



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 08:57 PM UTC

PDB ID : 5J44 / pdb_00005j44
Title : Crystal structure of the Secreted Extracellular protein A (SepA) from *Shigella flexneri*
Authors : Birtley, J.R.; Stern, L.J.; McCormick, B.; Maldonado-Contreras, A.
Deposited on : 2016-03-31
Resolution : 2.91 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

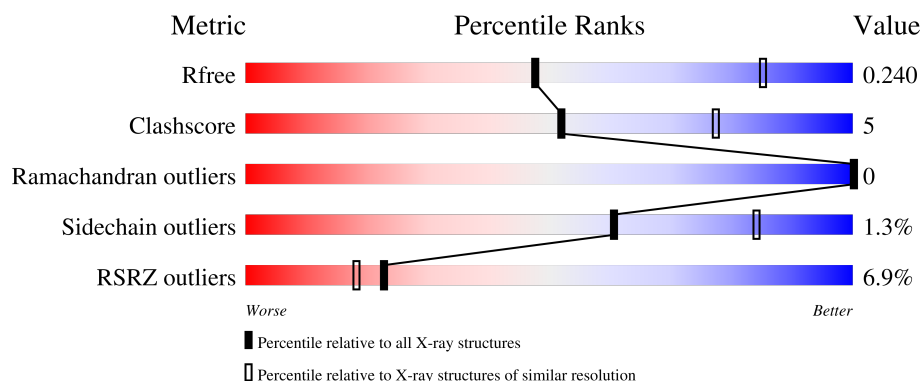
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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}	180053	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1033	2% 84% 13% .
1	B	1033	11% 85% 12% .

2 Entry composition [i](#)

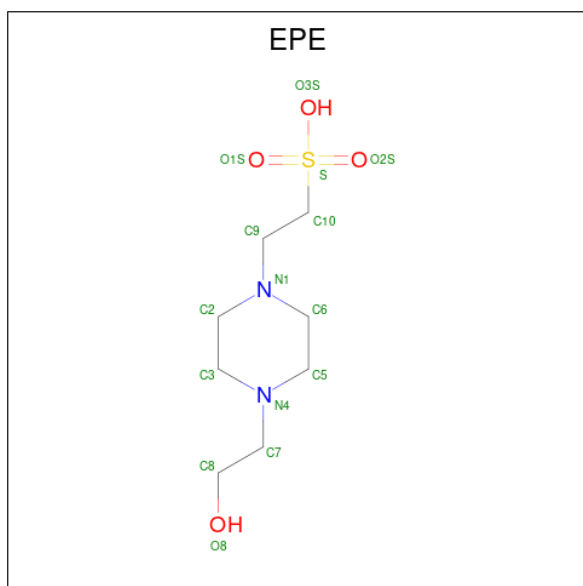
There are 3 unique types of molecules in this entry. The entry contains 15034 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine protease SepA autotransporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1006	Total	C	N	O	S	0	0	0
			7500	4650	1290	1543	17			
1	B	1006	Total	C	N	O	S	0	0	0
			7500	4650	1290	1543	17			

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		

Continued on next page...

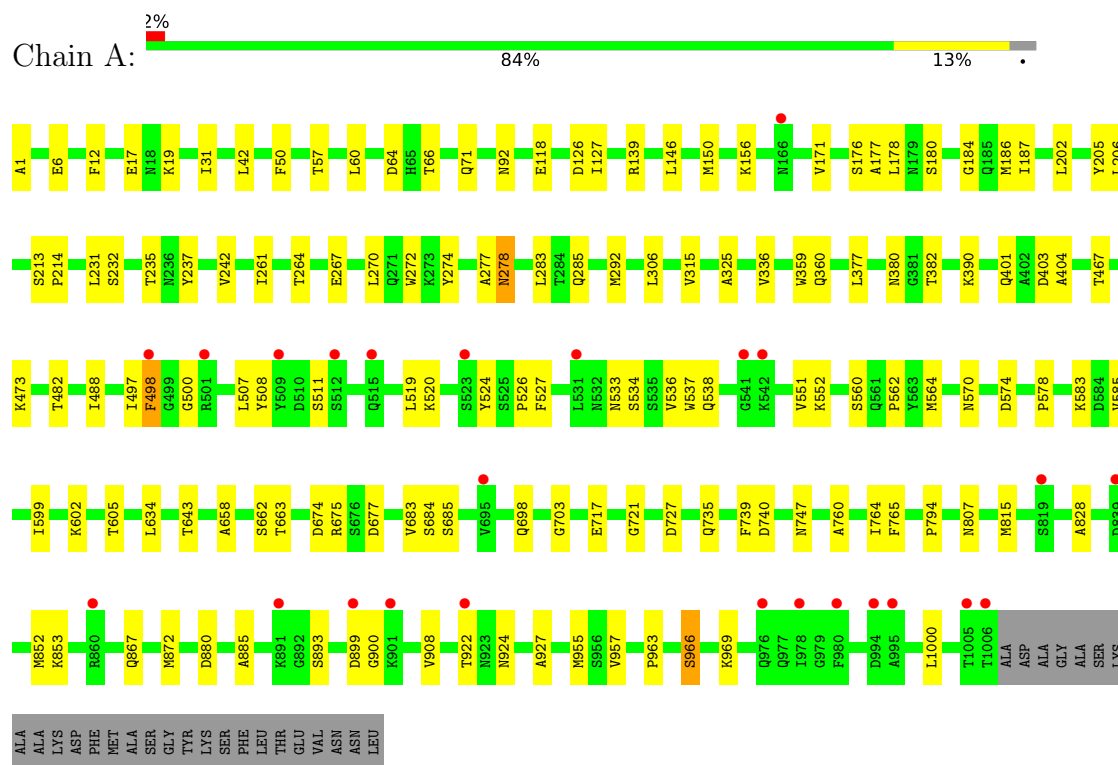
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	7	Total	O	0	0
			7	7		

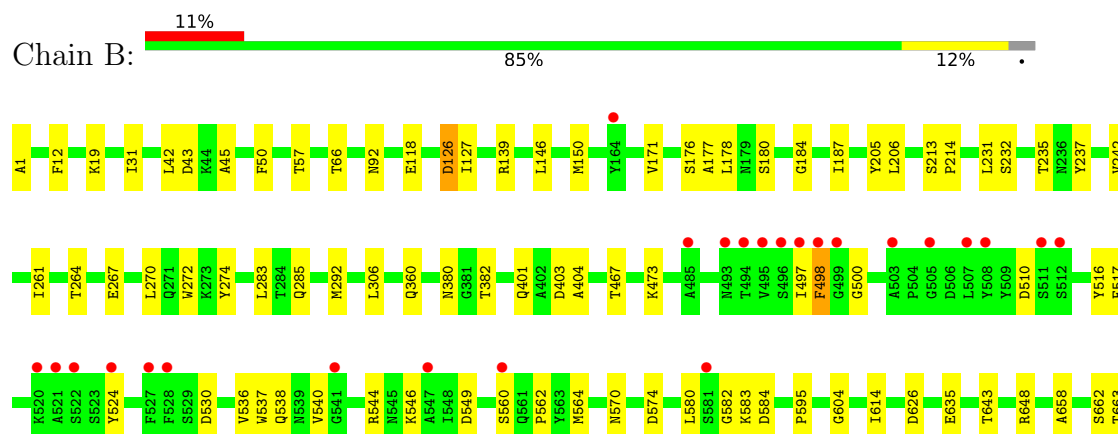
3 Residue-property plots

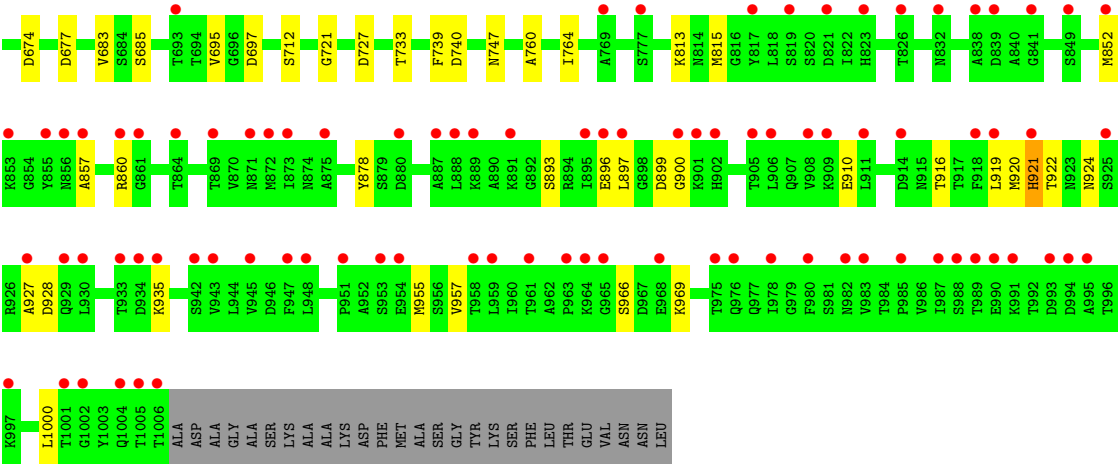
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Serine protease SepA autotransporter



• Molecule 1: Serine protease SepA autotransporter





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.52Å 143.52Å 269.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	72.76 – 2.91 72.76 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.9 (72.76-2.91) 100.0 (72.76-2.91)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	0.30	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.214 , 0.239 0.217 , 0.240	Depositor DCC
R_{free} test set	3584 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.334	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15034	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.09	0/7628	0.29	0/10353
1	B	0.08	0/7628	0.29	0/10353
All	All	0.09	0/15256	0.29	0/20706

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

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	7500	0	7282	82	1
1	B	7500	0	7282	71	0
2	A	15	0	17	1	0
3	A	12	0	0	1	0
3	B	7	0	0	0	0
All	All	15034	0	14581	152	1

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 5.

All (152) 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:B:584:ASP:OD2	1:B:604:GLY:HA3	1.79	0.82
1:A:277:ALA:O	1:A:278:ASN:ND2	2.12	0.80
1:A:482:THR:HG21	1:A:560:SER:HA	1.65	0.76
1:A:498:PHE:HA	1:A:526:PRO:HB3	1.70	0.74
1:A:178:LEU:HD13	1:A:187:ILE:HD12	1.69	0.73
1:B:178:LEU:HD13	1:B:187:ILE:HD12	1.69	0.72
1:A:899:ASP:OD2	1:A:900:GLY:N	2.20	0.71
1:B:127:ILE:HD11	1:B:139:ARG:HD3	1.75	0.68
1:A:533:ASN:OD1	1:A:534:SER:N	2.27	0.67
1:A:473:LYS:HD3	1:A:574:ASP:OD2	1.95	0.67
1:A:292:MET:HG3	1:A:306:LEU:HD11	1.76	0.67
1:B:580:LEU:N	1:B:584:ASP:OD1	2.20	0.66
1:B:674:ASP:HB3	1:B:677:ASP:HB2	1.77	0.66
1:B:564:MET:HB2	1:B:683:VAL:HG11	1.78	0.65
1:A:1:ALA:N	1:A:205:TYR:O	2.29	0.65
1:A:674:ASP:HB3	1:A:677:ASP:HB2	1.80	0.64
1:B:1:ALA:N	1:B:205:TYR:O	2.28	0.64
1:A:520:LYS:HE3	1:A:538:GLN:HB2	1.79	0.64
1:A:727:ASP:OD1	1:A:747:ASN:ND2	2.30	0.63
1:B:292:MET:HG3	1:B:306:LEU:HD11	1.80	0.63
1:A:127:ILE:HD11	1:A:139:ARG:HD3	1.80	0.61
1:A:562:PRO:O	1:A:685:SER:OG	2.17	0.61
1:B:50:PHE:HB3	1:B:146:LEU:HD22	1.82	0.61
1:B:206:LEU:HD12	1:B:231:LEU:HD13	1.84	0.59
1:B:896:GLU:HA	1:B:919:LEU:HB3	1.85	0.59
1:B:516:TYR:CZ	1:B:544:ARG:HB3	2.38	0.58
1:B:473:LYS:HD3	1:B:574:ASP:OD2	2.03	0.58
1:A:467:THR:HG22	1:A:570:ASN:HB2	1.86	0.58
1:A:50:PHE:HB3	1:A:146:LEU:HD22	1.86	0.58
1:B:580:LEU:HB2	1:B:584:ASP:HA	1.87	0.57
1:A:643:THR:HG23	1:A:663:THR:HB	1.88	0.56
1:B:562:PRO:HD3	1:B:583:LYS:HD3	1.87	0.55
1:A:658:ALA:HB1	1:A:662:SER:HB2	1.88	0.55
1:B:562:PRO:O	1:B:685:SER:OG	2.18	0.55
1:A:562:PRO:HD3	1:A:583:LYS:HD3	1.88	0.55
1:B:382:THR:HG22	1:B:401:GLN:HB2	1.88	0.55
1:A:922:THR:HG22	1:A:924:ASN:H	1.71	0.55
1:A:390:LYS:NZ	3:A:1201:HOH:O	2.39	0.54
1:B:43:ASP:C	1:B:45:ALA:H	2.16	0.53
1:A:957:VAL:HG23	1:A:1000:LEU:HB3	1.90	0.53
1:B:921:HIS:ND1	1:B:928:ASP:OD2	2.30	0.53
1:A:564:MET:HB2	1:A:683:VAL:HG11	1.89	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:897:LEU:HD12	1:B:920:MET:HG3	1.90	0.53
1:A:739:PHE:HB2	1:A:760:ALA:HA	1.90	0.52
1:B:727:ASP:OD1	1:B:747:ASN:ND2	2.40	0.51
1:B:922:THR:HG22	1:B:924:ASN:H	1.75	0.51
1:B:721:GLY:O	1:B:740:ASP:N	2.43	0.51
1:A:360:GLN:HG2	1:A:380:ASN:HB3	1.93	0.51
1:A:66:THR:OG1	1:A:214:PRO:HG3	2.11	0.51
1:A:206:LEU:HD12	1:A:231:LEU:HD13	1.92	0.51
1:B:66:THR:OG1	1:B:214:PRO:HG3	2.11	0.50
1:B:12:PHE:HB3	1:B:171:VAL:HG13	1.93	0.50
1:B:658:ALA:HB1	1:B:662:SER:HB2	1.93	0.50
1:A:270:LEU:HD23	1:A:285:GLN:HB2	1.94	0.50
1:B:739:PHE:HB2	1:B:760:ALA:HA	1.93	0.50
1:B:403:ASP:OD1	1:B:404:ALA:N	2.43	0.50
1:A:17:GLU:OE1	1:A:19:LYS:NZ	2.42	0.50
1:A:497:ILE:O	1:A:527:PHE:N	2.35	0.49
1:B:272:TRP:HE1	1:B:292:MET:HE2	1.77	0.49
1:A:178:LEU:HB3	1:A:187:ILE:HB	1.93	0.49
1:B:922:THR:HG23	1:B:927:ALA:HB2	1.94	0.49
1:A:924:ASN:N	1:A:924:ASN:HD22	2.11	0.48
1:A:403:ASP:OD1	1:A:404:ALA:N	2.43	0.48
1:A:922:THR:HG23	1:A:927:ALA:HB2	1.95	0.48
1:B:126:ASP:OD1	1:B:126:ASP:N	2.46	0.48
1:A:146:LEU:O	1:A:213:SER:HB2	2.13	0.48
1:A:150:MET:HE3	1:B:150:MET:HG3	1.96	0.48
1:A:599:ILE:HG13	1:A:634:LEU:HD21	1.95	0.48
1:B:536:VAL:HG23	1:B:537:TRP:CD1	2.49	0.48
1:A:12:PHE:HB3	1:A:171:VAL:HG13	1.95	0.48
1:B:235:THR:HG23	1:B:237:TYR:H	1.79	0.48
1:B:924:ASN:HD22	1:B:924:ASN:N	2.11	0.48
1:A:261:ILE:HD13	1:A:283:LEU:HD22	1.96	0.47
1:B:524:TYR:HB2	1:B:530:ASP:OD2	2.14	0.47
1:B:497:ILE:HG22	1:B:498:PHE:H	1.79	0.47
1:B:957:VAL:HG23	1:B:1000:LEU:HB3	1.96	0.47
1:A:272:TRP:HE1	1:A:292:MET:HE2	1.79	0.47
1:B:899:ASP:CG	1:B:900:GLY:H	2.22	0.47
1:B:146:LEU:O	1:B:213:SER:HB2	2.15	0.47
1:B:232:SER:HB2	1:B:242:VAL:HG23	1.97	0.47
1:A:721:GLY:O	1:A:740:ASP:N	2.47	0.47
1:B:274:TYR:CD1	1:B:292:MET:HE1	2.49	0.47
1:B:360:GLN:HG2	1:B:380:ASN:HB3	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:963:PRO:O	1:A:966:SER:OG	2.29	0.46
1:A:176:SER:OG	1:A:177:ALA:N	2.49	0.46
1:B:178:LEU:HB3	1:B:187:ILE:HB	1.97	0.46
1:A:765:PHE:HB2	2:A:1101:EPE:H81	1.97	0.46
1:A:274:TYR:CD1	1:A:292:MET:HE1	2.50	0.46
1:A:872:MET:HE2	1:A:893:SER:HB3	1.98	0.46
1:B:648:ARG:NH2	1:B:697:ASP:OD2	2.49	0.46
1:B:910:GLU:HG3	1:B:935:LYS:HB3	1.98	0.46
1:A:599:ILE:HD12	1:A:634:LEU:HD11	1.98	0.45
1:B:176:SER:OG	1:B:177:ALA:N	2.49	0.45
1:B:739:PHE:HD2	1:B:764:ILE:HD11	1.81	0.45
1:B:272:TRP:NE1	1:B:292:MET:HE2	2.32	0.45
1:B:813:LYS:HA	1:B:857:ALA:HB2	1.99	0.45
1:A:235:THR:HG23	1:A:237:TYR:H	1.81	0.45
1:A:500:GLY:HA3	1:A:524:TYR:CZ	2.52	0.45
1:A:828:ALA:HA	1:A:867:GLN:O	2.17	0.45
1:B:516:TYR:CE2	1:B:544:ARG:HB3	2.52	0.45
1:A:272:TRP:NE1	1:A:292:MET:HE2	2.33	0.44
1:A:232:SER:HB2	1:A:242:VAL:HG23	1.98	0.44
1:A:872:MET:HE2	1:A:872:MET:HB3	1.86	0.44
1:B:270:LEU:HD23	1:B:285:GLN:HB2	2.00	0.44
1:A:675:ARG:HB2	1:A:684:SER:HB2	1.99	0.43
1:A:186:MET:HG2	1:A:242:VAL:HA	1.98	0.43
1:A:382:THR:HG22	1:A:401:GLN:HB2	1.99	0.43
1:A:6:GLU:HG3	1:A:156:LYS:HE3	2.01	0.43
1:A:31:ILE:HD13	1:A:202:LEU:HG	2.00	0.43
1:A:60:LEU:HB3	1:A:64:ASP:OD2	2.18	0.43
1:A:315:VAL:HB	1:A:336:VAL:HG22	2.01	0.43
1:B:500:GLY:HA3	1:B:524:TYR:CZ	2.53	0.43
1:A:359:TRP:HB2	1:A:377:LEU:HD11	1.99	0.43
1:A:508:TYR:HE2	1:A:519:LEU:HD22	1.83	0.43
1:B:180:SER:HB3	1:B:184:GLY:HA2	2.00	0.43
1:B:31:ILE:HD11	1:B:42:LEU:HG	2.01	0.43
1:A:880:ASP:O	1:A:899:ASP:HB2	2.18	0.42
1:B:42:LEU:HD23	1:B:42:LEU:HA	1.89	0.42
1:A:815:MET:HA	1:A:852:MET:HE2	2.01	0.42
1:A:71:GLN:NE2	1:A:325:ALA:O	2.38	0.42
1:B:264:THR:HB	1:B:267:GLU:HG3	2.01	0.42
1:B:261:ILE:HD13	1:B:283:LEU:HD22	2.02	0.42
1:B:643:THR:HG23	1:B:663:THR:HB	2.01	0.42
1:A:536:VAL:HG23	1:A:537:TRP:CD1	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ASN:ND2	1:A:118:GLU:HG2	2.35	0.42
1:A:180:SER:HB3	1:A:184:GLY:HA2	2.01	0.42
1:B:626:ASP:OD1	1:B:626:ASP:N	2.53	0.41
1:B:860:ARG:HA	1:B:878:TYR:HB2	2.03	0.41
1:A:885:ALA:HB3	1:A:908:VAL:HG12	2.02	0.41
1:B:92:ASN:ND2	1:B:118:GLU:HG2	2.35	0.41
1:B:467:THR:HA	1:B:570:ASN:O	2.20	0.41
1:A:126:ASP:OD1	1:A:126:ASP:N	2.54	0.41
1:A:264:THR:HB	1:A:267:GLU:HG3	2.01	0.41
1:A:739:PHE:HD2	1:A:764:ILE:HD11	1.85	0.41
1:B:815:MET:HA	1:B:852:MET:HE2	2.00	0.41
1:A:578:PRO:HA	1:A:602:LYS:HB3	2.02	0.41
1:B:510:ASP:HB2	1:B:517:PHE:HE2	1.86	0.41
1:B:595:PRO:O	1:B:635:GLU:HB2	2.20	0.41
1:B:663:THR:HG23	1:B:712:SER:HB2	2.03	0.41
1:B:893:SER:HB2	1:B:916:THR:HG23	2.02	0.41
1:A:488:ILE:HG21	1:A:552:LYS:HG2	2.02	0.41
1:A:507:LEU:HD13	1:A:551:VAL:HG21	2.03	0.41
1:A:698:GLN:HG2	1:A:717:GLU:OE2	2.21	0.41
1:A:794:PRO:HA	1:A:815:MET:O	2.21	0.41
1:B:19:LYS:HD3	1:B:614:ILE:HG22	2.03	0.41
1:B:292:MET:HB3	1:B:292:MET:HE3	1.79	0.41
1:B:560:SER:OG	1:B:582:GLY:HA3	2.22	0.40
1:A:585:VAL:HG22	1:A:605:THR:HB	2.03	0.40
1:A:31:ILE:HD11	1:A:42:LEU:HG	2.04	0.40
1:A:467:THR:CG2	1:A:570:ASN:HB2	2.50	0.40
1:A:500:GLY:HA3	1:A:524:TYR:CE1	2.56	0.40
1:A:703:GLY:O	1:A:721:GLY:HA3	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:727:ASP:OD2	1:A:853:LYS:NZ[4_556]	1.88	0.32

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	1004/1033 (97%)	965 (96%)	39 (4%)	0	100	100
1	B	1004/1033 (97%)	961 (96%)	43 (4%)	0	100	100
All	All	2008/2066 (97%)	1926 (96%)	82 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	816/835 (98%)	807 (99%)	9 (1%)	65	86
1	B	816/835 (98%)	803 (98%)	13 (2%)	55	81
All	All	1632/1670 (98%)	1610 (99%)	22 (1%)	61	84

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	THR
1	A	278	ASN
1	A	498	PHE
1	A	511	SER
1	A	735	GLN
1	A	807	ASN
1	A	955	MET
1	A	966	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	969	LYS
1	B	57	THR
1	B	126	ASP
1	B	498	PHE
1	B	538	GLN
1	B	540	VAL
1	B	546	LYS
1	B	549	ASP
1	B	695	VAL
1	B	733	THR
1	B	921	HIS
1	B	955	MET
1	B	966	SER
1	B	969	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	240	ASN
1	A	251	GLN
1	A	469	ASN
1	A	481	GLN
1	A	570	ASN
1	A	631	GLN
1	A	871	ASN
1	A	924	ASN
1	A	949	ASN
1	B	159	ASN
1	B	179	ASN
1	B	240	ASN
1	B	380	ASN
1	B	469	ASN
1	B	570	ASN
1	B	631	GLN
1	B	832	ASN
1	B	871	ASN
1	B	941	ASN
1	B	949	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	EPE	A	1101	-	15,15,15	0.81	1 (6%)	19,20,20	1.86	5 (26%)

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	EPE	A	1101	-	-	3/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	EPE	C10-S	2.62	1.81	1.77

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	EPE	C5-N4-C3	4.13	117.73	108.84
2	A	1101	EPE	C7-N4-C3	3.91	121.67	111.24
2	A	1101	EPE	C7-N4-C5	3.48	120.50	111.24
2	A	1101	EPE	C6-N1-C2	2.61	114.47	108.84
2	A	1101	EPE	O3S-S-C10	2.06	110.04	106.00

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	EPE	C10-C9-N1-C2
2	A	1101	EPE	C10-C9-N1-C6
2	A	1101	EPE	C8-C7-N4-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	EPE	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1006/1033 (97%)	-0.00	25 (2%) 58 48	28, 51, 106, 161	0
1	B	1006/1033 (97%)	0.49	114 (11%) 10 8	25, 65, 164, 212	0
All	All	2012/2066 (97%)	0.25	139 (6%) 23 18	25, 56, 150, 212	0

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	901	LYS	4.9
1	B	945	VAL	4.9
1	B	496	SER	4.5
1	B	497	ILE	4.4
1	B	498	PHE	4.3
1	B	891	LYS	4.3
1	B	838	ALA	4.1
1	B	512	SER	4.1
1	B	897	LEU	3.8
1	B	906	LEU	3.8
1	B	852	MET	3.8
1	B	914	ASP	3.7
1	A	901	LYS	3.7
1	B	853	LYS	3.6
1	B	499	GLY	3.6
1	B	826	THR	3.5
1	B	905	THR	3.5
1	A	860	ARG	3.4
1	B	855	TYR	3.4
1	B	817	TYR	3.3
1	B	493	ASN	3.3
1	B	889	LYS	3.3
1	B	978	ILE	3.3
1	B	934	ASP	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	911	LEU	3.2
1	B	927	ALA	3.2
1	B	521	ALA	3.1
1	B	921	HIS	3.1
1	B	1005	THR	3.1
1	B	997	LYS	3.0
1	A	978	ILE	3.0
1	B	547	ALA	3.0
1	B	961	THR	3.0
1	A	523	SER	3.0
1	B	958	THR	3.0
1	B	895	ILE	2.9
1	B	948	LEU	2.9
1	B	959	LEU	2.9
1	A	166	ASN	2.9
1	B	823	HIS	2.9
1	A	509	TYR	2.9
1	B	503	ALA	2.9
1	B	995	ALA	2.9
1	B	983	VAL	2.9
1	A	839	ASP	2.8
1	B	953	SER	2.8
1	A	976	GLN	2.8
1	B	964	LYS	2.8
1	B	485	ALA	2.8
1	B	1004	GLN	2.8
1	B	857	ALA	2.8
1	B	873	ILE	2.8
1	B	991	LYS	2.8
1	A	1006	THR	2.8
1	A	994	ASP	2.7
1	B	976	GLN	2.7
1	B	918	PHE	2.7
1	B	869	THR	2.7
1	B	900	GLY	2.7
1	B	980	PHE	2.7
1	B	832	ASN	2.7
1	B	541	GLY	2.7
1	B	1006	THR	2.7
1	B	947	PHE	2.7
1	B	985	PRO	2.7
1	A	531	LEU	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	849	SER	2.7
1	B	527	PHE	2.6
1	B	1002	GLY	2.6
1	B	494	THR	2.6
1	B	963	PRO	2.6
1	B	919	LEU	2.6
1	B	943	VAL	2.6
1	B	508	TYR	2.6
1	B	511	SER	2.6
1	B	925	SER	2.6
1	B	505	GLY	2.6
1	B	887	ALA	2.6
1	B	951	PRO	2.5
1	B	524	TYR	2.5
1	B	933	THR	2.5
1	B	954	GLU	2.5
1	B	968	GLU	2.5
1	B	581	SER	2.5
1	B	841	GLY	2.5
1	A	995	ALA	2.5
1	B	693	THR	2.5
1	B	994	ASP	2.5
1	B	861	GLY	2.5
1	B	942	SER	2.5
1	A	515	GLN	2.4
1	A	542	LYS	2.4
1	A	819	SER	2.4
1	A	980	PHE	2.4
1	A	922	THR	2.4
1	B	839	ASP	2.4
1	B	1001	THR	2.4
1	B	888	LEU	2.4
1	B	902	HIS	2.4
1	A	541	GLY	2.3
1	B	896	GLU	2.3
1	B	560	SER	2.3
1	B	819	SER	2.3
1	A	891	LYS	2.3
1	B	495	VAL	2.3
1	B	860	ARG	2.3
1	B	880	ASP	2.3
1	B	777	SER	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	501	ARG	2.3
1	A	899	ASP	2.3
1	B	908	VAL	2.3
1	A	498	PHE	2.3
1	B	975	THR	2.3
1	B	989	THR	2.3
1	B	929	GLN	2.2
1	B	935	LYS	2.2
1	B	993	ASP	2.2
1	B	988	SER	2.2
1	B	520	LYS	2.2
1	B	164	TYR	2.1
1	B	871	ASN	2.1
1	B	909	LYS	2.1
1	B	965	GLY	2.1
1	B	528	PHE	2.1
1	B	930	LEU	2.1
1	A	512	SER	2.1
1	B	987	ILE	2.1
1	B	507	LEU	2.1
1	B	769	ALA	2.1
1	B	875	ALA	2.1
1	B	522	SER	2.1
1	B	872	MET	2.0
1	A	1005	THR	2.0
1	B	864	THR	2.0
1	B	990	GLU	2.0
1	A	695	VAL	2.0
1	B	856	ASN	2.0
1	B	982	ASN	2.0
1	B	821	ASP	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 oligosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	EPE	A	1101	15/15	0.66	0.27	49,73,151,154	0

6.5 Other polymers

There are no such residues in this entry.