



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:43 pm GMT

PDB ID : 4L9K
Title : X-ray study of human serum albumin complexed with camptothecin
Authors : Wang, Z.; Ho, J.X.; Ruble, J.; Rose, J.P.; Carter, D.C.
Deposited on : 2013-06-18
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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

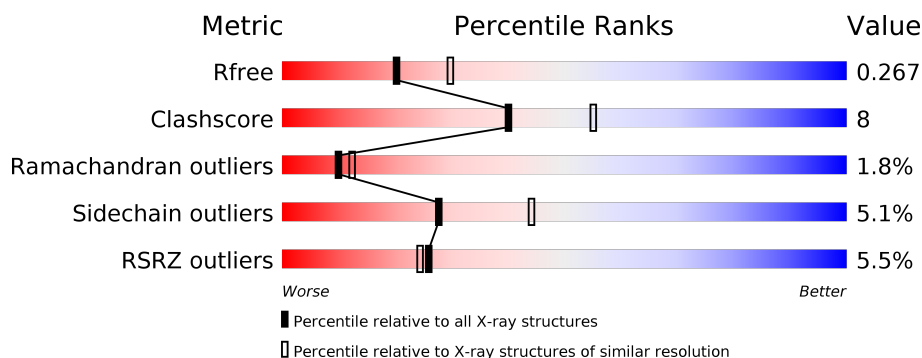
1 Overall quality at a glance

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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (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	585	<div> <div>6%</div> <div> <div></div> <div>79%</div> <div>17%</div> <div>..</div> </div> </div>
1	B	585	<div> <div>5%</div> <div> <div></div> <div>77%</div> <div>19%</div> <div>..</div> </div> </div>

2 Entry composition [i](#)

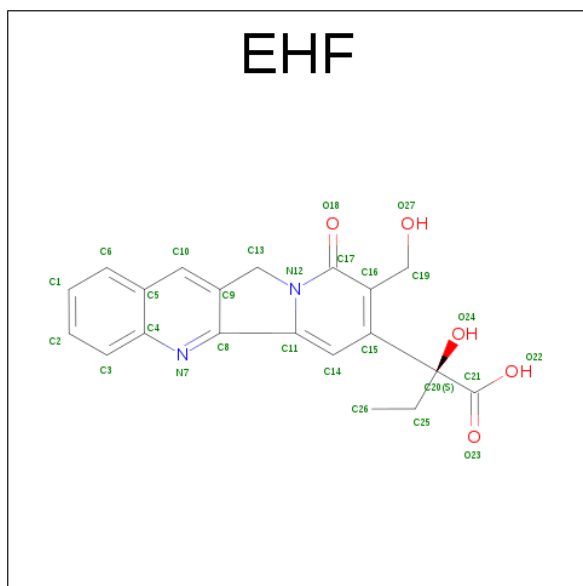
There are 3 unique types of molecules in this entry. The entry contains 9371 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SERUM ALBUMIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	578	Total	C	N	O	S	0	0	0
			4599	2903	776	879	41			
1	B	578	Total	C	N	O	S	0	0	0
			4599	2903	776	879	41			

- Molecule 2 is (2S)-2-HYDROXY-2-[8-(HYDROXYMETHYL)-9-OXO-9,11-DIHYDROIN DOLIZINO[1,2-B]QUINOLIN-7-YL]BUTANOIC ACID (three-letter code: EHF) (formula: $C_{20}H_{18}N_2O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			27	20	2	5		
2	B	1	Total	C	N	O	0	0
			27	20	2	5		

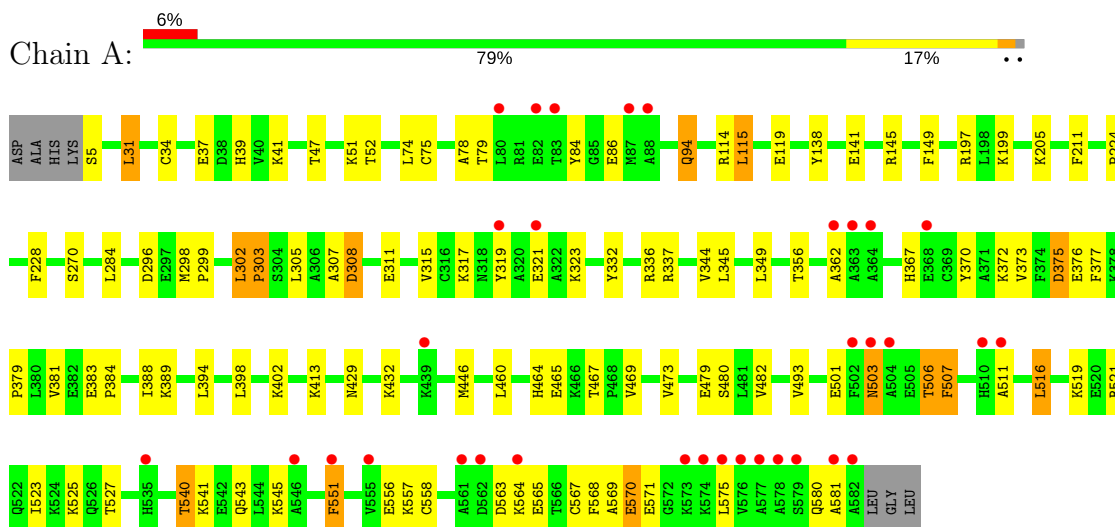
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	72	Total 72	O 72	0	0
3	B	47	Total 47	O 47	0	0

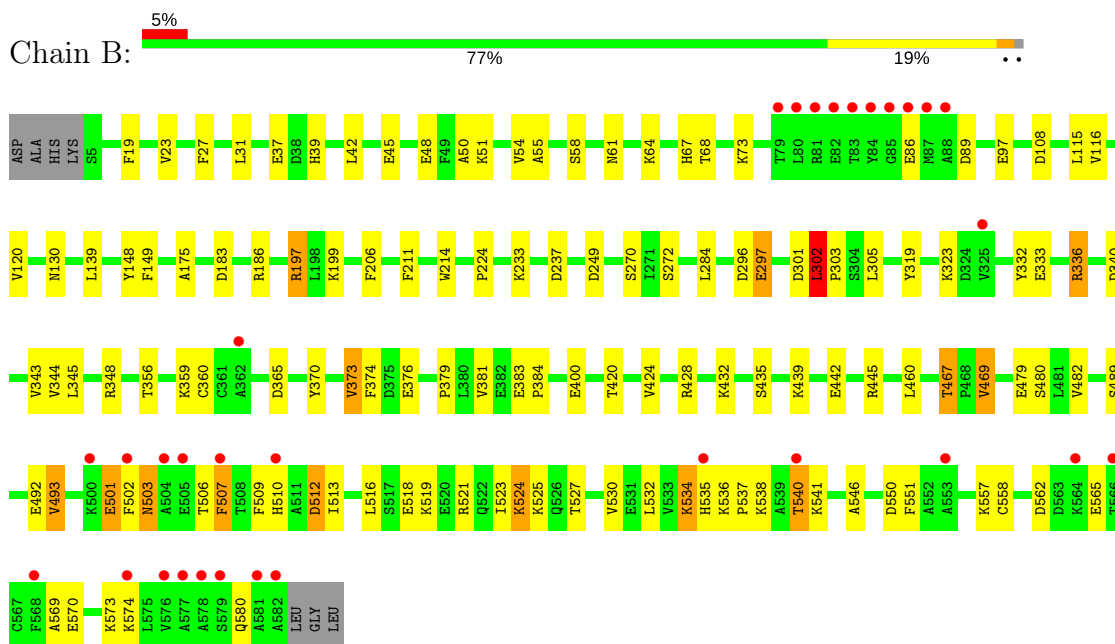
3 Residue-property plots

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



• Molecule 1: SERUM ALBUMIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.97Å 59.46Å 96.04Å 74.97° 87.90° 75.48°	Depositor
Resolution (Å)	28.71 – 2.40 28.71 – 2.40	Depositor EDS
% Data completeness (in resolution range)	93.1 (28.71-2.40) 79.8 (28.71-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.214 , 0.269 0.209 , 0.267	Depositor DCC
R_{free} test set	1849 reflections (4.17%)	DCC
Wilson B-factor (Å ²)	46.2	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9371	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.51	0/4688	0.64	0/6324
1	B	0.48	0/4688	0.65	0/6324
All	All	0.50	0/9376	0.65	0/12648

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	4599	0	4518	68	0
1	B	4599	0	4518	82	0
2	A	27	0	17	3	0
2	B	27	0	17	3	0
3	A	72	0	0	11	0
3	B	47	0	0	8	0
All	All	9371	0	9070	152	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 8.

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:A:114:ARG:NH2	3:A:770:HOH:O	1.98	0.97
1:B:61:ASN:HB3	1:B:64:LYS:HD2	1.45	0.96
1:B:97:GLU:OE2	3:B:712:HOH:O	1.91	0.89
1:B:513:ILE:HA	1:B:516:LEU:HD12	1.59	0.84
1:A:31:LEU:HD23	1:A:74:LEU:HD22	1.61	0.82
1:A:307:ALA:HA	1:A:311:GLU:HG2	1.63	0.80
1:B:540:THR:OG1	1:B:541:LYS:N	2.12	0.79
1:A:479:GLU:O	3:A:736:HOH:O	2.02	0.78
1:A:5:SER:N	3:A:749:HOH:O	2.18	0.75
1:A:356:THR:HG21	1:A:373:VAL:HG22	1.70	0.74
1:A:308:ASP:OD1	1:A:308:ASP:N	2.21	0.72
1:A:31:LEU:HD21	1:A:78:ALA:HB2	1.71	0.72
2:A:601:EHF:O23	3:A:742:HOH:O	2.06	0.72
1:B:400:GLU:OE2	1:B:432:LYS:NZ	2.15	0.71
1:B:37:GLU:OE2	3:B:716:HOH:O	2.12	0.68
1:B:509:PHE:CD2	1:B:551:PHE:HZ	2.12	0.67
1:B:301:ASP:OD1	1:B:302:LEU:N	2.23	0.67
1:B:97:GLU:OE1	3:B:732:HOH:O	2.13	0.67
1:B:149:PHE:CE2	2:B:601:EHF:H1	2.30	0.67
1:A:540:THR:OG1	1:A:541:LYS:N	2.30	0.65
1:B:516:LEU:O	1:B:521:ARG:NH2	2.29	0.65
1:A:516:LEU:O	1:A:521:ARG:NH2	2.30	0.64
1:A:567:CYS:HA	1:A:570:GLU:HB2	1.78	0.63
1:A:34:CYS:HG	1:A:84:TYR:HH	1.48	0.62
1:B:467:THR:OG1	1:B:467:THR:O	2.09	0.62
1:B:513:ILE:HG13	1:B:524:LYS:HE2	1.84	0.60
1:A:413:LYS:HB3	1:A:493:VAL:HG22	1.83	0.59
1:A:199:LYS:HG3	1:A:211:PHE:HE1	1.68	0.59
1:A:298:MET:SD	3:A:765:HOH:O	2.57	0.59
1:B:510:HIS:NE2	1:B:512:ASP:OD1	2.36	0.58
1:B:67:HIS:NE2	1:B:249:ASP:OD1	2.36	0.58
1:B:519:LYS:O	1:B:523:ILE:HG12	2.03	0.58
1:A:34:CYS:HB2	1:A:39:HIS:NE2	2.19	0.57
1:B:345:LEU:HD21	1:B:381:VAL:HG22	1.85	0.57
1:A:302:LEU:HD21	1:A:336:ARG:NH1	2.18	0.57
1:A:86:GLU:N	1:A:86:GLU:OE1	2.39	0.56
1:B:206:PHE:O	3:B:708:HOH:O	2.18	0.56
1:B:86:GLU:O	1:B:89:ASP:HB3	2.06	0.56
1:A:376:GLU:O	1:A:379:PRO:HD2	2.07	0.55
1:B:233:LYS:NZ	1:B:237:ASP:OD2	2.41	0.54
1:B:537:PRO:O	1:B:538:LYS:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:373:VAL:HG23	1:B:374:PHE:HD1	1.72	0.54
1:B:45:GLU:OE1	1:B:73:LYS:HE2	2.08	0.54
1:A:370:TYR:O	1:A:373:VAL:HG23	2.08	0.54
1:A:429:ASN:HA	1:A:432:LYS:HD2	1.89	0.53
1:B:340:ASP:OD2	3:B:723:HOH:O	2.18	0.53
1:B:42:LEU:HD22	1:B:73:LYS:HG3	1.90	0.53
1:B:64:LYS:HE3	1:B:68:THR:HG21	1.91	0.53
1:B:301:ASP:CG	1:B:302:LEU:H	2.12	0.53
1:B:524:LYS:HA	1:B:527:THR:HB	1.90	0.53
1:A:571:GLU:O	1:A:575:LEU:HG	2.08	0.53
1:B:400:GLU:OE1	1:B:435:SER:OG	2.25	0.53
1:B:359:LYS:NZ	1:B:360:CYS:SG	2.82	0.52
1:A:47:THR:HG22	1:A:51:LYS:NZ	2.25	0.52
1:B:356:THR:HG21	1:B:373:VAL:CG1	2.40	0.52
1:B:376:GLU:O	1:B:379:PRO:HD2	2.10	0.52
1:B:199:LYS:HG3	1:B:211:PHE:HE1	1.75	0.51
1:B:492:GLU:HB3	3:B:741:HOH:O	2.11	0.51
1:A:31:LEU:HG	1:A:34:CYS:SG	2.50	0.51
1:A:34:CYS:SG	1:A:84:TYR:OH	2.61	0.51
1:B:536:LYS:NZ	1:B:580:GLN:HG3	2.26	0.50
1:A:205:LYS:HE3	3:A:716:HOH:O	2.10	0.50
1:A:319:TYR:CE2	1:A:323:LYS:HE3	2.46	0.50
1:B:120:VAL:HG21	1:B:175:ALA:HB2	1.94	0.49
1:B:530:VAL:O	1:B:534:LYS:HB2	2.11	0.49
1:B:518:GLU:OE1	1:B:521:ARG:NH1	2.45	0.49
1:A:307:ALA:HA	1:A:311:GLU:CG	2.37	0.49
1:B:503:ASN:OD1	1:B:507:PHE:HB2	2.12	0.49
1:B:370:TYR:O	1:B:373:VAL:HG22	2.13	0.49
1:B:64:LYS:HE3	1:B:68:THR:CG2	2.42	0.49
1:A:465:GLU:OE1	3:A:716:HOH:O	2.19	0.49
1:A:503:ASN:HD21	1:A:507:PHE:HB2	1.77	0.48
1:B:50:ALA:O	1:B:54:VAL:HG23	2.13	0.48
1:A:519:LYS:O	1:A:523:ILE:HG12	2.13	0.48
1:B:305:LEU:HD12	1:B:305:LEU:HA	1.44	0.48
1:B:573:LYS:HA	1:B:573:LYS:HD3	1.66	0.47
1:A:119:GLU:OE2	1:B:120:VAL:HB	2.14	0.47
1:A:383:GLU:HB3	1:A:384:PRO:HD3	1.97	0.47
1:A:540:THR:HG23	1:A:543:GLN:OE1	2.15	0.47
1:A:384:PRO:O	1:A:388:ILE:HG13	2.15	0.47
1:A:394:LEU:HG	1:A:398:LEU:HD12	1.97	0.47
1:B:149:PHE:HE2	2:B:601:EHF:H1	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:PRO:HD2	1:A:296:ASP:HB3	1.96	0.47
1:A:345:LEU:O	1:A:349:LEU:HG	2.16	0.46
1:B:31:LEU:HA	1:B:31:LEU:HD23	1.71	0.45
1:A:563:ASP:CG	1:A:564:LYS:H	2.20	0.45
1:A:503:ASN:ND2	1:A:507:PHE:HB2	2.31	0.45
1:A:302:LEU:HA	1:A:303:PRO:HD3	1.88	0.45
1:A:402:LYS:HE2	1:A:545:LYS:NZ	2.31	0.45
1:B:502:PHE:HB3	1:B:503:ASN:H	1.58	0.45
1:A:228:PHE:HB2	1:A:332:TYR:CE2	2.51	0.45
1:B:348:ARG:HG3	1:B:482:VAL:CG1	2.47	0.45
1:B:435:SER:O	1:B:439:LYS:HD3	2.17	0.45
1:B:546:ALA:O	1:B:550:ASP:HB2	2.17	0.44
1:A:75:CYS:O	1:A:79:THR:HG23	2.17	0.44
1:B:148:TYR:O	3:B:724:HOH:O	2.21	0.44
1:B:420:THR:O	1:B:424:VAL:HG23	2.16	0.44
1:B:383:GLU:HB3	1:B:384:PRO:HD3	2.00	0.44
1:A:506:THR:OG1	1:A:506:THR:O	2.34	0.44
1:B:332:TYR:O	1:B:336:ARG:HB2	2.18	0.44
1:B:565:GLU:HA	1:B:565:GLU:OE2	2.18	0.44
1:A:305:LEU:HD12	1:A:305:LEU:HA	1.78	0.44
1:A:302:LEU:HD23	1:A:337:ARG:HG2	2.00	0.44
1:B:297:GLU:H	1:B:297:GLU:HG2	1.51	0.44
1:B:48:GLU:HA	1:B:51:LYS:HE3	1.99	0.44
1:A:149:PHE:CE2	2:A:601:EHF:H1	2.52	0.44
1:A:317:LYS:NZ	1:A:321:GLU:HG3	2.33	0.44
1:A:228:PHE:HD1	1:A:332:TYR:CG	2.36	0.44
1:B:513:ILE:HG13	1:B:524:LYS:CE	2.48	0.44
1:A:551:PHE:HA	1:A:551:PHE:HD2	1.69	0.43
1:A:388:ILE:HD13	1:A:446:MET:HA	1.99	0.43
1:B:381:VAL:O	1:B:384:PRO:HD2	2.18	0.43
1:A:479:GLU:HG2	3:A:736:HOH:O	2.18	0.43
1:B:305:LEU:HD11	1:B:333:GLU:HB3	2.00	0.43
1:A:299:PRO:HB2	1:A:302:LEU:HD13	2.00	0.43
1:A:302:LEU:HD22	3:A:765:HOH:O	2.19	0.43
1:A:141:GLU:OE1	1:A:145:ARG:NH1	2.37	0.43
1:B:507:PHE:CZ	1:B:532:LEU:HD23	2.54	0.43
1:B:525:LYS:HG2	1:B:551:PHE:CE2	2.53	0.43
2:B:601:EHF:H7	2:B:601:EHF:H14	1.78	0.43
1:A:511:ALA:HA	1:A:568:PHE:CE2	2.54	0.42
1:A:565:GLU:HA	1:A:565:GLU:OE2	2.19	0.42
1:B:86:GLU:N	1:B:86:GLU:OE1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:534:LYS:HB3	1:B:535:HIS:CE1	2.54	0.42
1:A:377:PHE:O	1:A:381:VAL:HG23	2.19	0.42
1:B:27:PHE:HB3	1:B:39:HIS:ND1	2.35	0.42
1:A:372:LYS:HD2	1:A:375:ASP:OD2	2.20	0.42
1:B:108:ASP:OD1	1:B:197:ARG:HD2	2.20	0.42
2:A:601:EHF:H14	2:A:601:EHF:H7	1.62	0.42
1:B:570:GLU:O	1:B:574:LYS:HG2	2.20	0.42
1:A:94:GLN:HG2	1:A:94:GLN:H	1.72	0.41
1:B:224:PRO:HD2	1:B:296:ASP:HB3	2.02	0.41
1:A:525:LYS:HB3	1:A:525:LYS:HE2	1.80	0.41
1:A:362:ALA:HB3	3:A:717:HOH:O	2.21	0.41
1:B:442:GLU:HA	1:B:445:ARG:HD2	2.02	0.41
1:A:523:ILE:O	1:A:527:THR:OG1	2.26	0.41
1:B:525:LYS:HE2	1:B:525:LYS:HB3	1.80	0.41
1:A:317:LYS:HZ2	1:A:321:GLU:HG3	1.85	0.41
1:A:138:TYR:OH	3:A:703:HOH:O	2.17	0.41
1:B:319:TYR:CE2	1:B:323:LYS:HE3	2.55	0.41
1:B:501:GLU:N	1:B:535:HIS:HB3	2.36	0.41
1:B:139:LEU:HA	1:B:139:LEU:HD23	1.87	0.41
1:B:108:ASP:OD2	1:B:197:ARG:NH1	2.54	0.41
1:B:302:LEU:HA	1:B:302:LEU:HD12	1.77	0.41
1:B:214:TRP:CD1	1:B:343:VAL:HG11	2.56	0.41
1:B:493:VAL:HG12	3:B:741:HOH:O	2.21	0.41
1:A:115:LEU:HA	1:A:115:LEU:HD12	1.82	0.40
1:A:464:HIS:CG	1:A:473:VAL:HG11	2.55	0.40
1:B:373:VAL:HG23	1:B:374:PHE:CD1	2.54	0.40
1:B:428:ARG:HD2	1:B:523:ILE:HD12	2.04	0.40
1:B:183:ASP:OD1	1:B:186:ARG:NH1	2.54	0.40
1:B:19:PHE:O	1:B:23:VAL:HG23	2.21	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	576/585 (98%)	528 (92%)	38 (7%)	10 (2%)	11	13
1	B	576/585 (98%)	529 (92%)	36 (6%)	11 (2%)	9	11
All	All	1152/1170 (98%)	1057 (92%)	74 (6%)	21 (2%)	10	12

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	303	PRO
1	A	501	GLU
1	A	581	ALA
1	B	55	ALA
1	B	303	PRO
1	B	501	GLU
1	A	503	ASN
1	A	569	ALA
1	B	480	SER
1	B	569	ALA
1	A	302	LEU
1	A	480	SER
1	B	503	ASN
1	B	562	ASP
1	A	469	VAL
1	A	507	PHE
1	A	580	GLN
1	B	507	PHE
1	B	302	LEU
1	B	469	VAL
1	B	365	ASP

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	506/511 (99%)	480 (95%)	26 (5%)	28	44
1	B	506/511 (99%)	480 (95%)	26 (5%)	28	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1012/1022 (99%)	960 (95%)	52 (5%)	28	44

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LEU
1	A	37	GLU
1	A	41	LYS
1	A	52	THR
1	A	94	GLN
1	A	115	LEU
1	A	197	ARG
1	A	270	SER
1	A	284	LEU
1	A	308	ASP
1	A	315	VAL
1	A	344	VAL
1	A	367	HIS
1	A	375	ASP
1	A	389	LYS
1	A	460	LEU
1	A	467	THR
1	A	482	VAL
1	A	506	THR
1	A	516	LEU
1	A	540	THR
1	A	551	PHE
1	A	556	GLU
1	A	557	LYS
1	A	558	CYS
1	A	570	GLU
1	B	58	SER
1	B	115	LEU
1	B	116	VAL
1	B	130	ASN
1	B	197	ARG
1	B	270	SER
1	B	272	SER
1	B	284	LEU
1	B	297	GLU
1	B	302	LEU
1	B	336	ARG

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Mol	Chain	Res	Type
1	B	344	VAL
1	B	373	VAL
1	B	460	LEU
1	B	467	THR
1	B	469	VAL
1	B	479	GLU
1	B	489	SER
1	B	493	VAL
1	B	506	THR
1	B	512	ASP
1	B	524	LYS
1	B	534	LYS
1	B	540	THR
1	B	557	LYS
1	B	558	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	ASN
1	B	130	ASN
1	B	386	ASN
1	B	405	ASN

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](#)

2 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	EHF	A	601	-	22,30,30	2.09	5 (22%)	20,46,46	2.69	6 (30%)
2	EHF	B	601	-	22,30,30	2.18	7 (31%)	20,46,46	2.76	4 (20%)

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	EHF	A	601	-	-	0/11/25/25	0/3/4/4
2	EHF	B	601	-	-	0/11/25/25	0/3/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	EHF	O24-C20	-3.93	1.39	1.43
2	B	601	EHF	C5-C4	-2.22	1.38	1.42
2	A	601	EHF	C17-N12	-2.12	1.35	1.38
2	B	601	EHF	C17-N12	-2.07	1.35	1.38
2	A	601	EHF	C10-C5	2.10	1.46	1.42
2	B	601	EHF	C19-C16	2.22	1.54	1.51
2	A	601	EHF	C16-C15	2.80	1.43	1.38
2	B	601	EHF	C16-C15	2.86	1.43	1.38
2	B	601	EHF	C10-C9	3.08	1.42	1.37
2	A	601	EHF	C10-C9	3.45	1.43	1.37
2	B	601	EHF	O18-C17	5.85	1.39	1.24
2	A	601	EHF	O18-C17	6.15	1.39	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	EHF	O27-C19-C16	-2.64	104.28	111.70
2	A	601	EHF	C9-C10-C5	-2.34	117.16	121.29
2	A	601	EHF	C10-C5-C4	2.01	120.71	118.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	EHF	C3-C4-C5	2.17	121.18	119.04
2	B	601	EHF	C8-N7-C4	2.44	122.33	117.17
2	A	601	EHF	C3-C4-C5	2.61	121.62	119.04
2	B	601	EHF	C9-C13-N12	6.43	108.39	102.54
2	A	601	EHF	C9-C13-N12	6.45	108.41	102.54
2	A	601	EHF	C11-C8-N7	8.08	130.12	118.19
2	B	601	EHF	C11-C8-N7	8.93	131.38	118.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	EHF	3	0
2	B	601	EHF	3	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	578/585 (98%)	0.03	33 (5%)	24 23	34, 56, 112, 129	0
1	B	578/585 (98%)	0.08	31 (5%)	26 25	38, 60, 114, 136	0
All	All	1156/1170 (98%)	0.05	64 (5%)	26 24	34, 58, 114, 136	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	577	ALA	7.9
1	A	502	PHE	7.8
1	B	83	THR	7.0
1	A	582	ALA	6.6
1	B	87	MET	5.8
1	B	84	TYR	5.8
1	A	83	THR	5.6
1	B	79	THR	5.6
1	B	582	ALA	5.5
1	B	502	PHE	5.4
1	B	88	ALA	5.3
1	B	81	ARG	5.3
1	A	578	ALA	5.0
1	B	80	LEU	4.9
1	A	577	ALA	4.7
1	B	576	VAL	4.7
1	B	564	LYS	4.2
1	B	579	SER	4.2
1	B	82	GLU	4.1
1	A	82	GLU	4.0
1	A	581	ALA	4.0
1	A	88	ALA	4.0
1	A	87	MET	3.9
1	A	362	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	86	GLU	3.7
1	A	80	LEU	3.6
1	A	555	VAL	3.5
1	A	575	LEU	3.3
1	A	504	ALA	3.3
1	A	574	LYS	3.3
1	B	85	GLY	3.2
1	B	504	ALA	3.2
1	B	566	THR	3.1
1	A	363	ALA	3.0
1	A	576	VAL	2.9
1	B	540	THR	2.9
1	A	561	ALA	2.8
1	A	546	ALA	2.8
1	A	364	ALA	2.8
1	B	535	HIS	2.8
1	A	579	SER	2.7
1	A	551	PHE	2.6
1	A	573	LYS	2.6
1	B	505	GLU	2.5
1	B	507	PHE	2.5
1	B	500	LYS	2.4
1	A	564	LYS	2.4
1	A	562	ASP	2.4
1	B	568	PHE	2.4
1	B	578	ALA	2.4
1	B	574	LYS	2.4
1	A	511	ALA	2.3
1	B	553	ALA	2.3
1	A	510	HIS	2.3
1	A	319	TYR	2.3
1	B	325	VAL	2.2
1	A	321	GLU	2.2
1	A	439	LYS	2.2
1	A	535	HIS	2.2
1	B	510	HIS	2.1
1	A	503	ASN	2.1
1	B	581	ALA	2.1
1	A	368	GLU	2.1
1	B	362	ALA	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](#)

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(\AA^2)	Q<0.9
2	EHF	B	601	27/27	0.94	0.15	0.75	49,59,67,72	0
2	EHF	A	601	27/27	0.95	0.16	0.53	40,53,61,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.