



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:04 PM UTC

PDB ID : 1BM0 / pdb_00001bm0
Title : CRYSTAL STRUCTURE OF HUMAN SERUM ALBUMIN
Authors : Sugio, S.; Kashima, A.; Mochizuki, S.; Noda, M.; Kobayashi, K.
Deposited on : 1998-07-28
Resolution : 2.50 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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

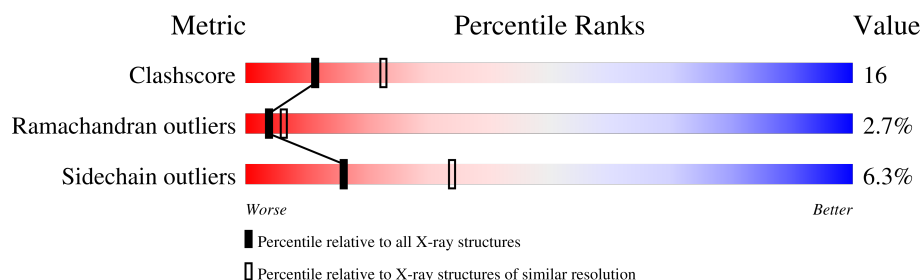
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	585	 57% 36% 5%
1	B	585	 58% 37%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9202 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 water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	O	0	0
			1	1		
2	B	3	Total	O	0	0
			3	3		

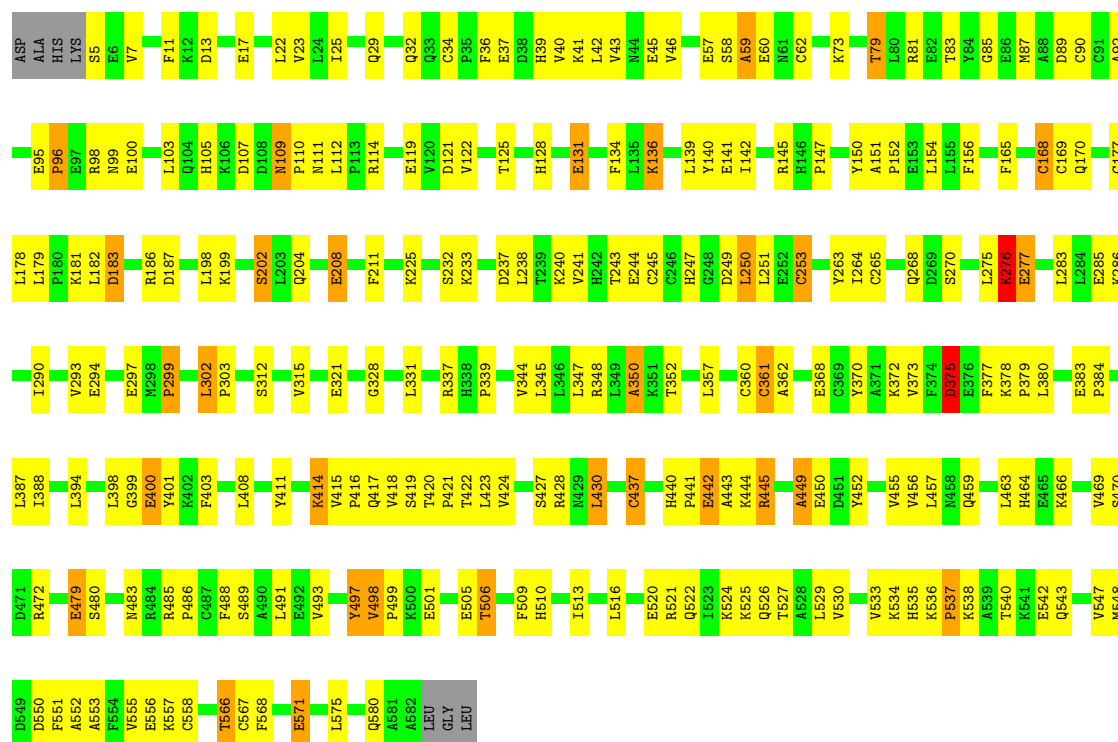
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

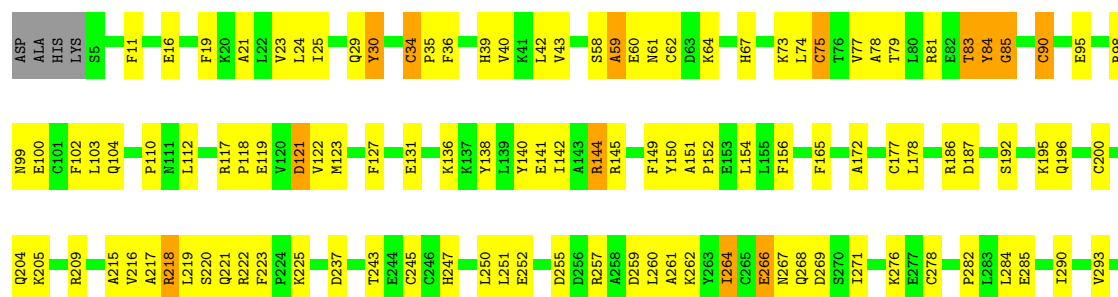
• Molecule 1: SERUM ALBUMIN

Chain A: 



• Molecule 1: SERUM ALBUMIN

Chain B: 





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.36Å 96.89Å 59.24Å 91.04° 103.40° 74.94°	Depositor
Resolution (Å)	50.00 – 2.50	Depositor
% Data completeness (in resolution range)	77.1 (50.00-2.50)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.207 , 0.292	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9202	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.83	0/4688	1.26	38/6324 (0.6%)
1	B	0.85	0/4688	1.23	35/6324 (0.6%)
All	All	0.84	0/9376	1.24	73/12648 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	415	VAL	CA-C-N	11.63	132.07	119.28
1	A	415	VAL	C-N-CA	11.63	132.07	119.28
1	A	250	LEU	N-CA-C	8.81	122.04	111.82
1	A	204	GLN	N-CA-C	8.81	120.88	111.28
1	B	522	GLN	N-CA-C	-8.40	101.16	111.40
1	A	418	VAL	N-CA-C	8.36	121.67	109.63
1	B	104	GLN	N-CA-C	-7.80	103.22	112.89
1	A	208	GLU	N-CA-C	7.67	119.65	111.28
1	A	13	ASP	N-CA-C	7.40	119.34	111.28
1	A	529	LEU	N-CA-C	-7.32	103.24	111.07
1	A	339	PRO	N-CA-C	-7.29	106.24	114.92
1	B	437	CYS	N-CA-C	7.27	123.68	114.31
1	A	136	LYS	N-CA-C	-7.26	103.30	111.07
1	A	505	GLU	N-CA-C	7.19	122.40	112.04
1	B	34	CYS	CA-C-N	7.12	127.16	119.89
1	B	34	CYS	C-N-CA	7.12	127.16	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	178	LEU	N-CA-C	7.11	119.69	111.02
1	B	339	PRO	N-CA-C	-7.10	104.72	114.80
1	A	277	GLU	N-CA-C	7.02	119.97	111.82
1	A	238	LEU	N-CA-C	-6.96	103.77	111.36
1	B	121	ASP	N-CA-C	-6.93	103.66	111.07
1	B	469	VAL	N-CA-C	6.89	118.21	111.67
1	A	32	GLN	N-CA-C	6.81	118.78	111.36
1	B	136	LYS	N-CA-C	-6.75	103.16	111.40
1	A	479	GLU	N-CA-C	6.62	119.34	111.33
1	B	177	CYS	N-CA-C	-6.41	102.97	111.24
1	A	498	VAL	CA-C-N	6.38	127.25	120.11
1	A	498	VAL	C-N-CA	6.38	127.25	120.11
1	B	529	LEU	N-CA-C	-6.34	104.29	111.14
1	A	170	GLN	N-CA-C	-6.31	105.71	113.41
1	B	430	LEU	N-CA-C	-6.29	104.52	111.82
1	B	497	TYR	N-CA-C	6.16	119.41	110.42
1	A	352	THR	N-CA-C	-6.00	104.43	110.97
1	A	445	ARG	N-CA-C	5.98	118.28	111.11
1	B	192	SER	N-CA-C	-5.97	104.70	112.23
1	A	368	GLU	N-CA-C	5.93	118.70	111.82
1	A	168	CYS	N-CA-C	5.91	119.31	111.75
1	A	328	GLY	N-CA-C	-5.90	105.22	112.77
1	B	564	LYS	N-CA-C	-5.90	102.72	111.81
1	A	345	LEU	N-CA-C	-5.78	104.90	111.14
1	A	497	TYR	N-CA-C	5.78	118.97	110.30
1	A	399	GLY	N-CA-C	-5.76	105.43	112.68
1	A	430	LEU	N-CA-C	-5.75	104.92	111.07
1	B	459	GLN	N-CA-C	-5.74	104.02	111.02
1	A	375	ASP	N-CA-C	-5.72	105.03	112.23
1	B	469	VAL	CB-CA-C	-5.69	105.09	111.80
1	B	550	ASP	N-CA-C	-5.64	105.03	111.07
1	B	75	CYS	N-CA-C	5.63	119.63	112.87
1	B	458	ASN	N-CA-C	-5.63	104.52	111.33
1	B	90	CYS	N-CA-C	5.58	119.59	112.34
1	A	571	GLU	N-CA-C	-5.56	104.85	111.69
1	A	437	CYS	N-CA-C	5.55	120.71	113.88
1	B	172	ALA	N-CA-C	-5.49	104.99	110.97
1	B	269	ASP	N-CA-C	5.45	117.98	111.71
1	B	365	ASP	CA-C-N	5.44	126.64	119.84
1	B	365	ASP	C-N-CA	5.44	126.64	119.84
1	A	360	CYS	N-CA-C	5.42	117.27	111.36
1	B	266	GLU	N-CA-C	-5.41	105.02	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	209	ARG	N-CA-C	-5.36	106.00	112.54
1	A	251	LEU	N-CA-C	-5.36	105.35	111.14
1	B	360	CYS	N-CA-C	5.34	117.86	111.71
1	A	34	CYS	CA-C-N	5.33	125.27	119.78
1	A	34	CYS	C-N-CA	5.33	125.27	119.78
1	B	307	ALA	N-CA-C	5.24	117.00	111.28
1	A	362	ALA	N-CA-C	-5.21	108.19	114.75
1	B	278	CYS	CB-CA-C	-5.21	102.67	110.90
1	A	302	LEU	CA-C-N	5.20	126.34	119.84
1	A	302	LEU	C-N-CA	5.20	126.34	119.84
1	B	390	GLN	N-CA-C	5.12	116.94	111.36
1	B	445	ARG	N-CA-C	5.08	117.59	111.40
1	B	577	ALA	N-CA-C	-5.07	105.45	111.69
1	A	350	ALA	N-CA-C	-5.03	105.69	111.07
1	B	426	VAL	N-CA-C	5.02	115.24	110.42

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	332	TYR	Sidechain

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	4599	0	4518	153	0
1	B	4599	0	4518	140	0
2	A	1	0	0	0	0
2	B	3	0	0	0	0
All	All	9202	0	9036	293	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 16.

All (293) 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:417:GLN:HB3	1:A:469:VAL:HG12	1.44	0.99
1:A:156:PHE:HE1	1:A:285:GLU:HG3	1.34	0.91
1:A:240:LYS:O	1:A:244:GLU:HG3	1.73	0.88
1:A:370:TYR:O	1:A:373:VAL:HG23	1.75	0.87
1:A:417:GLN:HB2	1:A:470:SER:HB3	1.58	0.85
1:B:119:GLU:HB2	1:B:122:VAL:HG23	1.61	0.82
1:A:424:VAL:O	1:A:428:ARG:HG3	1.79	0.82
1:A:36:PHE:O	1:A:40:VAL:HG23	1.82	0.80
1:A:59:ALA:HB3	1:A:62:CYS:SG	2.23	0.79
1:A:41:LYS:HZ2	1:A:42:LEU:HD23	1.47	0.79
1:A:151:ALA:HB2	1:A:250:LEU:HD13	1.65	0.77
1:B:90:CYS:O	1:B:98:ARG:HG3	1.85	0.77
1:B:42:LEU:HD22	1:B:73:LYS:HG3	1.68	0.75
1:B:571:GLU:O	1:B:575:LEU:HG	1.87	0.75
1:A:156:PHE:CE1	1:A:285:GLU:HG3	2.22	0.74
1:B:200:CYS:O	1:B:204:GLN:HG3	1.86	0.74
1:A:119:GLU:HB2	1:A:122:VAL:HG23	1.70	0.74
1:B:420:THR:O	1:B:424:VAL:HG23	1.88	0.73
1:A:525:LYS:HE2	1:A:552:ALA:HA	1.71	0.72
1:B:307:ALA:HA	1:B:311:GLU:HB2	1.70	0.72
1:B:383:GLU:HB3	1:B:384:PRO:HD3	1.71	0.72
1:B:356:THR:HG21	1:B:373:VAL:HG22	1.70	0.72
1:B:418:VAL:HB	1:B:423:LEU:HD21	1.70	0.71
1:A:387:LEU:HD22	1:A:485:ARG:NH1	2.05	0.71
1:B:319:TYR:CE1	1:B:323:LYS:HB2	2.26	0.71
1:A:81:ARG:HB2	1:A:85:GLY:HA2	1.75	0.69
1:A:464:HIS:HE1	1:A:470:SER:H	1.41	0.69
1:A:442:GLU:HA	1:A:445:ARG:HD2	1.73	0.69
1:A:312:SER:O	1:A:315:VAL:HG23	1.93	0.68
1:B:156:PHE:HE1	1:B:285:GLU:HG3	1.57	0.68
1:A:384:PRO:O	1:A:388:ILE:HG12	1.93	0.68
1:B:303:PRO:HG2	1:B:337:ARG:HH22	1.59	0.67
1:A:498:VAL:HG13	1:A:498:VAL:O	1.95	0.65
1:A:87:MET:HE1	1:A:105:HIS:HB3	1.77	0.65
1:B:218:ARG:HH21	1:B:221:GLN:HB2	1.62	0.65
1:A:268:GLN:OE1	1:A:276:LYS:HA	1.97	0.64
1:A:387:LEU:HD22	1:A:485:ARG:HH11	1.62	0.64
1:B:149:PHE:HD1	1:B:150:TYR:N	1.96	0.64
1:B:319:TYR:O	1:B:323:LYS:HB3	1.98	0.64
1:A:141:GLU:HB3	1:A:145:ARG:NH1	2.12	0.64
1:A:383:GLU:HB3	1:A:384:PRO:HD3	1.80	0.63
1:B:543:GLN:O	1:B:546:ALA:HB3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:ILE:HD12	1:A:449:ALA:HB1	1.81	0.63
1:B:83:THR:HB	1:B:84:TYR:CE1	2.34	0.63
1:B:370:TYR:O	1:B:373:VAL:HG23	1.98	0.63
1:B:259:ASP:O	1:B:262:LYS:HB3	1.99	0.63
1:A:141:GLU:HB3	1:A:145:ARG:HH12	1.64	0.62
1:A:571:GLU:O	1:A:575:LEU:HG	1.99	0.62
1:A:5:SER:HA	1:A:62:CYS:O	2.00	0.62
1:A:177:CYS:O	1:A:181:LYS:HD2	2.00	0.61
1:A:41:LYS:NZ	1:A:42:LEU:HD23	2.15	0.61
1:B:25:ILE:HD13	1:B:154:LEU:HD23	1.83	0.60
1:B:312:SER:O	1:B:315:VAL:HG23	2.02	0.60
1:B:413:LYS:O	1:B:416:PRO:HD3	2.00	0.60
1:B:475:LYS:O	1:B:479:GLU:HB2	2.02	0.59
1:A:151:ALA:HB3	1:A:152:PRO:HD3	1.83	0.59
1:A:394:LEU:HD11	1:A:398:LEU:HD11	1.85	0.59
1:A:373:VAL:HG12	1:A:377:PHE:CE1	2.38	0.59
1:B:25:ILE:CD1	1:B:154:LEU:HD23	2.33	0.58
1:B:417:GLN:HB2	1:B:470:SER:HB2	1.84	0.58
1:B:528:ALA:O	1:B:532:LEU:HG	2.04	0.58
1:B:225:LYS:HG2	1:B:299:PRO:HG3	1.85	0.58
1:B:472:ARG:CZ	1:B:491:LEU:HD22	2.34	0.57
1:A:419:SER:OG	1:A:421:PRO:HD2	2.04	0.57
1:A:440:HIS:HB3	1:A:444:LYS:HB2	1.87	0.57
1:B:372:LYS:O	1:B:375:ASP:HB2	2.04	0.57
1:A:265:CYS:O	1:A:268:GLN:HB2	2.05	0.57
1:B:222:ARG:HG2	1:B:223:PHE:CE1	2.40	0.57
1:A:414:LYS:HD2	1:A:491:LEU:HB2	1.87	0.57
1:A:299:PRO:HB2	1:A:302:LEU:HG	1.87	0.56
1:A:81:ARG:C	1:A:83:THR:H	2.13	0.56
1:B:268:GLN:OE1	1:B:276:LYS:HA	2.06	0.56
1:B:319:TYR:CD1	1:B:323:LYS:HB2	2.40	0.56
1:A:276:LYS:HD3	1:A:277:GLU:HG3	1.88	0.56
1:A:552:ALA:O	1:A:556:GLU:HG2	2.05	0.56
1:B:110:PRO:HB2	1:B:112:LEU:HG	1.87	0.55
1:B:19:PHE:O	1:B:23:VAL:HG23	2.07	0.55
1:B:39:HIS:O	1:B:43:VAL:HG23	2.04	0.55
1:B:384:PRO:O	1:B:388:ILE:HG12	2.07	0.55
1:B:112:LEU:HD22	1:B:144:ARG:HH21	1.71	0.55
1:A:414:LYS:C	1:A:416:PRO:HD3	2.32	0.55
1:B:551:PHE:O	1:B:555:VAL:HG23	2.07	0.54
1:A:225:LYS:NZ	1:A:297:GLU:HB2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:498:VAL:HG13	1:B:498:VAL:O	2.06	0.54
1:B:99:ASN:O	1:B:102:PHE:N	2.40	0.54
1:A:464:HIS:CE1	1:A:470:SER:H	2.23	0.54
1:A:25:ILE:O	1:A:29:GLN:HG3	2.08	0.54
1:A:103:LEU:HD11	1:A:247:HIS:CD2	2.44	0.53
1:B:61:ASN:HB3	1:B:64:LYS:HD2	1.89	0.53
1:B:251:LEU:O	1:B:255:ASP:HB2	2.09	0.53
1:A:459:GLN:O	1:A:463:LEU:HG	2.09	0.53
1:B:449:ALA:O	1:B:453:LEU:HG	2.08	0.53
1:A:497:TYR:O	1:A:499:PRO:HD3	2.09	0.53
1:B:567:CYS:O	1:B:571:GLU:HB2	2.09	0.53
1:A:186:ARG:HD3	1:A:186:ARG:C	2.34	0.52
1:A:378:LYS:HB2	1:A:379:PRO:HD3	1.91	0.52
1:B:408:LEU:HD23	1:B:529:LEU:HD23	1.91	0.52
1:A:516:LEU:O	1:A:521:ARG:NH2	2.42	0.52
1:B:119:GLU:HB2	1:B:122:VAL:CG2	2.36	0.52
1:A:110:PRO:HB2	1:A:112:LEU:HG	1.92	0.52
1:B:333:GLU:O	1:B:336:ARG:HG2	2.09	0.52
1:B:378:LYS:HB2	1:B:379:PRO:HD3	1.92	0.51
1:A:344:VAL:HG21	1:A:450:GLU:HG2	1.92	0.51
1:A:225:LYS:HZ1	1:A:297:GLU:HB2	1.75	0.51
1:B:533:VAL:O	1:B:537:PRO:HG3	2.10	0.51
1:B:30:TYR:HD2	1:B:74:LEU:HD11	1.76	0.51
1:A:247:HIS:O	1:A:247:HIS:CG	2.63	0.51
1:A:286:LYS:O	1:A:290:ILE:HG13	2.11	0.51
1:B:521:ARG:O	1:B:525:LYS:HD3	2.11	0.51
1:A:303:PRO:HG2	1:A:337:ARG:HH22	1.75	0.51
1:B:140:TYR:CE2	1:B:144:ARG:NH1	2.79	0.50
1:B:151:ALA:HB3	1:B:152:PRO:HD3	1.94	0.50
1:A:331:LEU:HD21	1:A:347:LEU:CD2	2.42	0.50
1:A:401:TYR:CE1	1:A:522:GLN:HB3	2.46	0.50
1:A:567:CYS:O	1:A:571:GLU:HB2	2.11	0.50
1:A:331:LEU:HD13	1:A:350:ALA:HB2	1.94	0.50
1:B:437:CYS:HA	1:B:440:HIS:HD2	1.77	0.50
1:B:343:VAL:O	1:B:347:LEU:HG	2.12	0.49
1:B:259:ASP:O	1:B:262:LYS:HE3	2.12	0.49
1:A:401:TYR:HE1	1:A:522:GLN:HB3	1.77	0.49
1:A:45:GLU:OE1	1:A:73:LYS:HD2	2.13	0.49
1:A:95:GLU:OE1	1:A:99:ASN:HB2	2.13	0.49
1:A:265:CYS:SG	1:A:286:LYS:HD2	2.52	0.49
1:A:414:LYS:O	1:A:416:PRO:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:ARG:NH2	1:A:450:GLU:OE2	2.44	0.49
1:A:533:VAL:O	1:A:537:PRO:HG3	2.12	0.49
1:A:87:MET:CE	1:A:105:HIS:HB3	2.42	0.49
1:A:198:LEU:HD22	1:A:455:VAL:HG22	1.94	0.49
1:B:345:LEU:HD11	1:B:349:LEU:HD21	1.95	0.49
1:B:441:PRO:O	1:B:443:ALA:N	2.45	0.49
1:A:472:ARG:HE	1:A:491:LEU:HD22	1.78	0.48
1:B:81:ARG:C	1:B:83:THR:H	2.21	0.48
1:A:441:PRO:O	1:A:443:ALA:N	2.47	0.48
1:B:112:LEU:CD2	1:B:144:ARG:HH21	2.26	0.48
1:B:262:LYS:C	1:B:262:LYS:HD2	2.38	0.48
1:A:383:GLU:CD	1:A:485:ARG:HH22	2.20	0.48
1:A:430:LEU:HD23	1:A:456:VAL:HG11	1.96	0.48
1:B:448:CYS:O	1:B:452:TYR:HB2	2.13	0.48
1:A:25:ILE:HD13	1:A:154:LEU:HD23	1.96	0.48
1:A:109:ASN:C	1:A:109:ASN:HD22	2.22	0.48
1:A:90:CYS:O	1:A:98:ARG:HG3	2.14	0.48
1:B:237:ASP:HB3	1:B:260:LEU:HD13	1.95	0.48
1:B:141:GLU:HA	1:B:141:GLU:OE1	2.14	0.47
1:B:149:PHE:CD1	1:B:150:TYR:N	2.79	0.47
1:A:168:CYS:SG	1:A:177:CYS:C	2.97	0.47
1:A:96:PRO:O	1:A:100:GLU:HB2	2.14	0.47
1:A:244:GLU:O	1:A:249:ASP:N	2.47	0.47
1:B:95:GLU:OE1	1:B:95:GLU:HA	2.15	0.47
1:B:196:GLN:HE21	1:B:196:GLN:HA	1.80	0.47
1:A:39:HIS:O	1:A:43:VAL:HG23	2.14	0.47
1:B:19:PHE:CD1	1:B:19:PHE:C	2.92	0.47
1:B:77:VAL:O	1:B:84:TYR:CE1	2.68	0.47
1:B:138:TYR:O	1:B:142:ILE:HG12	2.14	0.47
1:B:306:ALA:O	1:B:311:GLU:N	2.48	0.47
1:B:424:VAL:O	1:B:428:ARG:HG3	2.14	0.47
1:B:149:PHE:HD1	1:B:150:TYR:H	1.63	0.47
1:B:367:HIS:O	1:B:371:ALA:HB2	2.15	0.47
1:B:400:GLU:O	1:B:403:PHE:HB3	2.15	0.47
1:B:464:HIS:HE1	1:B:470:SER:H	1.63	0.47
1:B:23:VAL:O	1:B:24:LEU:C	2.58	0.47
1:B:36:PHE:O	1:B:40:VAL:HG23	2.15	0.46
1:A:558:CYS:SG	1:A:567:CYS:C	2.98	0.46
1:B:112:LEU:HD22	1:B:144:ARG:NH2	2.29	0.46
1:B:260:LEU:O	1:B:261:ALA:C	2.58	0.46
1:A:139:LEU:O	1:A:140:TYR:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:ARG:HE	1:B:218:ARG:HA	1.81	0.46
1:B:457:LEU:O	1:B:460:LEU:HB3	2.15	0.46
1:A:79:THR:O	1:A:79:THR:HG22	2.15	0.46
1:A:485:ARG:HB3	1:A:486:PRO:HD3	1.97	0.46
1:A:81:ARG:C	1:A:83:THR:N	2.74	0.46
1:B:11:PHE:CZ	1:B:16:GLU:HB2	2.51	0.46
1:B:156:PHE:CE1	1:B:285:GLU:HG3	2.44	0.46
1:A:450:GLU:OE2	1:A:485:ARG:NE	2.49	0.46
1:B:150:TYR:OH	1:B:257:ARG:HD2	2.16	0.46
1:B:483:ASN:C	1:B:486:PRO:HD2	2.41	0.46
1:B:544:LEU:HD23	1:B:544:LEU:HA	1.79	0.45
1:A:199:LYS:HG2	1:A:211:PHE:HE1	1.81	0.45
1:A:543:GLN:O	1:A:547:VAL:HG23	2.15	0.45
1:B:30:TYR:HE1	1:B:103:LEU:HD23	1.81	0.45
1:A:237:ASP:O	1:A:241:VAL:HG23	2.16	0.45
1:B:243:THR:O	1:B:247:HIS:HB2	2.16	0.45
1:A:331:LEU:HD21	1:A:347:LEU:HD23	1.99	0.45
1:A:377:PHE:O	1:A:380:LEU:HB2	2.16	0.45
1:A:441:PRO:C	1:A:443:ALA:N	2.75	0.45
1:A:408:LEU:HD11	1:A:526:GLN:HG2	1.99	0.45
1:A:414:LYS:HE2	1:A:414:LYS:HB2	1.59	0.45
1:A:536:LYS:HG2	1:A:536:LYS:O	2.17	0.45
1:B:59:ALA:HB3	1:B:62:CYS:SG	2.57	0.45
1:A:542:GLU:HG3	1:A:543:GLN:N	2.32	0.44
1:B:564:LYS:O	1:B:565:GLU:HB2	2.17	0.44
1:B:21:ALA:O	1:B:25:ILE:HG13	2.18	0.44
1:B:282:PRO:HB2	1:B:285:GLU:OE1	2.18	0.44
1:A:23:VAL:HG12	1:A:43:VAL:HG22	1.99	0.44
1:A:131:GLU:O	1:A:134:PHE:HB3	2.17	0.44
1:A:7:VAL:O	1:A:11:PHE:HB2	2.18	0.44
1:A:165:PHE:O	1:A:169:CYS:SG	2.76	0.44
1:B:266:GLU:C	1:B:268:GLN:H	2.25	0.44
1:B:378:LYS:O	1:B:379:PRO:C	2.60	0.44
1:A:464:HIS:CD2	1:A:464:HIS:C	2.95	0.44
1:B:350:ALA:O	1:B:353:TYR:N	2.50	0.44
1:B:267:ASN:O	1:B:271:ILE:HG13	2.18	0.44
1:B:392:CYS:O	1:B:396:GLU:HG2	2.18	0.44
1:B:539:ALA:O	1:B:543:GLN:NE2	2.51	0.44
1:A:125:THR:O	1:A:128:HIS:N	2.51	0.44
1:A:244:GLU:HB2	1:A:253:CYS:HB2	2.00	0.44
1:A:178:LEU:O	1:A:179:LEU:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:ILE:O	1:B:29:GLN:HG3	2.17	0.43
1:B:196:GLN:HE21	1:B:196:GLN:CA	2.31	0.43
1:A:372:LYS:O	1:A:375:ASP:HB2	2.19	0.43
1:A:400:GLU:O	1:A:403:PHE:HB3	2.19	0.43
1:B:373:VAL:C	1:B:375:ASP:H	2.26	0.43
1:B:491:LEU:HA	1:B:491:LEU:HD23	1.71	0.43
1:A:150:TYR:CD1	1:A:152:PRO:HD2	2.53	0.43
1:B:378:LYS:HE3	1:B:378:LYS:HB3	1.77	0.43
1:A:422:THR:O	1:A:423:LEU:C	2.60	0.43
1:A:107:ASP:O	1:A:147:PRO:HG3	2.19	0.43
1:B:127:PHE:CE1	1:B:131:GLU:HG3	2.54	0.43
1:A:441:PRO:C	1:A:443:ALA:H	2.26	0.43
1:A:498:VAL:O	1:A:498:VAL:CG1	2.66	0.43
1:A:513:ILE:HG21	1:A:568:PHE:HZ	1.84	0.43
1:B:217:ALA:O	1:B:220:SER:HB2	2.18	0.43
1:A:357:LEU:O	1:A:361:CYS:HB2	2.19	0.42
1:A:408:LEU:HD23	1:A:427:SER:CB	2.49	0.42
1:A:550:ASP:O	1:A:553:ALA:HB3	2.20	0.42
1:B:305:LEU:HD13	1:B:334:TYR:CD2	2.53	0.42
1:B:459:GLN:O	1:B:460:LEU:C	2.62	0.42
1:A:268:GLN:OE1	1:A:276:LYS:CA	2.65	0.42
1:A:497:TYR:CD2	1:A:537:PRO:HG2	2.54	0.42
1:A:535:HIS:C	1:A:537:PRO:HD3	2.44	0.42
1:B:75:CYS:HA	1:B:78:ALA:HB3	2.01	0.42
1:B:215:ALA:O	1:B:216:VAL:C	2.62	0.42
1:B:348:ARG:NH2	1:B:486:PRO:HD3	2.34	0.42
1:B:441:PRO:C	1:B:443:ALA:H	2.26	0.42
1:B:34:CYS:HA	1:B:35:PRO:HD3	1.85	0.42
1:A:437:CYS:HA	1:A:440:HIS:HD2	1.84	0.42
1:A:513:ILE:HG21	1:A:568:PHE:CZ	2.55	0.42
1:B:536:LYS:HE3	1:B:540:THR:HG22	2.02	0.42
1:A:183:ASP:O	1:A:187:ASP:HB2	2.19	0.42
1:A:457:LEU:HD13	1:A:488:PHE:CD2	2.54	0.42
1:B:34:CYS:HB3	1:B:39:HIS:CE1	2.55	0.42
1:B:141:GLU:O	1:B:145:ARG:HD2	2.20	0.42
1:B:553:ALA:O	1:B:554:PHE:C	2.63	0.42
1:A:275:LEU:O	1:A:276:LYS:C	2.61	0.42
1:B:117:ARG:HA	1:B:118:PRO:HD3	1.87	0.42
1:A:199:LYS:O	1:A:202:SER:HB2	2.20	0.42
1:A:380:LEU:HD23	1:A:380:LEU:HA	1.89	0.42
1:A:420:THR:HG23	1:A:530:VAL:HG11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:551:PHE:O	1:A:555:VAL:HG23	2.20	0.42
1:A:344:VAL:CG2	1:A:450:GLU:HG2	2.49	0.42
1:A:408:LEU:HD23	1:A:427:SER:HB2	2.02	0.41
1:A:293:VAL:HG22	1:A:294:GLU:H	1.86	0.41
1:B:205:LYS:HE2	1:B:465:GLU:OE2	2.20	0.41
1:A:89:ASP:O	1:A:92:ALA:HB3	2.19	0.41
1:A:121:ASP:O	1:A:122:VAL:C	2.63	0.41
1:A:417:GLN:HB3	1:A:469:VAL:CG1	2.32	0.41
1:A:417:GLN:O	1:A:469:VAL:HG11	2.21	0.41
1:A:420:THR:N	1:A:421:PRO:CD	2.83	0.41
1:A:452:TYR:O	1:A:456:VAL:HG23	2.19	0.41
1:A:420:THR:CG2	1:A:527:THR:HG23	2.50	0.41
1:A:485:ARG:O	1:A:486:PRO:C	2.63	0.41
1:B:366:PRO:C	1:B:368:GLU:N	2.78	0.41
1:A:114:ARG:NH1	1:A:520:GLU:OE2	2.50	0.41
1:A:165:PHE:CE2	1:A:182:LEU:HD21	2.56	0.41
1:A:302:LEU:HA	1:A:303:PRO:HD2	1.84	0.41
1:A:22:LEU:CD2	1:A:151:ALA:HB1	2.50	0.41
1:A:483:ASN:C	1:A:486:PRO:HD2	2.46	0.41
1:B:268:GLN:HE21	1:B:268:GLN:HB2	1.65	0.41
1:B:394:LEU:HA	1:B:394:LEU:HD12	1.79	0.41
1:B:435:SER:O	1:B:439:LYS:HE2	2.20	0.41
1:B:302:LEU:HA	1:B:303:PRO:HD2	1.83	0.41
1:B:307:ALA:O	1:B:312:SER:N	2.51	0.41
1:B:81:ARG:C	1:B:83:THR:N	2.78	0.41
1:A:36:PHE:CZ	1:A:136:LYS:HB3	2.55	0.41
1:A:250:LEU:N	1:A:250:LEU:HD23	2.36	0.41
1:A:263:TYR:O	1:A:264:ILE:C	2.64	0.41
1:A:509:PHE:CD1	1:A:509:PHE:N	2.88	0.41
1:B:99:ASN:O	1:B:100:GLU:C	2.63	0.41
1:B:333:GLU:O	1:B:337:ARG:HG3	2.20	0.41
1:A:142:ILE:HD13	1:A:142:ILE:HA	1.78	0.41
1:B:383:GLU:HB3	1:B:384:PRO:CD	2.47	0.40
1:A:424:VAL:HG21	1:A:527:THR:HA	2.02	0.40
1:A:524:LYS:HD3	1:A:524:LYS:HA	1.96	0.40
1:B:11:PHE:CD1	1:B:11:PHE:C	3.00	0.40
1:B:123:MET:HB3	1:B:165:PHE:HE2	1.85	0.40
1:A:411:TYR:O	1:A:414:LYS:HB3	2.21	0.40
1:B:84:TYR:O	1:B:85:GLY:C	2.63	0.40
1:B:196:GLN:HA	1:B:196:GLN:NE2	2.35	0.40
1:B:441:PRO:C	1:B:443:ALA:N	2.77	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:566:THR:HB	1:B:567:CYS:H	1.76	0.40
1:B:543:GLN:HG3	1:B:544:LEU:N	2.36	0.40
1:B:264:ILE:HD12	1:B:290:ILE:HG21	2.03	0.40
1:B:350:ALA:O	1:B:351:LYS:C	2.65	0.40
1:B:416:PRO:O	1:B:534:LYS:HE2	2.21	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	576/585 (98%)	496 (86%)	60 (10%)	20 (4%)	3	4
1	B	576/585 (98%)	500 (87%)	65 (11%)	11 (2%)	6	11
All	All	1152/1170 (98%)	996 (86%)	125 (11%)	31 (3%)	4	6

All (31) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	501	GLU
1	B	60	GLU
1	B	501	GLU
1	B	538	LYS
1	B	566	THR
1	A	60	GLU
1	A	276	LYS
1	A	442	GLU
1	A	506	THR
1	A	566	THR
1	B	442	GLU
1	B	444	LYS
1	A	79	THR

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Mol	Chain	Res	Type
1	B	59	ALA
1	A	17	GLU
1	A	59	ALA
1	A	283	LEU
1	A	321	GLU
1	A	480	SER
1	B	303	PRO
1	A	361	CYS
1	A	400	GLU
1	A	449	ALA
1	A	538	LYS
1	B	321	GLU
1	B	373	VAL
1	A	202	SER
1	A	466	LYS
1	A	537	PRO
1	B	85	GLY
1	A	493	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	506/511 (99%)	476 (94%)	30 (6%)	18	37
1	B	506/511 (99%)	472 (93%)	34 (7%)	15	31
All	All	1012/1022 (99%)	948 (94%)	64 (6%)	16	34

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	GLU
1	A	46	VAL
1	A	57	GLU
1	A	58	SER
1	A	96	PRO

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Mol	Chain	Res	Type
1	A	109	ASN
1	A	111	ASN
1	A	131	GLU
1	A	183	ASP
1	A	208	GLU
1	A	232	SER
1	A	233	LYS
1	A	243	THR
1	A	245	CYS
1	A	253	CYS
1	A	270	SER
1	A	276	LYS
1	A	299	PRO
1	A	375	ASP
1	A	414	LYS
1	A	479	GLU
1	A	489	SER
1	A	506	THR
1	A	510	HIS
1	A	534	LYS
1	A	540	THR
1	A	548	MET
1	A	557	LYS
1	A	566	THR
1	A	580	GLN
1	B	30	TYR
1	B	58	SER
1	B	67	HIS
1	B	79	THR
1	B	83	THR
1	B	84	TYR
1	B	121	ASP
1	B	144	ARG
1	B	186	ARG
1	B	187	ASP
1	B	195	LYS
1	B	218	ARG
1	B	219	LEU
1	B	245	CYS
1	B	250	LEU
1	B	252	GLU
1	B	264	ILE

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Mol	Chain	Res	Type
1	B	284	LEU
1	B	293	VAL
1	B	308	ASP
1	B	324	ASP
1	B	344	VAL
1	B	370	TYR
1	B	375	ASP
1	B	419	SER
1	B	427	SER
1	B	436	LYS
1	B	474	THR
1	B	479	GLU
1	B	515	THR
1	B	548	MET
1	B	557	LYS
1	B	566	THR
1	B	568	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	94	GLN
1	A	105	HIS
1	A	109	ASN
1	A	196	GLN
1	A	318	ASN
1	A	386	ASN
1	A	464	HIS
1	A	580	GLN
1	B	33	GLN
1	B	105	HIS
1	B	109	ASN
1	B	196	GLN
1	B	221	GLN
1	B	386	ASN
1	B	440	HIS
1	B	580	GLN

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 oligosaccharides 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 ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.