



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 10:40 AM UTC

PDB ID : 1BJ5 / pdb_00001bj5
Title : HUMAN SERUM ALBUMIN COMPLEXED WITH MYRISTIC ACID
Authors : Curry, S.; Mandelkow, H.; Brick, P.; Franks, N.
Deposited on : 1998-07-02
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
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

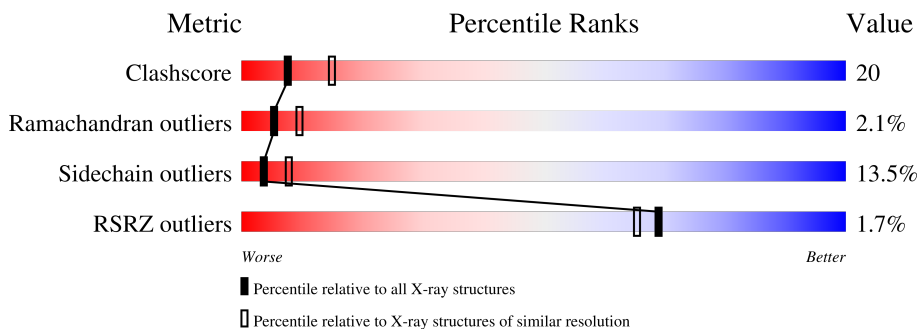
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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)
RSRZ outliers	180081	5833 (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 $\leq 5\%$. 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	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4544 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 HUMAN SERUM ALBUMIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	0	0	0
			4475	2829	755	850	41			

- Molecule 2 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).

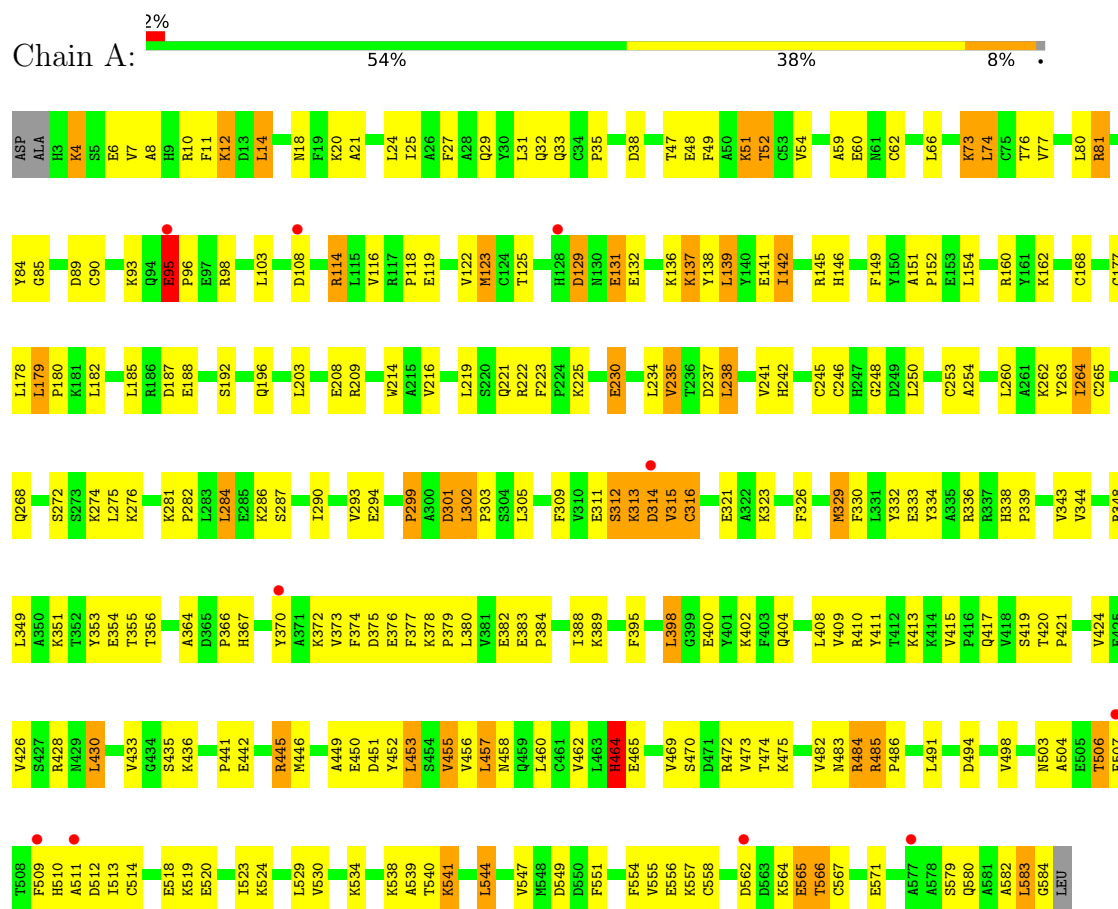


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			14	12	2		
2	A	1	Total	C	O	0	0
			13	11	2		
2	A	1	Total	C	O	0	0
			13	11	2		
2	A	1	Total	C	O	0	0
			13	11	2		
2	A	1	Total	C	O	0	0
			16	14	2		

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: HUMAN SERUM ALBUMIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	189.18Å 38.96Å 96.40Å 90.00° 105.31° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	90.8 (20.00-2.50) 90.6 (20.00-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.49Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.224 , 0.279 0.217 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	48.1	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 54.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4544	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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: MYR

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	0.43	0/4562	0.99	26/6181 (0.4%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	VAL	N-CA-C	-10.13	103.10	111.81
1	A	301	ASP	N-CA-C	-9.02	101.25	112.88
1	A	313	LYS	N-CA-C	-8.45	99.37	110.43
1	A	4	LYS	N-CA-C	-8.12	103.51	113.50
1	A	178	LEU	N-CA-C	7.29	118.87	111.07
1	A	95	GLU	N-CA-C	6.84	124.93	109.81
1	A	566	THR	N-CA-C	-6.58	103.31	112.45
1	A	583	LEU	N-CA-C	-6.52	105.44	113.19
1	A	541	LYS	N-CA-C	-6.51	104.60	112.54
1	A	95	GLU	CA-C-N	-6.42	112.56	119.24
1	A	95	GLU	C-N-CA	-6.42	112.56	119.24
1	A	131	GLU	N-CA-C	6.36	117.87	111.07
1	A	323	LYS	N-CA-C	6.35	119.01	111.33
1	A	139	LEU	N-CA-C	-5.95	104.87	111.36
1	A	250	LEU	N-CA-C	5.86	117.34	111.07
1	A	146	HIS	CA-C-N	5.79	125.41	119.56
1	A	146	HIS	C-N-CA	5.79	125.41	119.56
1	A	179	LEU	N-CA-C	5.78	120.76	113.25
1	A	302	LEU	N-CA-C	5.64	119.65	109.44
1	A	562	ASP	N-CA-C	5.49	122.49	110.80
1	A	316	CYS	N-CA-C	-5.38	105.58	111.82
1	A	12	LYS	N-CA-C	5.23	117.66	111.33
1	A	168	CYS	N-CA-C	5.18	118.76	112.23
1	A	108	ASP	N-CA-C	5.16	116.59	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	464	HIS	N-CA-C	-5.12	106.29	112.54
1	A	445	ARG	N-CA-C	5.11	116.70	111.03

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	4475	0	4264	179	0
2	A	69	0	101	6	0
All	All	4544	0	4365	179	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 20.

All (179) 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:424:VAL:O	1:A:428:ARG:HG3	1.82	0.80
1:A:564:LYS:O	1:A:565:GLU:HB2	1.82	0.80
1:A:305:LEU:HD21	1:A:333:GLU:HB3	1.65	0.78
1:A:151:ALA:HB3	1:A:152:PRO:HD3	1.64	0.77
1:A:114:ARG:HH21	1:A:116:VAL:HG12	1.48	0.76
1:A:12:LYS:HE2	1:A:54:VAL:HG13	1.68	0.76
1:A:398:LEU:HB3	1:A:402:LYS:HB3	1.69	0.74
1:A:118:PRO:HD2	1:A:123:MET:HE3	1.70	0.74
1:A:462:VAL:O	1:A:465:GLU:HB3	1.88	0.73
1:A:254:ALA:HB1	2:A:1002:MYR:H51	1.71	0.73
1:A:356:THR:HG21	1:A:373:VAL:CG2	2.19	0.72
1:A:119:GLU:O	1:A:122:VAL:HG22	1.88	0.72
1:A:518:GLU:HA	1:A:518:GLU:OE1	1.89	0.72
1:A:400:GLU:O	1:A:404:GLN:HG3	1.90	0.72
1:A:348:ARG:HG3	1:A:482:VAL:HG13	1.71	0.71
1:A:272:SER:HB3	1:A:275:LEU:HG	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ALA:O	1:A:12:LYS:HG3	1.93	0.67
1:A:313:LYS:O	1:A:314:ASP:HB2	1.94	0.67
1:A:137:LYS:O	1:A:141:GLU:HG2	1.95	0.66
1:A:138:TYR:O	1:A:142:ILE:HG12	1.96	0.65
1:A:530:VAL:HG12	1:A:534:LYS:HE3	1.79	0.65
1:A:551:PHE:O	1:A:555:VAL:HG23	1.97	0.64
1:A:10:ARG:O	1:A:14:LEU:HB2	1.97	0.64
1:A:567:CYS:O	1:A:571:GLU:HB2	1.97	0.64
1:A:225:LYS:HG3	1:A:299:PRO:HD3	1.78	0.64
1:A:485:ARG:H	1:A:486:PRO:CD	2.11	0.64
1:A:214:TRP:CD1	1:A:343:VAL:HG11	2.33	0.63
1:A:149:PHE:CD2	1:A:154:LEU:HD13	2.36	0.61
1:A:484:ARG:O	1:A:484:ARG:HG2	2.00	0.61
1:A:293:VAL:HG22	1:A:294:GLU:H	1.66	0.61
1:A:81:ARG:NH2	1:A:89:ASP:OD1	2.32	0.60
1:A:25:ILE:O	1:A:29:GLN:HG3	2.01	0.60
1:A:452:TYR:O	1:A:455:VAL:HG23	2.00	0.60
1:A:364:ALA:O	1:A:366:PRO:HD3	2.02	0.60
1:A:442:GLU:HA	1:A:445:ARG:HD2	1.84	0.59
1:A:141:GLU:O	1:A:145:ARG:HD2	2.02	0.59
1:A:409:VAL:O	1:A:413:LYS:HG3	2.02	0.59
1:A:293:VAL:HG22	1:A:294:GLU:N	2.17	0.59
1:A:131:GLU:OE2	1:A:162:LYS:HE3	2.02	0.59
1:A:458:ASN:O	1:A:462:VAL:HG23	2.03	0.58
1:A:77:VAL:O	1:A:80:LEU:HB2	2.04	0.58
1:A:114:ARG:NH2	1:A:116:VAL:HG12	2.19	0.57
1:A:540:THR:HG22	1:A:541:LYS:H	1.68	0.57
1:A:35:PRO:O	1:A:38:ASP:HB2	2.04	0.57
1:A:114:ARG:O	1:A:114:ARG:HG3	2.04	0.56
1:A:237:ASP:O	1:A:241:VAL:HG23	2.05	0.56
1:A:520:GLU:HA	1:A:520:GLU:OE1	2.04	0.56
1:A:80:LEU:HD12	1:A:84:TYR:CD2	2.40	0.56
1:A:313:LYS:O	1:A:314:ASP:CB	2.53	0.56
1:A:417:GLN:NE2	1:A:494:ASP:OD2	2.34	0.56
1:A:315:VAL:HG11	1:A:370:TYR:CZ	2.41	0.56
1:A:21:ALA:O	1:A:25:ILE:HG13	2.06	0.56
1:A:420:THR:N	1:A:421:PRO:HD2	2.22	0.55
1:A:540:THR:HG22	1:A:541:LYS:N	2.21	0.55
1:A:125:THR:O	1:A:129:ASP:OD1	2.24	0.55
1:A:315:VAL:HG13	1:A:316:CYS:N	2.22	0.55
1:A:378:LYS:HB3	1:A:379:PRO:HD3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:PHE:O	1:A:52:THR:HB	2.07	0.54
1:A:27:PHE:CE1	1:A:74:LEU:HD12	2.43	0.54
1:A:118:PRO:HB2	1:A:122:VAL:CG2	2.39	0.53
1:A:464:HIS:HE1	1:A:470:SER:O	1.92	0.53
1:A:272:SER:HB3	1:A:275:LEU:CG	2.37	0.53
1:A:564:LYS:O	1:A:565:GLU:CB	2.55	0.53
1:A:582:ALA:C	1:A:584:GLY:H	2.15	0.53
1:A:81:ARG:O	1:A:85:GLY:HA2	2.09	0.53
1:A:118:PRO:CD	1:A:123:MET:HE3	2.39	0.53
1:A:547:VAL:HG21	1:A:583:LEU:HD21	1.90	0.53
1:A:73:LYS:O	1:A:76:THR:HB	2.08	0.53
1:A:138:TYR:HB3	2:A:1001:MYR:H101	1.91	0.52
1:A:373:VAL:O	1:A:376:GLU:N	2.38	0.52
1:A:219:LEU:HD12	1:A:235:VAL:HG23	1.90	0.52
1:A:411:TYR:HE2	1:A:430:LEU:HD23	1.75	0.52
1:A:10:ARG:HG3	1:A:66:LEU:HD11	1.92	0.51
1:A:286:LYS:O	1:A:290:ILE:HG13	2.10	0.51
1:A:12:LYS:CE	1:A:54:VAL:HG13	2.39	0.51
1:A:395:PHE:O	1:A:398:LEU:O	2.27	0.51
1:A:95:GLU:OE1	1:A:98:ARG:NH2	2.44	0.51
1:A:222:ARG:HH11	1:A:222:ARG:HG2	1.75	0.51
1:A:398:LEU:CB	1:A:402:LYS:HB3	2.39	0.51
1:A:378:LYS:HB3	1:A:379:PRO:CD	2.40	0.51
1:A:449:ALA:O	1:A:453:LEU:HB2	2.10	0.51
1:A:433:VAL:HG22	1:A:452:TYR:HB3	1.91	0.51
1:A:216:VAL:CG2	1:A:235:VAL:HG21	2.41	0.50
1:A:419:SER:OG	1:A:421:PRO:HD2	2.11	0.50
1:A:284:LEU:HG	1:A:284:LEU:O	2.09	0.50
1:A:356:THR:HG21	1:A:373:VAL:HG23	1.93	0.50
1:A:311:GLU:O	1:A:312:SER:C	2.54	0.50
1:A:372:LYS:O	1:A:375:ASP:HB2	2.12	0.50
1:A:142:ILE:N	1:A:142:ILE:HD13	2.27	0.50
1:A:349:LEU:HD23	1:A:380:LEU:HD23	1.94	0.49
1:A:582:ALA:C	1:A:584:GLY:N	2.70	0.49
1:A:388:ILE:HD13	2:A:1003:MYR:H72	1.95	0.49
1:A:415:VAL:HG11	1:A:473:VAL:HG23	1.95	0.49
1:A:348:ARG:HG3	1:A:482:VAL:CG1	2.42	0.49
1:A:513:ILE:CD1	1:A:555:VAL:HG13	2.42	0.49
1:A:95:GLU:O	1:A:96:PRO:C	2.53	0.48
1:A:222:ARG:HG2	1:A:222:ARG:NH1	2.28	0.48
1:A:315:VAL:CG1	1:A:316:CYS:N	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ALA:HB3	1:A:152:PRO:CD	2.40	0.47
1:A:519:LYS:O	1:A:523:ILE:HG13	2.15	0.47
1:A:530:VAL:CG1	1:A:534:LYS:HE3	2.44	0.47
1:A:33:GLN:HA	1:A:33:GLN:OE1	2.14	0.47
1:A:554:PHE:HE2	1:A:571:GLU:C	2.22	0.47
1:A:430:LEU:CD1	1:A:456:VAL:HG11	2.45	0.46
1:A:556:GLU:O	1:A:558:CYS:N	2.47	0.46
1:A:48:GLU:HA	1:A:48:GLU:OE1	2.15	0.46
1:A:245:CYS:HA	1:A:253:CYS:HB2	1.98	0.46
1:A:332:TYR:O	1:A:336:ARG:HG2	2.15	0.46
1:A:383:GLU:HB3	1:A:384:PRO:HD3	1.97	0.46
1:A:415:VAL:HG23	1:A:415:VAL:O	2.16	0.46
1:A:299:PRO:C	1:A:301:ASP:H	2.24	0.46
1:A:315:VAL:HG23	1:A:326:PHE:HZ	1.81	0.46
1:A:453:LEU:O	1:A:457:LEU:HB2	2.16	0.45
1:A:24:LEU:HD23	1:A:139:LEU:HD23	1.98	0.45
1:A:539:ALA:HB3	1:A:544:LEU:HD13	1.97	0.45
1:A:344:VAL:HG22	1:A:450:GLU:OE2	2.16	0.45
1:A:309:PHE:HB3	1:A:353:TYR:OH	2.17	0.45
1:A:281:LYS:HB3	1:A:282:PRO:HD2	1.98	0.45
1:A:114:ARG:HE	1:A:116:VAL:HG12	1.82	0.45
1:A:59:ALA:HB3	1:A:62:CYS:SG	2.56	0.45
1:A:510:HIS:O	1:A:512:ASP:N	2.50	0.45
1:A:177:CYS:O	1:A:180:PRO:HD2	2.16	0.44
1:A:290:ILE:O	1:A:293:VAL:HG12	2.18	0.44
1:A:539:ALA:CB	1:A:544:LEU:HD13	2.48	0.44
1:A:223:PHE:CD1	1:A:272:SER:HB2	2.52	0.44
1:A:378:LYS:O	1:A:382:GLU:HG3	2.17	0.44
1:A:415:VAL:HG21	2:A:1004:MYR:H101	1.99	0.44
1:A:238:LEU:HD22	1:A:242:HIS:HD2	1.83	0.44
1:A:411:TYR:CE2	1:A:430:LEU:HD23	2.52	0.44
1:A:464:HIS:CE1	1:A:470:SER:H	2.35	0.44
1:A:138:TYR:CB	2:A:1001:MYR:H101	2.48	0.44
1:A:420:THR:HG23	1:A:530:VAL:CG1	2.48	0.44
1:A:230:GLU:OE1	1:A:263:TYR:OH	2.36	0.43
1:A:549:ASP:C	1:A:551:PHE:H	2.26	0.43
1:A:136:LYS:HD3	1:A:136:LYS:HA	1.75	0.43
1:A:485:ARG:H	1:A:486:PRO:HD2	1.83	0.43
1:A:334:TYR:CE1	1:A:338:HIS:HD2	2.36	0.43
1:A:388:ILE:O	1:A:389:LYS:C	2.61	0.43
1:A:503:ASN:HB3	1:A:506:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:CYS:O	1:A:98:ARG:HG3	2.19	0.43
1:A:234:LEU:O	1:A:238:LEU:HB2	2.19	0.43
1:A:458:ASN:HA	1:A:484:ARG:HH12	1.83	0.43
1:A:520:GLU:O	1:A:524:LYS:HG3	2.18	0.43
1:A:154:LEU:HD12	1:A:154:LEU:HA	1.90	0.43
1:A:329:MET:O	1:A:333:GLU:HG2	2.19	0.42
1:A:384:PRO:O	1:A:388:ILE:HG12	2.19	0.42
1:A:219:LEU:HD12	1:A:235:VAL:CG2	2.49	0.42
1:A:513:ILE:HD11	1:A:555:VAL:HG13	2.01	0.42
1:A:6:GLU:HB3	1:A:66:LEU:HG	2.01	0.42
1:A:11:PHE:CZ	1:A:51:LYS:HD2	2.54	0.42
1:A:20:LYS:HE2	1:A:47:THR:HG21	2.02	0.42
1:A:160:ARG:HH22	1:A:188:GLU:CD	2.27	0.42
1:A:464:HIS:CE1	1:A:469:VAL:H	2.37	0.42
1:A:27:PHE:HE1	1:A:74:LEU:HD12	1.82	0.42
1:A:221:GLN:CG	1:A:339:PRO:HA	2.50	0.42
1:A:485:ARG:HB3	1:A:486:PRO:HD3	2.01	0.42
1:A:549:ASP:C	1:A:551:PHE:N	2.77	0.42
1:A:118:PRO:HG2	1:A:123:MET:HE3	2.01	0.42
1:A:208:GLU:O	1:A:209:ARG:C	2.62	0.42
1:A:265:CYS:O	1:A:268:GLN:HB2	2.20	0.41
1:A:118:PRO:HG2	1:A:123:MET:HG3	2.02	0.41
1:A:579:SER:O	1:A:580:GLN:C	2.62	0.41
1:A:395:PHE:CZ	1:A:435:SER:HA	2.55	0.41
1:A:260:LEU:O	1:A:264:ILE:HG13	2.20	0.41
1:A:238:LEU:HD22	1:A:242:HIS:CD2	2.56	0.41
1:A:299:PRO:C	1:A:301:ASP:N	2.78	0.41
1:A:415:VAL:HG11	1:A:473:VAL:CG2	2.51	0.41
1:A:59:ALA:O	1:A:60:GLU:C	2.63	0.41
1:A:18:ASN:H	1:A:18:ASN:ND2	2.19	0.41
1:A:32:GLN:H	1:A:32:GLN:HG3	1.68	0.41
1:A:472:ARG:HB3	1:A:491:LEU:HD21	2.03	0.41
1:A:507:PHE:HD1	2:A:1005:MYR:H101	1.85	0.41
1:A:330:PHE:HZ	1:A:377:PHE:CE2	2.38	0.41
1:A:483:ASN:C	1:A:486:PRO:HD2	2.46	0.40
1:A:246:CYS:C	1:A:248:GLY:N	2.79	0.40
1:A:373:VAL:HG12	1:A:374:PHE:N	2.35	0.40
1:A:216:VAL:HG23	1:A:235:VAL:HG21	2.03	0.40
1:A:441:PRO:O	1:A:442:GLU:C	2.64	0.40
1:A:420:THR:HG23	1:A:530:VAL:HB	2.04	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	580/585 (99%)	514 (89%)	54 (9%)	12 (2%)	5 9

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	GLU
1	A	303	PRO
1	A	276	LYS
1	A	312	SER
1	A	314	ASP
1	A	511	ALA
1	A	557	LYS
1	A	565	GLU
1	A	367	HIS
1	A	504	ALA
1	A	485	ARG
1	A	299	PRO

5.3.2 Protein sidechains [i](#)

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	467/511 (91%)	404 (86%)	63 (14%)	4 8

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	7	VAL
1	A	14	LEU
1	A	31	LEU
1	A	51	LYS
1	A	52	THR
1	A	73	LYS
1	A	74	LEU
1	A	81	ARG
1	A	93	LYS
1	A	95	GLU
1	A	103	LEU
1	A	114	ARG
1	A	123	MET
1	A	129	ASP
1	A	132	GLU
1	A	137	LYS
1	A	142	ILE
1	A	179	LEU
1	A	182	LEU
1	A	185	LEU
1	A	187	ASP
1	A	192	SER
1	A	196	GLN
1	A	203	LEU
1	A	230	GLU
1	A	235	VAL
1	A	238	LEU
1	A	262	LYS
1	A	264	ILE
1	A	274	LYS
1	A	284	LEU
1	A	287	SER
1	A	302	LEU
1	A	321	GLU
1	A	329	MET
1	A	351	LYS
1	A	354	GLU
1	A	355	THR
1	A	398	LEU
1	A	408	LEU
1	A	410	ARG
1	A	426	VAL

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Mol	Chain	Res	Type
1	A	430	LEU
1	A	436	LYS
1	A	446	MET
1	A	451	ASP
1	A	453	LEU
1	A	455	VAL
1	A	457	LEU
1	A	460	LEU
1	A	464	HIS
1	A	474	THR
1	A	475	LYS
1	A	484	ARG
1	A	498	VAL
1	A	506	THR
1	A	509	PHE
1	A	514	CYS
1	A	529	LEU
1	A	538	LYS
1	A	544	LEU
1	A	566	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	HIS
1	A	18	ASN
1	A	61	ASN
1	A	105	HIS
1	A	242	HIS
1	A	247	HIS
1	A	268	GLN
1	A	295	ASN
1	A	338	HIS
1	A	535	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	MYR	A	1003	-	12,12,15	0.73	0	12,12,15	0.68	0
2	MYR	A	1001	-	13,13,15	0.60	0	13,13,15	0.73	0
2	MYR	A	1002	-	12,12,15	0.68	0	12,12,15	0.74	0
2	MYR	A	1004	-	12,12,15	0.68	0	12,12,15	0.71	0
2	MYR	A	1005	-	15,15,15	0.57	0	15,15,15	0.75	0

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	MYR	A	1003	-	-	7/10/10/13	-
2	MYR	A	1001	-	-	7/11/11/13	-
2	MYR	A	1002	-	-	4/10/10/13	-
2	MYR	A	1004	-	-	7/10/10/13	-
2	MYR	A	1005	-	-	6/13/13/13	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1003	MYR	C1-C2-C3-C4
2	A	1005	MYR	C1-C2-C3-C4
2	A	1004	MYR	C1-C2-C3-C4
2	A	1005	MYR	C10-C11-C12-C13
2	A	1001	MYR	C5-C6-C7-C8
2	A	1002	MYR	C2-C3-C4-C5
2	A	1003	MYR	C6-C7-C8-C9
2	A	1001	MYR	C4-C5-C6-C7
2	A	1003	MYR	C5-C6-C7-C8
2	A	1004	MYR	C4-C5-C6-C7
2	A	1001	MYR	C1-C2-C3-C4
2	A	1004	MYR	C6-C7-C8-C9
2	A	1003	MYR	C11-C10-C9-C8
2	A	1004	MYR	C2-C3-C4-C5
2	A	1001	MYR	C2-C3-C4-C5
2	A	1005	MYR	C6-C7-C8-C9
2	A	1005	MYR	C4-C5-C6-C7
2	A	1004	MYR	C11-C10-C9-C8
2	A	1005	MYR	C11-C10-C9-C8
2	A	1001	MYR	C7-C8-C9-C10
2	A	1004	MYR	O1-C1-C2-C3
2	A	1002	MYR	O2-C1-C2-C3
2	A	1001	MYR	O1-C1-C2-C3
2	A	1002	MYR	C4-C5-C6-C7
2	A	1003	MYR	O1-C1-C2-C3
2	A	1001	MYR	O2-C1-C2-C3
2	A	1003	MYR	O2-C1-C2-C3
2	A	1004	MYR	O2-C1-C2-C3
2	A	1002	MYR	O1-C1-C2-C3
2	A	1003	MYR	C4-C5-C6-C7
2	A	1005	MYR	C7-C8-C9-C10

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1003	MYR	1	0
2	A	1001	MYR	2	0
2	A	1002	MYR	1	0
2	A	1004	MYR	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1005	MYR	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	582/585 (99%)	0.03	10 (1%) 69 65	21, 49, 82, 99	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	562	ASP	2.7
1	A	509	PHE	2.7
1	A	108	ASP	2.5
1	A	314	ASP	2.5
1	A	511	ALA	2.3
1	A	95	GLU	2.2
1	A	507	PHE	2.2
1	A	577	ALA	2.1
1	A	370	TYR	2.1
1	A	128	HIS	2.1

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 [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. 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	MYR	A	1002	13/16	0.80	0.15	49,54,56,56	0
2	MYR	A	1005	16/16	0.86	0.12	47,51,66,66	0
2	MYR	A	1001	14/16	0.88	0.12	42,55,59,60	0
2	MYR	A	1004	13/16	0.89	0.10	40,43,54,54	0
2	MYR	A	1003	13/16	0.90	0.11	36,39,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.