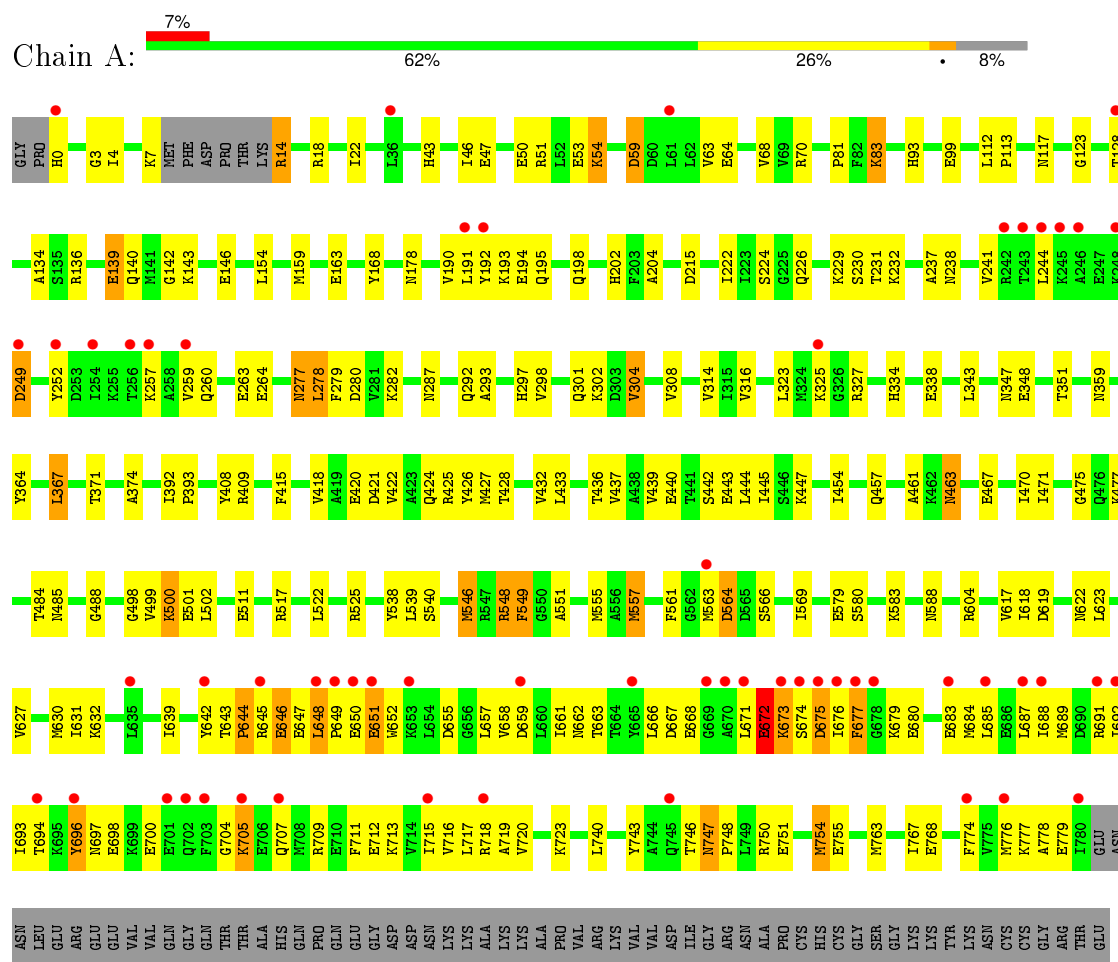
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	129	Total	O	0	0
			129	129		

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: Preprotein translocase secA subunit



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.23Å 107.19Å 72.05Å 90.00° 94.96° 90.00°	Depositor
Resolution (Å)	50.00 – 2.18 44.98 – 2.20	Depositor EDS
% Data completeness (in resolution range)	90.1 (50.00-2.18) 90.5 (44.98-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.241 , 0.273 0.239 , 0.270	Depositor DCC
R_{free} test set	2967 reflections (5.72%)	DCC
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 57335 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6316	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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](#)

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	0/6273	0.57	0/8434

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	6187	0	6184	218	0
2	A	129	0	0	6	0
All	All	6316	0	6184	218	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 18.

All (218) 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:630:MET:HE2	1:A:768:GLU:HA	1.35	1.07
1:A:83:LYS:H	1:A:83:LYS:CD	1.84	0.86
1:A:658:VAL:HG11	1:A:672:GLU:HG2	1.58	0.86
1:A:83:LYS:H	1:A:83:LYS:HD3	1.39	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:630:MET:CE	1:A:768:GLU:HA	2.05	0.84
1:A:159:MET:HE2	1:A:163:GLU:HG2	1.57	0.84
1:A:83:LYS:HD3	1:A:83:LYS:N	1.91	0.84
1:A:644:PRO:CB	1:A:647:GLU:HB2	2.11	0.81
1:A:671:LEU:HD11	1:A:691:ARG:HG3	1.62	0.81
1:A:644:PRO:HB2	1:A:647:GLU:HB2	1.64	0.80
1:A:693:ILE:HG22	1:A:697:ASN:HD21	1.48	0.79
1:A:238:ASN:OD1	1:A:297:HIS:HE1	1.66	0.78
1:A:433:LEU:HD21	1:A:525:ARG:HD3	1.65	0.77
1:A:93:HIS:HD2	1:A:117:ASN:HD21	1.32	0.76
1:A:694:THR:HA	1:A:697:ASN:HD22	1.51	0.74
1:A:159:MET:CE	1:A:163:GLU:HG2	2.17	0.73
1:A:622:ASN:HA	1:A:709:ARG:HD2	1.71	0.72
1:A:436:THR:HG21	1:A:442:SER:OG	1.89	0.72
1:A:557:MET:HE1	1:A:561:PHE:HB2	1.71	0.71
1:A:648:LEU:H	1:A:649:PRO:CD	2.05	0.69
1:A:747:ASN:HD22	1:A:748:PRO:CD	2.05	0.69
1:A:675:ASP:O	1:A:679:LYS:HG3	1.93	0.68
1:A:642:TYR:HD1	1:A:657:LEU:HB2	1.57	0.68
1:A:657:LEU:O	1:A:661:ILE:HG12	1.94	0.67
1:A:128:THR:CG2	1:A:134:ALA:HB2	2.25	0.67
1:A:415:PHE:CD2	1:A:445:ILE:HD11	2.31	0.65
1:A:457:GLN:NE2	1:A:470:ILE:HD12	2.11	0.65
1:A:627:VAL:HG21	1:A:712:GLU:HG2	1.78	0.65
1:A:549:PHE:HZ	1:A:588:ASN:ND2	1.95	0.65
1:A:658:VAL:CG1	1:A:672:GLU:HG2	2.26	0.65
1:A:51:ARG:HA	1:A:54:LYS:HG2	1.78	0.64
1:A:557:MET:CE	1:A:561:PHE:HB2	2.27	0.64
1:A:128:THR:HG21	1:A:134:ALA:HB2	1.79	0.64
1:A:673:LYS:HD3	1:A:673:LYS:H	1.62	0.64
1:A:222:ILE:HG23	1:A:351:THR:HG23	1.80	0.64
1:A:747:ASN:HD22	1:A:748:PRO:HD2	1.62	0.64
1:A:83:LYS:HG2	2:A:2014:HOH:O	1.98	0.63
1:A:754:MET:HE2	1:A:755:GLU:HA	1.80	0.63
1:A:0:HIS:O	1:A:4:ILE:HG13	1.99	0.63
1:A:675:ASP:HB3	1:A:687:LEU:HD13	1.81	0.63
1:A:648:LEU:H	1:A:649:PRO:HD2	1.64	0.62
1:A:277:ASN:ND2	1:A:279:PHE:H	1.98	0.62
1:A:715:ILE:HA	1:A:718:ARG:HD3	1.80	0.62
1:A:301:GLN:HB2	1:A:304:VAL:HG13	1.83	0.61
1:A:278:LEU:HD22	1:A:287:ASN:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:617:VAL:O	1:A:713:LYS:HE2	2.00	0.60
1:A:178:ASN:H	1:A:178:ASN:HD22	1.50	0.60
1:A:252:TYR:HD2	1:A:259:VAL:HG22	1.66	0.60
1:A:93:HIS:CD2	1:A:117:ASN:HD21	2.16	0.60
1:A:676:ILE:O	1:A:677:PHE:HB2	2.02	0.60
1:A:190:VAL:HG22	1:A:195:GLN:HB2	1.84	0.59
1:A:252:TYR:CD2	1:A:259:VAL:HG22	2.37	0.59
1:A:644:PRO:HB3	1:A:647:GLU:HB2	1.82	0.59
1:A:433:LEU:CD2	1:A:525:ARG:HD3	2.32	0.58
1:A:693:ILE:HG22	1:A:697:ASN:ND2	2.19	0.58
1:A:426:TYR:CD2	1:A:454:ILE:HD12	2.39	0.57
1:A:675:ASP:CB	1:A:687:LEU:HD13	2.35	0.57
1:A:617:VAL:HG13	1:A:623:LEU:HD21	1.87	0.57
1:A:648:LEU:HB2	1:A:649:PRO:HD3	1.86	0.57
1:A:237:ALA:O	1:A:241:VAL:HG23	2.05	0.56
1:A:260:GLN:HE21	1:A:740:LEU:HD22	1.69	0.56
1:A:308:VAL:HG13	1:A:343:LEU:HD11	1.88	0.56
1:A:549:PHE:H	1:A:549:PHE:HD1	1.53	0.55
1:A:231:THR:HG23	1:A:347:ASN:ND2	2.22	0.55
1:A:630:MET:HE2	1:A:768:GLU:CA	2.23	0.55
1:A:190:VAL:O	1:A:618:ILE:HD11	2.07	0.54
1:A:70:ARG:HG3	1:A:81:PRO:HD2	1.89	0.54
1:A:627:VAL:O	1:A:631:ILE:HG13	2.07	0.54
1:A:754:MET:O	1:A:754:MET:HE3	2.07	0.54
1:A:277:ASN:HD22	1:A:277:ASN:C	2.11	0.54
1:A:226:GLN:H	1:A:226:GLN:CD	2.10	0.54
1:A:463:ASN:HD22	1:A:463:ASN:C	2.10	0.54
1:A:671:LEU:O	1:A:672:GLU:HB2	2.06	0.54
1:A:477:LYS:HE2	1:A:502:LEU:HD11	1.89	0.53
1:A:99:GLU:HA	1:A:371:THR:O	2.08	0.53
1:A:178:ASN:H	1:A:178:ASN:ND2	2.05	0.53
1:A:538:TYR:O	1:A:539:LEU:HD23	2.08	0.53
1:A:642:TYR:CD1	1:A:657:LEU:HB2	2.43	0.53
1:A:662:ASN:HB3	1:A:668:GLU:HA	1.91	0.53
1:A:231:THR:CG2	1:A:347:ASN:HD22	2.22	0.52
1:A:359:ASN:OD1	1:A:604:ARG:HD3	2.08	0.52
1:A:673:LYS:HD3	1:A:673:LYS:N	2.25	0.52
1:A:754:MET:HE2	1:A:755:GLU:CA	2.40	0.52
1:A:549:PHE:CD1	1:A:549:PHE:N	2.78	0.52
1:A:763:MET:O	1:A:767:ILE:HG13	2.10	0.52
1:A:93:HIS:HD2	1:A:117:ASN:ND2	2.04	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:LEU:HB2	1:A:113:PRO:HD3	1.92	0.52
1:A:704:GLY:HA2	1:A:707:GLN:NE2	2.25	0.51
1:A:674:SER:O	1:A:676:ILE:HG13	2.10	0.51
1:A:238:ASN:OD1	1:A:297:HIS:CE1	2.55	0.51
1:A:231:THR:HG23	1:A:347:ASN:HD22	1.76	0.51
1:A:14:ARG:HD3	1:A:14:ARG:N	2.25	0.51
1:A:292:GLN:HA	1:A:292:GLN:OE1	2.10	0.51
1:A:659:ASP:O	1:A:663:THR:HG22	2.11	0.51
1:A:673:LYS:CD	1:A:673:LYS:H	2.23	0.51
1:A:463:ASN:O	1:A:467:GLU:HG3	2.11	0.51
1:A:754:MET:HE3	1:A:754:MET:C	2.32	0.50
1:A:715:ILE:HA	1:A:718:ARG:CD	2.41	0.50
1:A:191:LEU:HD23	1:A:192:TYR:CE1	2.45	0.50
1:A:280:ASP:OD2	1:A:282:LYS:HD2	2.12	0.50
1:A:548:ARG:HB3	1:A:549:PHE:HD1	1.77	0.50
1:A:743:TYR:O	1:A:746:THR:HB	2.12	0.50
1:A:128:THR:HG21	1:A:134:ALA:CA	2.41	0.50
1:A:191:LEU:HD12	1:A:717:LEU:HD12	1.92	0.50
1:A:715:ILE:O	1:A:718:ARG:HG2	2.12	0.50
1:A:648:LEU:N	1:A:649:PRO:CD	2.70	0.50
1:A:260:GLN:HE21	1:A:740:LEU:CD2	2.25	0.50
1:A:54:LYS:HB3	1:A:54:LYS:NZ	2.27	0.50
1:A:564:ASP:HB2	1:A:566:SER:OG	2.12	0.50
1:A:563:MET:SD	1:A:569:ILE:HG12	2.52	0.49
1:A:190:VAL:CG2	1:A:195:GLN:HB2	2.42	0.49
1:A:774:PHE:O	1:A:778:ALA:HB3	2.13	0.49
1:A:128:THR:HG21	1:A:134:ALA:N	2.28	0.49
1:A:715:ILE:HD13	1:A:718:ARG:HD3	1.93	0.49
1:A:676:ILE:HG23	1:A:684:MET:CE	2.43	0.49
1:A:643:THR:N	1:A:644:PRO:HD3	2.28	0.49
1:A:301:GLN:HB2	1:A:304:VAL:CG1	2.42	0.49
1:A:685:LEU:HD13	1:A:685:LEU:C	2.34	0.48
1:A:461:ALA:HA	1:A:467:GLU:OE2	2.12	0.48
1:A:112:LEU:HB2	1:A:113:PRO:CD	2.42	0.48
1:A:424:GLN:NE2	1:A:424:GLN:HA	2.29	0.48
1:A:193:LYS:HE2	1:A:619:ASP:OD1	2.14	0.48
1:A:711:PHE:O	1:A:715:ILE:HG12	2.13	0.48
1:A:549:PHE:HZ	1:A:588:ASN:HD21	1.61	0.48
1:A:334:HIS:O	1:A:338:GLU:HG3	2.13	0.47
1:A:18:ARG:O	1:A:22:ILE:HG12	2.14	0.47
1:A:705:LYS:HD3	1:A:705:LYS:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ASN:HD22	1:A:278:LEU:N	2.12	0.47
1:A:128:THR:HG21	1:A:134:ALA:CB	2.44	0.47
1:A:546:MET:HG3	1:A:555:MET:SD	2.54	0.47
1:A:314:VAL:HG21	1:A:325:LYS:HE3	1.96	0.47
1:A:651:GLU:HG3	1:A:652:TRP:N	2.30	0.47
1:A:549:PHE:CZ	1:A:588:ASN:ND2	2.80	0.47
1:A:136:ARG:O	1:A:140:GLN:HG3	2.15	0.47
1:A:63:VAL:HG23	2:A:2072:HOH:O	2.15	0.47
1:A:522:LEU:O	1:A:525:ARG:HG3	2.15	0.47
1:A:64:GLU:O	1:A:68:VAL:HG23	2.15	0.47
1:A:444:LEU:HD13	1:A:444:LEU:C	2.35	0.47
1:A:204:ALA:HB2	1:A:364:TYR:CE2	2.50	0.47
1:A:671:LEU:HD22	1:A:674:SER:HB2	1.96	0.46
1:A:754:MET:CE	1:A:754:MET:C	2.84	0.46
1:A:224:SER:OG	2:A:2121:HOH:O	2.21	0.46
1:A:716:VAL:O	1:A:720:VAL:HG23	2.15	0.46
1:A:3:GLY:O	1:A:7:LYS:HG3	2.15	0.46
1:A:551:ALA:O	1:A:555:MET:HG2	2.15	0.46
1:A:230:SER:OG	1:A:232:LYS:HG2	2.15	0.46
1:A:677:PHE:C	1:A:679:LYS:H	2.19	0.46
1:A:650:GLU:O	1:A:651:GLU:HB3	2.15	0.46
1:A:277:ASN:HD21	1:A:279:PHE:HB2	1.81	0.45
1:A:316:VAL:HG22	1:A:323:LEU:CD2	2.46	0.45
1:A:425:ARG:HB2	1:A:432:VAL:HG21	1.99	0.45
1:A:457:GLN:HG3	2:A:2104:HOH:O	2.15	0.45
1:A:302:LYS:NZ	2:A:2128:HOH:O	2.45	0.45
1:A:671:LEU:HD22	1:A:674:SER:CB	2.47	0.45
1:A:751:GLU:OE1	1:A:755:GLU:OE2	2.35	0.45
1:A:51:ARG:HB3	2:A:2122:HOH:O	2.17	0.45
1:A:241:VAL:HG21	1:A:293:ALA:HB3	1.98	0.45
1:A:463:ASN:ND2	1:A:463:ASN:C	2.70	0.45
1:A:471:ILE:HG13	1:A:488:GLY:HA3	1.98	0.45
1:A:475:GLY:O	1:A:499:VAL:HG21	2.16	0.44
1:A:409:ARG:HD3	1:A:563:MET:O	2.18	0.44
1:A:18:ARG:HG3	1:A:18:ARG:HH11	1.83	0.44
1:A:154:LEU:O	1:A:159:MET:HE1	2.18	0.44
1:A:747:ASN:ND2	1:A:748:PRO:HD2	2.32	0.44
1:A:644:PRO:C	1:A:646:GLU:H	2.21	0.44
1:A:277:ASN:C	1:A:277:ASN:ND2	2.70	0.44
1:A:142:GLY:O	1:A:146:GLU:HG3	2.18	0.44
1:A:437:VAL:HB	1:A:511:GLU:OE1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:GLU:OE2	1:A:143:LYS:HE3	2.18	0.44
1:A:408:TYR:O	1:A:540:SER:HA	2.17	0.44
1:A:43:HIS:CD2	1:A:47:GLU:HG3	2.53	0.43
1:A:696:TYR:CD1	1:A:696:TYR:C	2.92	0.43
1:A:70:ARG:CG	1:A:81:PRO:HD2	2.48	0.43
1:A:639:ILE:O	1:A:643:THR:HG23	2.18	0.43
1:A:632:LYS:HD3	1:A:689:MET:HG3	2.00	0.43
1:A:191:LEU:HD12	1:A:717:LEU:CD1	2.48	0.43
1:A:719:ALA:O	1:A:723:LYS:HG2	2.18	0.43
1:A:244:LEU:HB3	1:A:249:ASP:HB3	2.00	0.43
1:A:392:ILE:HA	1:A:393:PRO:HD3	1.88	0.43
1:A:651:GLU:HG3	1:A:652:TRP:H	1.84	0.43
1:A:676:ILE:HG23	1:A:684:MET:HE2	2.00	0.42
1:A:747:ASN:HD22	1:A:748:PRO:N	2.17	0.42
1:A:680:GLU:HB2	1:A:683:GLU:HG3	2.01	0.42
1:A:747:ASN:HA	1:A:748:PRO:HD3	1.88	0.42
1:A:50:GLU:O	1:A:53:GLU:HB3	2.19	0.42
1:A:666:LEU:CD2	1:A:692:ILE:HD13	2.49	0.42
1:A:168:TYR:CZ	1:A:198:GLN:HG2	2.54	0.42
1:A:443:GLU:O	1:A:447:LYS:HG3	2.19	0.42
1:A:639:ILE:HA	1:A:657:LEU:CD1	2.49	0.42
1:A:371:THR:HG21	1:A:374:ALA:HB2	2.01	0.42
1:A:424:GLN:HE21	1:A:424:GLN:HA	1.83	0.42
1:A:421:ASP:O	1:A:425:ARG:HG2	2.20	0.42
1:A:439:VAL:HG22	1:A:440:GLU:OE2	2.20	0.41
1:A:123:GLY:O	1:A:202:HIS:HD2	2.03	0.41
1:A:657:LEU:C	1:A:657:LEU:HD23	2.40	0.41
1:A:231:THR:CG2	1:A:347:ASN:ND2	2.83	0.41
1:A:418:VAL:O	1:A:422:VAL:HG23	2.20	0.41
1:A:688:ILE:O	1:A:692:ILE:HG12	2.20	0.41
1:A:364:TYR:HB2	1:A:367:LEU:HD13	2.02	0.41
1:A:46:ILE:O	1:A:50:GLU:HG3	2.20	0.41
1:A:500:LYS:CE	1:A:500:LYS:H	2.34	0.41
1:A:327:ARG:HH11	1:A:327:ARG:HG3	1.86	0.41
1:A:264:GLU:CD	1:A:264:GLU:H	2.23	0.41
1:A:579:GLU:HG3	1:A:583:LYS:HE3	2.03	0.41
1:A:215:ASP:OD1	1:A:517:ARG:NH2	2.53	0.41
1:A:59:ASP:OD1	1:A:93:HIS:HE1	2.02	0.41
1:A:252:TYR:CD2	1:A:298:VAL:HG12	2.56	0.41
1:A:548:ARG:HB3	1:A:549:PHE:CD1	2.55	0.41
1:A:420:GLU:O	1:A:424:GLN:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:498:GLY:HA2	1:A:501:GLU:OE1	2.21	0.41
1:A:779:GLU:N	1:A:779:GLU:OE1	2.54	0.41
1:A:436:THR:HG22	1:A:484:THR:HA	2.02	0.41
1:A:424:GLN:O	1:A:428:THR:HG23	2.20	0.41
1:A:229:LYS:HG2	1:A:230:SER:N	2.36	0.41
1:A:257:LYS:O	1:A:259:VAL:HG23	2.20	0.40
1:A:178:ASN:N	1:A:178:ASN:ND2	2.68	0.40
1:A:563:MET:SD	1:A:569:ILE:CG1	3.10	0.40
1:A:667:ASP:HA	1:A:777:LYS:CE	2.51	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	771/844 (91%)	722 (94%)	36 (5%)	13 (2%)	11 7

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	549	PHE
1	A	672	GLU
1	A	485	ASN
1	A	645	ARG
1	A	651	GLU
1	A	675	ASP
1	A	677	PHE
1	A	700	GLU
1	A	249	ASP
1	A	698	GLU
1	A	548	ARG
1	A	644	PRO

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Mol	Chain	Res	Type
1	A	648	LEU

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	665/723 (92%)	636 (96%)	29 (4%)	35	39

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	54	LYS
1	A	59	ASP
1	A	83	LYS
1	A	139	GLU
1	A	194	GLU
1	A	263	GLU
1	A	277	ASN
1	A	278	LEU
1	A	304	VAL
1	A	348	GLU
1	A	367	LEU
1	A	427	MET
1	A	463	ASN
1	A	500	LYS
1	A	546	MET
1	A	557	MET
1	A	564	ASP
1	A	580	SER
1	A	646	GLU
1	A	655	ASP
1	A	672	GLU
1	A	673	LYS
1	A	696	TYR
1	A	705	LYS

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Mol	Chain	Res	Type
1	A	747	ASN
1	A	750	ARG
1	A	754	MET
1	A	776	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	6	ASN
1	A	43	HIS
1	A	93	HIS
1	A	178	ASN
1	A	202	HIS
1	A	236	GLN
1	A	260	GLN
1	A	277	ASN
1	A	287	ASN
1	A	297	HIS
1	A	347	ASN
1	A	383	ASN
1	A	386	ASN
1	A	395	ASN
1	A	424	GLN
1	A	457	GLN
1	A	463	ASN
1	A	588	ASN
1	A	595	GLN
1	A	605	GLN
1	A	613	GLN
1	A	697	ASN
1	A	707	GLN
1	A	747	ASN

5.3.3 RNA ⓘ

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	775/844 (91%)	0.54	58 (7%) 17 18	27, 48, 116, 132	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	671	LEU	9.7
1	A	649	PRO	7.8
1	A	648	LEU	7.3
1	A	780	ILE	6.7
1	A	675	ASP	5.4
1	A	645	ARG	5.1
1	A	696	TYR	5.0
1	A	651	GLU	4.6
1	A	0	HIS	4.3
1	A	677	PHE	4.2
1	A	650	GLU	4.2
1	A	670	ALA	4.0
1	A	745	GLN	3.9
1	A	692	ILE	3.8
1	A	694	THR	3.7
1	A	774	PHE	3.6
1	A	701	GLU	3.5
1	A	687	LEU	3.5
1	A	703	PHE	3.5
1	A	702	GLN	3.3
1	A	642	TYR	3.2
1	A	707	GLN	3.2
1	A	676	ILE	3.1
1	A	248	LYS	3.0
1	A	249	ASP	3.0
1	A	245	LYS	2.9
1	A	653	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	665	TYR	2.9
1	A	259	VAL	2.8
1	A	192	TYR	2.8
1	A	688	ILE	2.7
1	A	242	ARG	2.7
1	A	61	LEU	2.7
1	A	705	LYS	2.7
1	A	257	LYS	2.7
1	A	244	LEU	2.7
1	A	678	GLY	2.7
1	A	685	LEU	2.6
1	A	718	ARG	2.6
1	A	674	SER	2.6
1	A	715	ILE	2.6
1	A	669	GLY	2.5
1	A	243	THR	2.4
1	A	776	MET	2.3
1	A	691	ARG	2.3
1	A	128	THR	2.3
1	A	36	LEU	2.3
1	A	635	LEU	2.3
1	A	659	ASP	2.2
1	A	254	ILE	2.2
1	A	252	TYR	2.2
1	A	246	ALA	2.2
1	A	683	GLU	2.2
1	A	673	LYS	2.2
1	A	325	LYS	2.1
1	A	256	THR	2.0
1	A	563	MET	2.0
1	A	191	LEU	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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.