



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:14 PM GMT

PDB ID : 1EPU
Title : X-RAY crystal structure of neuronal SEC1 from squid
Authors : Bracher, A.; Perrakis, A.; Dresbach, T.; Betz, H.; Weissenhorn, W.
Deposited on : 2000-03-29
Resolution : 2.40 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
<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

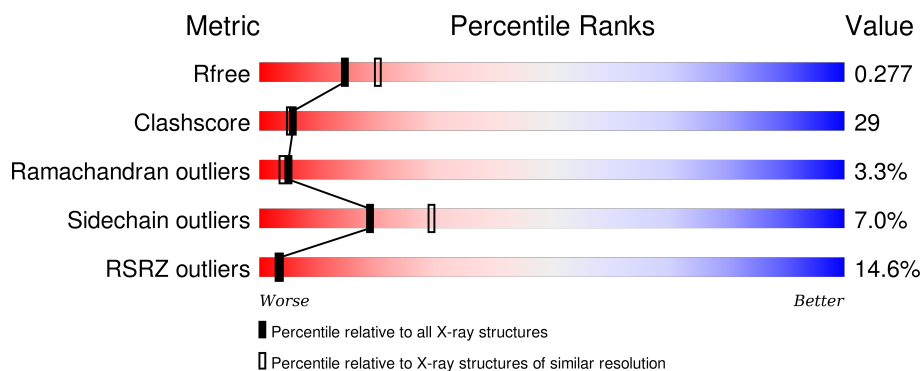
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (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. 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	591	<div> <div>13%</div> <div>47%</div> <div>40%</div> <div>5%</div> <div>8%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4481 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 S-SEC1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	546	Total	C	N	O	S	Se	0	0	0
			4412	2794	763	827	9	19			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	69	Total	O	0	0
			69	69		

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: S-SEC1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.06 Å 121.99 Å 69.05 Å 90.00° 104.53° 90.00°	Depositor
Resolution (Å)	25.00 – 2.40 24.79 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.5 (25.00-2.40) 99.3 (24.79-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.31 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.240 , 0.277 0.240 , 0.277	Depositor DCC
R_{free} test set	1542 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 34635 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4481	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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	0.36	0/4481	0.64	0/6017

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	4412	0	4414	258	0
2	A	69	0	0	5	0
All	All	4481	0	4414	258	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 29.

All (258) 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:577:THR:HG22	1:A:580:GLY:H	1.02	1.10
1:A:447:PRO:HG3	1:A:457:ILE:HB	1.42	0.98
1:A:122:ARG:H	1:A:122:ARG:HD2	1.29	0.96
1:A:312:ARG:HH22	1:A:328:MSE:HE3	1.30	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:ILE:HG23	1:A:164:PRO:HD3	1.51	0.92
1:A:141:ILE:HG12	1:A:552:MSE:HG2	1.54	0.90
1:A:577:THR:HG22	1:A:580:GLY:N	1.85	0.90
1:A:372:MSE:HE3	1:A:479:ARG:HB2	1.53	0.89
1:A:93:ASN:N	1:A:94:PRO:CD	2.38	0.86
1:A:297:SER:O	1:A:300:VAL:HG12	1.76	0.84
1:A:590:ASN:N	1:A:591:PRO:HD3	1.93	0.83
1:A:152:VAL:HG21	1:A:165:ASN:ND2	1.96	0.81
1:A:556:TYR:O	1:A:560:GLN:HG2	1.80	0.80
1:A:4:LYS:HE3	1:A:40:ALA:O	1.82	0.79
1:A:119:THR:O	1:A:122:ARG:HD3	1.81	0.79
1:A:257:GLU:O	1:A:260:VAL:HG12	1.84	0.76
1:A:93:ASN:H	1:A:94:PRO:HD3	1.47	0.75
1:A:249:MSE:HE1	1:A:293:ILE:HD13	1.68	0.75
1:A:163:ILE:CG2	1:A:164:PRO:HD3	2.17	0.74
1:A:445:GLY:O	1:A:457:ILE:HG21	1.88	0.74
1:A:242:HIS:HD2	1:A:367:GLU:OE2	1.69	0.74
1:A:262:LYS:HA	1:A:275:GLU:HA	1.69	0.74
1:A:110:GLU:HG3	1:A:111:LEU:H	1.50	0.74
1:A:399:ALA:O	1:A:403:ILE:HG13	1.89	0.73
1:A:249:MSE:HE1	1:A:293:ILE:CG1	2.19	0.72
1:A:232:ARG:O	1:A:232:ARG:HD3	1.87	0.72
1:A:249:MSE:HE1	1:A:293:ILE:HB	1.70	0.72
1:A:450:GLN:HG3	1:A:451:ASP:N	2.05	0.71
1:A:372:MSE:CE	1:A:479:ARG:HB2	2.20	0.71
1:A:469:ARG:HD2	2:A:594:HOH:O	1.90	0.71
1:A:368:GLN:HE22	1:A:480:TRP:H	1.38	0.71
1:A:78:GLU:O	1:A:82:LYS:HG2	1.91	0.71
1:A:402:LYS:O	1:A:406:ILE:HG12	1.90	0.70
1:A:81:VAL:HG12	1:A:85:MSE:HE2	1.74	0.70
1:A:2:ALA:O	1:A:4:LYS:N	2.25	0.69
1:A:441:MSE:HE2	1:A:446:VAL:CG2	2.23	0.69
1:A:586:ARG:NE	1:A:590:ASN:OD1	2.25	0.69
1:A:339:LEU:O	1:A:339:LEU:HD23	1.92	0.68
1:A:406:ILE:O	1:A:410:ILE:HG12	1.93	0.68
1:A:110:GLU:HG3	1:A:111:LEU:N	2.08	0.68
1:A:249:MSE:HE3	1:A:352:CYS:CB	2.23	0.68
1:A:479:ARG:NH2	2:A:617:HOH:O	2.27	0.68
1:A:44:MSE:O	1:A:48:MSE:HG2	1.94	0.68
1:A:372:MSE:HE1	1:A:480:TRP:N	2.08	0.67
1:A:403:ILE:HG23	1:A:438:ILE:CD1	2.24	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:MSE:HE3	1:A:352:CYS:HB3	1.76	0.67
1:A:327:GLN:H	1:A:327:GLN:CD	1.97	0.67
1:A:312:ARG:NH2	1:A:328:MSE:HE3	2.06	0.66
1:A:93:ASN:N	1:A:94:PRO:HD3	2.09	0.66
1:A:361:ASP:OD2	1:A:362:LYS:HG3	1.95	0.66
1:A:203:GLN:O	1:A:206:LEU:HD12	1.95	0.66
1:A:442:GLN:HB2	1:A:448:ILE:HD11	1.77	0.66
1:A:503:PHE:CZ	1:A:508:GLY:HA3	2.32	0.65
1:A:93:ASN:H	1:A:94:PRO:CD	2.06	0.64
1:A:249:MSE:HE1	1:A:293:ILE:CB	2.27	0.64
1:A:441:MSE:HE3	1:A:441:MSE:O	1.97	0.64
1:A:416:ILE:HG22	1:A:448:ILE:O	1.97	0.64
1:A:249:MSE:HE1	1:A:293:ILE:CD1	2.26	0.64
1:A:362:LYS:O	1:A:365:LYS:HG2	1.97	0.64
1:A:540:ILE:HD13	1:A:569:ILE:HB	1.79	0.64
1:A:389:VAL:HB	1:A:390:PRO:HD3	1.78	0.63
1:A:368:GLN:NE2	1:A:479:ARG:H	1.96	0.63
1:A:589:SER:C	1:A:591:PRO:HD3	2.19	0.63
1:A:218:GLU:C	1:A:220:PRO:HD2	2.18	0.63
1:A:441:MSE:HE1	1:A:444:LEU:HD22	1.80	0.62
1:A:202:VAL:O	1:A:206:LEU:HG	1.99	0.62
1:A:113:LYS:NZ	1:A:113:LYS:HA	2.15	0.62
1:A:334:GLN:HA	1:A:337:LYS:HD2	1.81	0.62
1:A:398:SER:O	1:A:402:LYS:HD3	2.00	0.62
1:A:384:HIS:O	1:A:388:ILE:HG12	2.00	0.62
1:A:441:MSE:CE	1:A:444:LEU:HB2	2.30	0.61
1:A:92:ASP:N	1:A:94:PRO:HD3	2.15	0.61
1:A:419:GLU:O	1:A:422:ALA:HB3	2.00	0.61
1:A:583:ARG:O	1:A:586:ARG:HB3	2.00	0.61
1:A:457:ILE:HD12	1:A:457:ILE:N	2.16	0.60
1:A:547:ILE:HG23	1:A:572:SER:HB2	1.82	0.60
1:A:439:ASN:O	1:A:448:ILE:HD11	2.01	0.60
1:A:450:GLN:HG3	1:A:451:ASP:H	1.66	0.60
1:A:152:VAL:HG21	1:A:165:ASN:HD22	1.67	0.60
1:A:441:MSE:HE3	1:A:444:LEU:HB2	1.84	0.59
1:A:232:ARG:NH2	1:A:551:GLU:OE1	2.35	0.59
1:A:224:ARG:HB2	1:A:537:PRO:CG	2.33	0.59
1:A:504:LEU:H	1:A:504:LEU:HD12	1.67	0.59
1:A:249:MSE:CE	1:A:293:ILE:HB	2.33	0.58
1:A:203:GLN:HA	1:A:206:LEU:HD11	1.85	0.58
1:A:447:PRO:CG	1:A:457:ILE:HB	2.26	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:GLN:HE21	1:A:479:ARG:H	1.50	0.58
1:A:259:ASP:O	1:A:277:LEU:HD12	2.03	0.58
1:A:441:MSE:HE2	1:A:446:VAL:HG21	1.84	0.58
1:A:392:LEU:HG	1:A:428:ALA:HB2	1.86	0.58
1:A:356:TYR:HA	1:A:360:VAL:HB	1.85	0.57
1:A:423:LYS:HD3	1:A:426:GLN:NE2	2.19	0.57
1:A:43:LYS:HE2	1:A:281:LYS:HB3	1.86	0.57
1:A:284:LEU:HB3	1:A:288:MSE:HE2	1.86	0.57
1:A:35:MSE:HE2	1:A:39:SER:OG	2.04	0.57
1:A:220:PRO:C	1:A:222:LYS:H	2.09	0.57
1:A:362:LYS:HA	1:A:365:LYS:HE2	1.87	0.56
1:A:388:ILE:HG22	1:A:392:LEU:HD22	1.86	0.56
1:A:289:ARG:HG3	1:A:290:HIS:CE1	2.40	0.56
1:A:219:GLY:O	1:A:221:GLN:N	2.38	0.56
1:A:285:TRP:O	1:A:289:ARG:HB3	2.05	0.56
1:A:447:PRO:HG3	1:A:457:ILE:CB	2.27	0.56
1:A:122:ARG:N	1:A:122:ARG:HD2	2.11	0.56
1:A:308:ALA:HB2	1:A:335:TYR:CE1	2.41	0.56
1:A:290:HIS:HE1	2:A:627:HOH:O	1.89	0.56
1:A:567:GLU:HG2	1:A:569:ILE:HD11	1.87	0.56
1:A:218:GLU:O	1:A:220:PRO:HD2	2.06	0.55
1:A:403:ILE:HG23	1:A:438:ILE:HD11	1.89	0.55
1:A:66:PRO:O	1:A:97:ARG:HB3	2.06	0.55
1:A:19:VAL:HG21	1:A:100:HIS:CG	2.42	0.55
1:A:44:MSE:HA	1:A:44:MSE:HE2	1.88	0.55
1:A:588:ILE:HD12	1:A:588:ILE:O	2.07	0.54
1:A:421:LEU:O	1:A:425:VAL:HG23	2.07	0.54
1:A:113:LYS:HZ3	1:A:113:LYS:HA	1.71	0.54
1:A:282:ASP:O	1:A:284:LEU:N	2.37	0.54
1:A:132:ILE:O	1:A:132:ILE:HG22	2.07	0.54
1:A:573:THR:OG1	1:A:574:HIS:HD2	1.90	0.54
1:A:457:ILE:H	1:A:457:ILE:HD12	1.73	0.54
1:A:93:ASN:O	1:A:94:PRO:C	2.46	0.53
1:A:187:ARG:HH12	1:A:496:LEU:HB3	1.73	0.53
1:A:11:ILE:O	1:A:15:VAL:HB	2.07	0.53
1:A:163:ILE:HG23	1:A:164:PRO:CD	2.31	0.53
1:A:564:ASN:HB3	1:A:566:TRP:HD1	1.72	0.53
1:A:393:LEU:HD23	1:A:427:HIS:O	2.09	0.53
1:A:382:ARG:HD3	1:A:382:ARG:N	2.23	0.53
1:A:29:ILE:HD13	1:A:70:ALA:HB1	1.90	0.53
1:A:77:THR:CG2	1:A:80:SER:H	2.23	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:ASP:C	1:A:284:LEU:H	2.13	0.52
1:A:249:MSE:CE	1:A:293:ILE:HD13	2.37	0.52
1:A:328:MSE:O	1:A:332:MSE:HG2	2.10	0.52
1:A:305:LYS:O	1:A:309:ASP:HB2	2.10	0.51
1:A:86:ALA:HA	1:A:89:GLN:HB2	1.92	0.51
1:A:135:LEU:HD22	1:A:135:LEU:N	2.26	0.51
1:A:333:PRO:O	1:A:337:LYS:HG3	2.10	0.51
1:A:365:LYS:HB3	1:A:477:MSE:HE1	1.93	0.51
1:A:289:ARG:HG2	1:A:290:HIS:N	2.26	0.50
1:A:386:ARG:HH11	1:A:386:ARG:HG3	1.75	0.50
1:A:140:GLN:HG3	1:A:556:TYR:CE1	2.47	0.50
1:A:34:SER:O	1:A:38:VAL:HG23	2.11	0.50
1:A:10:LYS:O	1:A:14:ASP:HB2	2.12	0.50
1:A:332:MSE:HE1	1:A:336:GLN:HE21	1.77	0.50
1:A:440:ASP:OD1	1:A:588:ILE:HD11	2.12	0.50
1:A:288:MSE:HE1	1:A:345:HIS:CD2	2.47	0.50
1:A:12:MSE:HE3	1:A:17:LEU:HD13	1.94	0.49
1:A:77:THR:HG22	1:A:80:SER:HB2	1.93	0.49
1:A:72:TYR:OH	1:A:88:PHE:HE1	1.94	0.49
1:A:311:LYS:O	1:A:331:LYS:HE2	2.12	0.49
1:A:332:MSE:N	1:A:333:PRO:CD	2.75	0.49
1:A:428:ALA:HB3	1:A:430:ILE:HG13	1.95	0.49
1:A:340:SER:HA	1:A:343:SER:OG	2.12	0.49
1:A:81:VAL:HG21	1:A:111:LEU:HD13	1.95	0.49
1:A:253:LEU:HB3	1:A:355:GLN:HG2	1.95	0.49
1:A:87:ASP:HB3	1:A:95:GLN:CB	2.43	0.49
1:A:77:THR:HG23	1:A:79:GLU:N	2.28	0.49
1:A:444:LEU:HD12	1:A:444:LEU:N	2.27	0.48
1:A:32:GLN:O	1:A:36:ARG:HG3	2.13	0.48
1:A:441:MSE:HE3	1:A:444:LEU:HD13	1.96	0.48
1:A:443:ASN:ND2	1:A:588:ILE:HD13	2.28	0.48
1:A:64:PRO:C	1:A:66:PRO:HD3	2.34	0.48
1:A:95:GLN:HA	1:A:95:GLN:OE1	2.14	0.48
1:A:3:LEU:O	1:A:7:VAL:HG23	2.13	0.48
1:A:93:ASN:N	1:A:94:PRO:HD2	2.27	0.48
1:A:362:LYS:NZ	1:A:362:LYS:CB	2.77	0.48
1:A:276:VAL:HG12	1:A:277:LEU:N	2.28	0.48
1:A:209:TYR:HB3	1:A:216:MSE:HE1	1.94	0.48
1:A:77:THR:HG22	1:A:80:SER:CB	2.43	0.47
1:A:410:ILE:CG2	1:A:448:ILE:HA	2.44	0.47
1:A:307:PHE:C	1:A:309:ASP:H	2.17	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:LEU:HD13	1:A:176:LEU:C	2.34	0.47
1:A:118:SER:C	1:A:120:THR:H	2.17	0.47
1:A:540:ILE:CD1	1:A:569:ILE:HB	2.45	0.47
1:A:384:HIS:CE1	1:A:412:HIS:HE1	2.33	0.47
1:A:441:MSE:HE2	1:A:446:VAL:HG23	1.95	0.47
1:A:26:LYS:O	1:A:53:THR:HG22	2.15	0.47
1:A:60:ARG:O	1:A:61:ARG:O	2.32	0.47
1:A:166:LYS:O	1:A:169:CYS:HB2	2.14	0.47
1:A:425:VAL:HG13	1:A:430:ILE:HB	1.98	0.46
1:A:122:ARG:H	1:A:122:ARG:CD	2.11	0.46
1:A:197:SER:O	1:A:201:LEU:HD23	2.14	0.46
1:A:141:ILE:HA	1:A:570:LEU:O	2.16	0.46
1:A:577:THR:HG23	2:A:609:HOH:O	2.15	0.46
1:A:171:GLU:O	1:A:175:THR:HG23	2.16	0.46
1:A:569:ILE:N	1:A:569:ILE:HD12	2.30	0.46
1:A:27:VAL:HG23	1:A:29:ILE:CD1	2.46	0.46
1:A:372:MSE:HB2	1:A:372:MSE:HE2	1.68	0.46
1:A:7:VAL:HG12	1:A:41:CYS:SG	2.56	0.46
1:A:232:ARG:HD3	1:A:232:ARG:HA	1.63	0.45
1:A:452:GLY:O	1:A:454:ARG:N	2.49	0.45
1:A:94:PRO:HB3	1:A:96:TYR:O	2.16	0.45
1:A:410:ILE:HD12	1:A:416:ILE:HG21	1.98	0.45
1:A:450:GLN:CG	1:A:451:ASP:H	2.25	0.45
1:A:581:LEU:O	1:A:585:LEU:HD23	2.17	0.45
1:A:303:LYS:O	1:A:306:GLN:HB3	2.16	0.45
1:A:416:ILE:HD11	1:A:420:ASN:CB	2.46	0.45
1:A:339:LEU:C	1:A:339:LEU:HD23	2.37	0.45
1:A:83:CYS:O	1:A:86:ALA:HB3	2.17	0.45
1:A:386:ARG:HH11	1:A:386:ARG:CG	2.30	0.45
1:A:230:LEU:HB2	1:A:543:VAL:HG22	1.99	0.45
1:A:37:MSE:SE	1:A:132:ILE:HG21	2.68	0.44
1:A:435:LYS:NZ	1:A:439:ASN:HD21	2.15	0.44
1:A:440:ASP:CG	1:A:588:ILE:HD11	2.38	0.44
1:A:224:ARG:HB2	1:A:537:PRO:HG3	1.98	0.44
1:A:65:LEU:N	1:A:66:PRO:HD3	2.32	0.44
1:A:303:LYS:HA	1:A:306:GLN:HB3	2.00	0.44
1:A:362:LYS:HB3	1:A:362:LYS:NZ	2.33	0.44
1:A:327:GLN:HB3	1:A:331:LYS:HE3	2.00	0.44
1:A:158:ARG:O	1:A:159:ALA:O	2.36	0.44
1:A:73:LEU:HD11	1:A:130:ILE:HD11	2.00	0.43
1:A:262:LYS:HA	1:A:275:GLU:CA	2.44	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:THR:O	1:A:77:THR:N	2.48	0.43
1:A:142:PHE:CZ	1:A:571:GLY:HA3	2.53	0.43
1:A:232:ARG:HB3	1:A:444:LEU:HD23	1.99	0.43
1:A:232:ARG:HH22	1:A:551:GLU:CD	2.22	0.43
1:A:134:PHE:CE1	1:A:176:LEU:HA	2.53	0.43
1:A:362:LYS:CA	1:A:365:LYS:HE2	2.49	0.43
1:A:12:MSE:O	1:A:17:LEU:HB2	2.18	0.43
1:A:148:ASP:CG	1:A:158:ARG:HH12	2.22	0.43
1:A:440:ASP:C	1:A:442:GLN:N	2.72	0.43
1:A:218:GLU:O	1:A:222:LYS:HB2	2.18	0.42
1:A:113:LYS:HE3	1:A:117:LYS:HG2	2.01	0.42
1:A:27:VAL:HG23	1:A:29:ILE:HD11	2.01	0.42
1:A:12:MSE:SE	1:A:47:ILE:HD13	2.69	0.42
1:A:62:ARG:O	1:A:95:GLN:NE2	2.52	0.42
1:A:407:LEU:O	1:A:411:ILE:HG13	2.18	0.42
1:A:338:GLU:O	1:A:341:LYS:N	2.44	0.42
1:A:567:GLU:HG2	1:A:569:ILE:CD1	2.48	0.42
1:A:113:LYS:CE	1:A:117:LYS:HG2	2.50	0.42
1:A:289:ARG:HG2	1:A:290:HIS:H	1.85	0.42
1:A:76:PRO:HG3	1:A:105:GLU:O	2.20	0.42
1:A:19:VAL:HG21	1:A:100:HIS:CD2	2.55	0.42
1:A:367:GLU:HG2	1:A:408:LEU:CD1	2.49	0.42
1:A:200:GLN:HG3	1:A:204:GLN:NE2	2.35	0.42
1:A:74:ILE:HD13	1:A:74:ILE:H	1.85	0.42
1:A:590:ASN:HA	1:A:590:ASN:HD22	1.59	0.41
1:A:416:ILE:O	1:A:450:GLN:N	2.48	0.41
1:A:171:GLU:OE2	1:A:209:TYR:HE1	2.02	0.41
1:A:458:PRO:C	1:A:460:PRO:HD3	2.41	0.41
1:A:503:PHE:CE2	1:A:508:GLY:HA3	2.56	0.41
1:A:334:GLN:HA	1:A:337:LYS:CD	2.50	0.41
1:A:104:THR:HG23	1:A:132:ILE:O	2.20	0.41
1:A:86:ALA:O	1:A:89:GLN:HB3	2.20	0.41
1:A:311:LYS:O	1:A:312:ARG:HG3	2.21	0.41
1:A:139:SER:O	1:A:140:GLN:HG2	2.21	0.41
1:A:220:PRO:C	1:A:222:LYS:N	2.74	0.41
1:A:308:ALA:HB2	1:A:335:TYR:HE1	1.84	0.41
1:A:573:THR:OG1	1:A:574:HIS:CD2	2.72	0.41
1:A:153:TYR:CE2	1:A:192:PHE:HE2	2.39	0.41
1:A:289:ARG:HG3	1:A:290:HIS:ND1	2.35	0.41
1:A:87:ASP:HB3	1:A:95:GLN:HB2	2.02	0.41
1:A:190:SER:OG	1:A:502:PRO:HG3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:PRO:O	1:A:222:LYS:N	2.55	0.41
1:A:32:GLN:NE2	2:A:656:HOH:O	2.53	0.40
1:A:451:ASP:C	1:A:453:GLY:H	2.23	0.40
1:A:140:GLN:C	1:A:141:ILE:HD12	2.42	0.40
1:A:77:THR:O	1:A:81:VAL:HG23	2.20	0.40
1:A:542:PHE:HA	1:A:571:GLY:O	2.20	0.40
1:A:422:ALA:O	1:A:426:GLN:HG3	2.22	0.40
1:A:62:ARG:N	1:A:62:ARG:CD	2.84	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	538/591 (91%)	471 (88%)	49 (9%)	18 (3%)	5 4

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	61	ARG
1	A	159	ALA
1	A	220	PRO
1	A	450	GLN
1	A	79	GLU
1	A	193	ASP
1	A	219	GLY
1	A	283	ASP
1	A	453	GLY
1	A	94	PRO
1	A	564	ASN
1	A	139	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	221	GLN
1	A	131	ASN
1	A	132	ILE
1	A	93	ASN
1	A	16	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	487/502 (97%)	453 (93%)	34 (7%)	19	29

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	VAL
1	A	25	TRP
1	A	62	ARG
1	A	63	GLU
1	A	74	ILE
1	A	84	LEU
1	A	94	PRO
1	A	113	LYS
1	A	122	ARG
1	A	140	GLN
1	A	145	ASP
1	A	153	TYR
1	A	191	ASP
1	A	206	LEU
1	A	228	LEU
1	A	232	ARG
1	A	241	LEU
1	A	244	LEU
1	A	246	PHE
1	A	283	ASP
1	A	329	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	354	LYS
1	A	355	GLN
1	A	359	HIS
1	A	382	ARG
1	A	386	ARG
1	A	391	ILE
1	A	402	LYS
1	A	421	LEU
1	A	504	LEU
1	A	544	VAL
1	A	577	THR
1	A	588	ILE
1	A	590	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	165	ASN
1	A	204	GLN
1	A	226	GLN
1	A	242	HIS
1	A	247	GLN
1	A	258	ASN
1	A	299	ASN
1	A	327	GLN
1	A	336	GLN
1	A	355	GLN
1	A	357	GLN
1	A	359	HIS
1	A	368	GLN
1	A	384	HIS
1	A	387	ASN
1	A	395	GLN
1	A	412	HIS
1	A	426	GLN
1	A	427	HIS
1	A	439	ASN
1	A	465	ASN
1	A	574	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 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	527/591 (89%)	0.70	77 (14%) 3 3	31, 65, 97, 129	1 (0%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	591	PRO	11.5
1	A	535	SER	6.6
1	A	534	LYS	6.5
1	A	309	ASP	6.1
1	A	263	TYR	5.3
1	A	455	ARG	5.0
1	A	312	ARG	4.8
1	A	310	GLU	4.8
1	A	220	PRO	4.5
1	A	311	LYS	4.3
1	A	71	VAL	4.2
1	A	219	GLY	4.2
1	A	454	ARG	4.1
1	A	101	ILE	4.0
1	A	92	ASP	3.9
1	A	453	GLY	3.9
1	A	382	ARG	3.9
1	A	451	ASP	3.8
1	A	214	PRO	3.7
1	A	471	ALA	3.6
1	A	93	ASN	3.6
1	A	72	TYR	3.6
1	A	357	GLN	3.6
1	A	89	GLN	3.5
1	A	215	THR	3.5
1	A	307	PHE	3.5
1	A	84	LEU	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	560	GLN	3.4
1	A	173	ILE	3.4
1	A	541	ILE	3.3
1	A	218	GLU	3.2
1	A	542	PHE	3.2
1	A	308	ALA	3.1
1	A	29	ILE	3.1
1	A	456	LYS	3.1
1	A	82	LYS	3.1
1	A	452	GLY	3.1
1	A	508	GLY	3.0
1	A	507	GLY	3.0
1	A	561	THR	3.0
1	A	70	ALA	3.0
1	A	562	ALA	3.0
1	A	590	ASN	2.9
1	A	306	GLN	2.9
1	A	285	TRP	2.9
1	A	407	LEU	2.8
1	A	571	GLY	2.8
1	A	241	LEU	2.8
1	A	228	LEU	2.7
1	A	177	CYS	2.7
1	A	88	PHE	2.6
1	A	540	ILE	2.6
1	A	281	LYS	2.6
1	A	73	LEU	2.6
1	A	283	ASP	2.5
1	A	450	GLN	2.5
1	A	499	ARG	2.4
1	A	432	ALA	2.4
1	A	160	GLN	2.3
1	A	43	LYS	2.3
1	A	419	GLU	2.3
1	A	27	VAL	2.3
1	A	28	LEU	2.3
1	A	570	LEU	2.3
1	A	341	LYS	2.3
1	A	227	LEU	2.2
1	A	406	ILE	2.2
1	A	339	LEU	2.2
1	A	544	VAL	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	240	LEU	2.2
1	A	472	ASP	2.1
1	A	383	ASP	2.1
1	A	572	SER	2.1
1	A	142	PHE	2.0
1	A	277	LEU	2.0
1	A	99	ALA	2.0
1	A	102	PHE	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 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.