



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:31 PM UTC

PDB ID : 1MAH / pdb_00001mah
Title : FASCICULIN2-MOUSE ACETYLCHOLINESTERASE COMPLEX
Authors : Bourne, Y.; Taylor, P.; Marchot, P.
Deposited on : 1995-11-21
Resolution : 3.20 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)	:	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

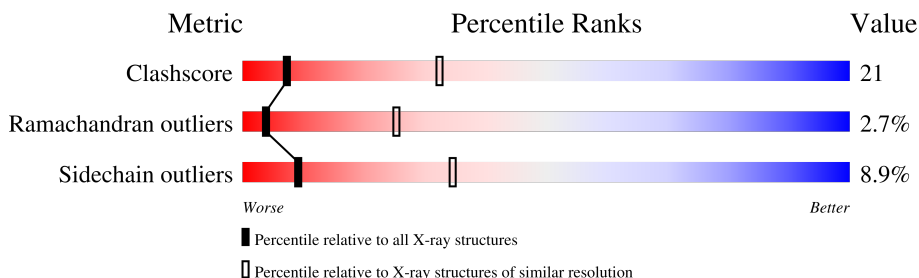
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)

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	543	
2	F	61	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4590 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 ACETYLCHOLINESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	533	Total	C	N	O	S	0	0	0
			4116	2648	699	755	14			

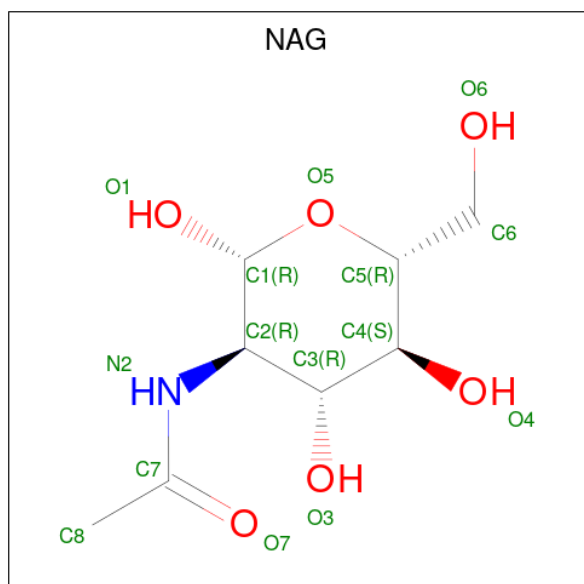
- Molecule 2 is a protein called FASCICULIN 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	61	Total	C	N	O	S	0	0	0
			460	273	87	90	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	47	ASN	TYR	conflict	UNP P01403

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



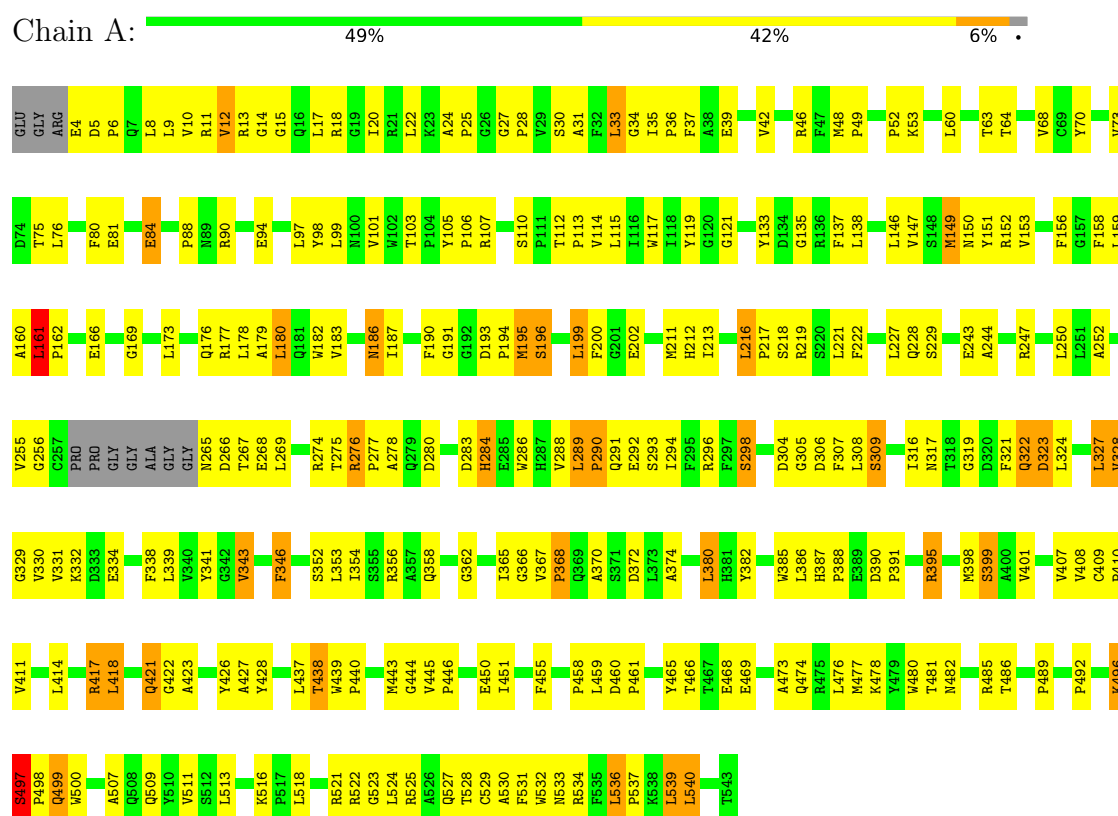
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

3 Residue-property plots

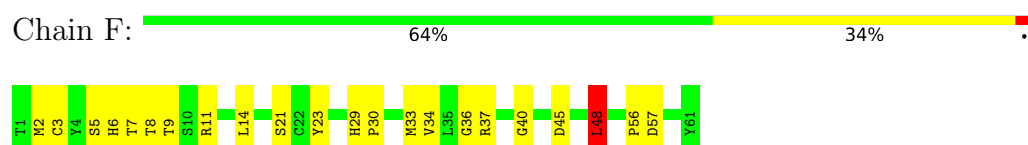
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: ACETYLCHOLINESTERASE



• Molecule 2: FASCICULIN 2



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	75.50Å 75.50Å 556.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 3.20	Depositor
% Data completeness (in resolution range)	85.0 (10.00-3.20)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.184 , 0.294	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4590	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0/4239	1.12	32/5801 (0.6%)
2	F	0.51	0/469	1.06	2/632 (0.3%)
All	All	0.51	0/4708	1.12	34/6433 (0.5%)

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	276	ARG	CA-C-N	10.03	130.66	119.93
1	A	276	ARG	C-N-CA	10.03	130.66	119.93
1	A	298	SER	N-CA-C	9.36	121.56	111.36
1	A	367	VAL	CA-C-N	8.20	127.84	119.56
1	A	367	VAL	C-N-CA	8.20	127.84	119.56
2	F	23	TYR	N-CA-C	7.53	121.54	110.17
1	A	500	TRP	CA-C-N	7.44	128.04	120.38
1	A	500	TRP	C-N-CA	7.44	128.04	120.38
1	A	343	VAL	N-CA-C	-7.13	100.49	107.55
1	A	496	LYS	N-CA-C	-6.99	97.44	108.63
1	A	64	THR	N-CA-C	6.68	118.35	108.60
1	A	307	PHE	N-CA-C	-6.57	102.77	111.24
1	A	8	LEU	N-CA-C	-6.36	103.65	112.30
1	A	276	ARG	N-CA-C	6.31	117.60	109.72
1	A	284	HIS	N-CA-C	6.28	120.98	112.88
2	F	48	LEU	N-CA-C	6.22	118.83	108.13
1	A	34	GLY	N-CA-C	6.06	123.13	114.64
1	A	422	GLY	N-CA-C	6.04	123.38	115.47
1	A	191	GLY	N-CA-C	-6.02	105.81	115.08
1	A	445	VAL	CA-C-N	5.92	126.74	120.11
1	A	445	VAL	C-N-CA	5.92	126.74	120.11
1	A	84	GLU	N-CA-C	5.81	118.39	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	497	SER	N-CA-C	5.58	122.15	109.81
1	A	368	PRO	N-CA-C	5.57	120.82	113.86
1	A	244	ALA	N-CA-C	-5.53	105.15	111.07
1	A	346	PHE	N-CA-C	5.45	118.34	110.28
1	A	27	GLY	CA-C-N	5.42	125.36	119.78
1	A	27	GLY	C-N-CA	5.42	125.36	119.78
1	A	158	PHE	N-CA-C	5.23	121.45	113.19
1	A	516	LYS	CA-C-N	5.23	125.16	119.78
1	A	516	LYS	C-N-CA	5.23	125.16	119.78
1	A	229	SER	N-CA-C	5.16	118.52	111.39
1	A	161	LEU	N-CA-C	-5.15	99.87	108.94
1	A	327	LEU	N-CA-C	-5.10	100.59	108.90

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	4116	0	3967	172	0
2	F	460	0	431	21	0
3	A	14	0	13	0	0
All	All	4590	0	4411	185	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 21.

All (185) 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:113:PRO:HA	1:A:196:SER:HB2	1.60	0.83
1:A:216:LEU:HD12	1:A:217:PRO:HD3	1.61	0.83
1:A:113:PRO:HA	1:A:196:SER:CB	2.12	0.79
1:A:211:MET:SD	1:A:308:LEU:HD11	2.23	0.79
1:A:329:GLY:HA3	1:A:428:TYR:CE1	2.18	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:LEU:HD13	1:A:31:ALA:HB3	1.66	0.77
1:A:113:PRO:HG3	1:A:485:ARG:HG2	1.69	0.74
1:A:352:SER:O	1:A:395:ARG:HG3	1.89	0.72
2:F:6:HIS:CE1	2:F:37:ARG:HG3	2.26	0.71
1:A:177:ARG:O	1:A:180:LEU:HB2	1.92	0.70
1:A:193:ASP:OD1	1:A:195:MET:SD	2.50	0.70
1:A:84:GLU:HB3	2:F:11:ARG:HH21	1.56	0.69
1:A:161:LEU:HD21	1:A:269:LEU:HD23	1.74	0.68
1:A:213:ILE:HG22	1:A:222:PHE:CZ	2.28	0.68
2:F:6:HIS:HE1	2:F:37:ARG:HG3	1.59	0.67
1:A:321:PHE:HB3	1:A:423:ALA:HB2	1.77	0.67
1:A:530:ALA:O	1:A:534:ARG:HB2	1.96	0.65
1:A:216:LEU:CD1	1:A:217:PRO:HD3	2.27	0.65
1:A:199:LEU:HD11	1:A:222:PHE:CD2	2.32	0.64
1:A:182:TRP:O	1:A:186:ASN:HB2	1.97	0.64
1:A:68:VAL:HG23	1:A:90:ARG:HB2	1.81	0.63
1:A:255:VAL:HG11	1:A:276:ARG:HG3	1.82	0.62
1:A:75:THR:HG21	2:F:6:HIS:CD2	2.35	0.61
1:A:458:PRO:HA	1:A:465:TYR:CD2	2.35	0.61
1:A:103:THR:HG21	1:A:190:PHE:HB3	1.83	0.61
1:A:195:MET:SD	1:A:195:MET:N	2.74	0.60
1:A:473:ALA:O	1:A:477:MET:HG3	2.01	0.60
1:A:532:TRP:O	1:A:537:PRO:HD3	2.02	0.60
1:A:31:ALA:HB1	1:A:33:LEU:CD1	2.32	0.59
1:A:84:GLU:HB3	2:F:11:ARG:NH2	2.18	0.58
1:A:252:ALA:HB1	1:A:269:LEU:HD11	1.86	0.57
1:A:213:ILE:HG22	1:A:222:PHE:CE2	2.39	0.57
1:A:149:MET:HE2	1:A:149:MET:N	2.20	0.57
1:A:149:MET:HE2	1:A:149:MET:H	1.71	0.56
1:A:160:ALA:HB2	1:A:169:GLY:HA3	1.88	0.56
1:A:265:ASN:HB3	1:A:268:GLU:HB3	1.88	0.56
2:F:3:CYS:O	2:F:14:LEU:HD12	2.06	0.56
1:A:218:SER:O	1:A:221:LEU:HG	2.05	0.55
1:A:20:ILE:HB	1:A:63:THR:HG22	1.88	0.55
1:A:112:THR:HG23	1:A:113:PRO:HD2	1.89	0.55
1:A:179:ALA:O	1:A:183:VAL:HG23	2.07	0.55
1:A:407:VAL:O	1:A:411:VAL:HG23	2.06	0.55
1:A:73:VAL:HG23	2:F:9:THR:HA	1.89	0.54
1:A:356:ARG:HD2	1:A:388:PRO:O	2.07	0.54
1:A:322:GLN:O	1:A:323:ASP:HB3	2.06	0.54
1:A:407:VAL:O	1:A:410:PRO:HD2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:TYR:CE2	1:A:153:VAL:HG12	2.43	0.54
1:A:317:ASN:HA	1:A:417:ARG:HE	1.73	0.53
1:A:12:VAL:O	1:A:14:GLY:N	2.42	0.53
1:A:293:SER:HA	1:A:365:ILE:HG23	1.89	0.53
2:F:6:HIS:NE2	2:F:36:GLY:HA2	2.23	0.53
1:A:39:GLU:HG2	1:A:52:PRO:O	2.09	0.53
1:A:113:PRO:HA	1:A:196:SER:HB3	1.91	0.53
1:A:529:CYS:HB3	1:A:533:ASN:HD22	1.74	0.53
1:A:10:VAL:HG22	1:A:107:ARG:NH1	2.24	0.53
1:A:213:ILE:HG22	1:A:222:PHE:HZ	1.73	0.52
1:A:46:ARG:O	1:A:274:ARG:NH1	2.40	0.52
1:A:30:SER:HB2	1:A:103:THR:OG1	2.08	0.52
1:A:528:THR:O	1:A:531:PHE:HB3	2.10	0.52
2:F:6:HIS:HD2	2:F:7:THR:O	1.92	0.52
1:A:482:ASN:O	1:A:486:THR:HG22	2.10	0.52
1:A:329:GLY:HA3	1:A:428:TYR:CZ	2.45	0.51
1:A:12:VAL:HG13	1:A:186:ASN:OD1	2.10	0.51
1:A:177:ARG:HA	1:A:180:LEU:HD22	1.92	0.51
1:A:529:CYS:HB3	1:A:533:ASN:ND2	2.26	0.51
2:F:45:ASP:OD1	2:F:48:LEU:HG	2.10	0.51
1:A:31:ALA:HB1	1:A:33:LEU:HD11	1.93	0.51
1:A:183:VAL:HG13	1:A:187:ILE:HB	1.93	0.51
1:A:250:LEU:HD23	1:A:288:VAL:HA	1.93	0.51
1:A:81:GLU:HB3	1:A:438:THR:HG21	1.92	0.50
1:A:354:ILE:CG1	1:A:358:GLN:HB2	2.41	0.50
1:A:176:GLN:OE1	1:A:212:HIS:HE1	1.94	0.50
2:F:21:SER:O	2:F:40:GLY:N	2.44	0.50
1:A:536:LEU:HD13	1:A:540:LEU:HD13	1.94	0.50
1:A:292:GLU:HA	2:F:30:PRO:O	2.11	0.49
1:A:68:VAL:HG11	1:A:88:PRO:HB3	1.92	0.49
1:A:80:PHE:CE1	1:A:438:THR:HB	2.47	0.49
1:A:286:TRP:CZ2	2:F:33:MET:HE3	2.48	0.49
1:A:328:VAL:O	1:A:427:ALA:HA	2.13	0.49
1:A:496:LYS:C	1:A:498:PRO:HD2	2.38	0.49
1:A:11:ARG:NH1	1:A:15:GLY:HA2	2.28	0.49
1:A:119:TYR:HE2	1:A:150:ASN:HA	1.78	0.49
1:A:149:MET:H	1:A:149:MET:CE	2.25	0.49
1:A:459:LEU:O	1:A:461:PRO:HD3	2.13	0.48
1:A:4:GLU:O	1:A:5:ASP:HB2	2.12	0.48
1:A:97:LEU:HD21	1:A:152:ARG:HG3	1.96	0.48
1:A:133:TYR:HA	1:A:455:PHE:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:6:HIS:CD2	2:F:36:GLY:HA2	2.49	0.48
1:A:24:ALA:HB1	1:A:25:PRO:HD2	1.96	0.48
1:A:531:PHE:CZ	1:A:536:LEU:HD23	2.48	0.47
1:A:166:GLU:CG	1:A:267:THR:HG22	2.45	0.47
1:A:277:PRO:HB2	1:A:280:ASP:HB2	1.95	0.47
1:A:330:VAL:HG12	1:A:331:VAL:O	2.14	0.47
1:A:292:GLU:HB3	2:F:29:HIS:HB3	1.95	0.47
1:A:382:TYR:CD2	1:A:401:VAL:HG22	2.50	0.47
1:A:450:GLU:HG2	1:A:451:ILE:N	2.28	0.47
1:A:507:ALA:HA	1:A:522:ARG:HH21	1.80	0.47
1:A:70:TYR:CD2	1:A:278:ALA:HB1	2.50	0.46
2:F:34:VAL:HG12	2:F:36:GLY:H	1.80	0.46
1:A:22:LEU:HD13	1:A:31:ALA:CB	2.43	0.46
1:A:166:GLU:HG3	1:A:267:THR:HG22	1.98	0.46
1:A:330:VAL:HG13	1:A:334:GLU:OE2	2.14	0.46
1:A:137:PHE:CE2	1:A:460:ASP:HB2	2.51	0.46
1:A:202:GLU:HA	1:A:228:GLN:O	2.15	0.46
1:A:444:GLY:O	1:A:446:PRO:HD3	2.16	0.46
1:A:305:GLY:HA2	1:A:309:SER:HA	1.96	0.46
1:A:338:PHE:CD1	1:A:338:PHE:N	2.84	0.45
1:A:525:ARG:HH11	1:A:525:ARG:HG2	1.80	0.45
1:A:366:GLY:C	1:A:368:PRO:HD3	2.40	0.45
1:A:135:GLY:HA2	1:A:146:LEU:HD22	1.99	0.45
1:A:428:TYR:HB2	1:A:513:LEU:HD23	1.99	0.45
1:A:194:PRO:HD2	1:A:195:MET:SD	2.57	0.45
1:A:36:PRO:HB3	1:A:98:TYR:CE1	2.52	0.45
1:A:48:MET:HB3	1:A:49:PRO:HD2	2.00	0.44
1:A:252:ALA:CB	1:A:269:LEU:HD11	2.47	0.44
1:A:319:GLY:O	1:A:421:GLN:HG2	2.17	0.44
1:A:466:THR:OG1	1:A:469:GLU:HG3	2.18	0.44
1:A:156:PHE:HZ	1:A:278:ALA:HA	1.82	0.44
1:A:37:PHE:CD2	1:A:99:LEU:HD23	2.53	0.44
1:A:199:LEU:HD11	1:A:222:PHE:CE2	2.52	0.44
1:A:101:VAL:HG22	1:A:147:VAL:HG22	1.98	0.44
1:A:36:PRO:HA	1:A:98:TYR:CD1	2.53	0.43
1:A:439:TRP:HB3	1:A:443:MET:SD	2.59	0.43
1:A:173:LEU:O	1:A:176:GLN:HG2	2.19	0.43
2:F:2:MET:HB2	2:F:57:ASP:HB3	2.00	0.43
1:A:211:MET:HB2	1:A:211:MET:HE2	1.77	0.43
1:A:339:LEU:HD13	1:A:346:PHE:CE1	2.52	0.43
1:A:135:GLY:CA	1:A:146:LEU:HD22	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:PHE:HD1	1:A:200:PHE:H	1.64	0.43
1:A:414:LEU:O	1:A:418:LEU:HB2	2.18	0.43
2:F:5:SER:O	2:F:6:HIS:HB3	2.18	0.43
1:A:276:ARG:HA	1:A:277:PRO:HD3	1.67	0.43
1:A:387:HIS:N	1:A:388:PRO:CD	2.81	0.43
1:A:176:GLN:OE1	1:A:212:HIS:CE1	2.71	0.43
1:A:276:ARG:HD2	1:A:280:ASP:OD2	2.19	0.43
1:A:459:LEU:HD11	1:A:477:MET:SD	2.58	0.43
1:A:316:ILE:HG22	1:A:417:ARG:HG2	2.01	0.43
1:A:426:TYR:CE2	1:A:489:PRO:HD2	2.54	0.42
1:A:18:ARG:O	1:A:18:ARG:HG3	2.19	0.42
1:A:227:LEU:HD12	1:A:227:LEU:N	2.34	0.42
1:A:362:GLY:HA3	1:A:398:MET:HE3	2.00	0.42
1:A:409:CYS:HB3	1:A:533:ASN:HD21	1.84	0.42
2:F:6:HIS:CE1	2:F:37:ARG:HH11	2.37	0.42
1:A:42:VAL:HG12	1:A:94:GLU:HB2	2.00	0.42
1:A:177:ARG:NH2	1:A:217:PRO:HB2	2.34	0.42
1:A:509:GLN:HA	1:A:521:ARG:O	2.18	0.42
1:A:294:ILE:HD13	1:A:343:VAL:CG2	2.50	0.42
1:A:365:ILE:O	1:A:368:PRO:HD3	2.20	0.42
2:F:6:HIS:CE1	2:F:37:ARG:NH1	2.87	0.42
1:A:17:LEU:CD2	1:A:35:ILE:HG12	2.50	0.41
1:A:331:VAL:HG22	1:A:334:GLU:CD	2.45	0.41
1:A:481:THR:O	1:A:485:ARG:HG3	2.20	0.41
1:A:228:GLN:HE21	1:A:480:TRP:HE1	1.68	0.41
1:A:304:ASP:OD2	1:A:306:ASP:HB3	2.20	0.41
1:A:286:TRP:CH2	2:F:33:MET:HE3	2.55	0.41
1:A:390:ASP:HA	1:A:391:PRO:HD2	1.89	0.41
1:A:536:LEU:HD22	1:A:536:LEU:HA	1.87	0.41
1:A:289:LEU:HD13	1:A:298:SER:HB3	2.02	0.41
1:A:380:LEU:HA	1:A:385:TRP:HZ2	1.86	0.41
1:A:12:VAL:C	1:A:14:GLY:H	2.29	0.41
1:A:76:LEU:HD22	1:A:341:TYR:CE2	2.56	0.41
1:A:339:LEU:HD11	1:A:399:SER:HB2	2.02	0.41
1:A:385:TRP:C	1:A:388:PRO:HD3	2.46	0.41
1:A:30:SER:HB2	1:A:103:THR:HG1	1.84	0.41
1:A:105:TYR:HA	1:A:106:PRO:HA	1.89	0.40
1:A:289:LEU:HD21	1:A:296:ARG:O	2.21	0.40
1:A:366:GLY:O	1:A:368:PRO:HD3	2.21	0.40
1:A:497:SER:O	1:A:499:GLN:N	2.55	0.40
1:A:511:VAL:HG11	1:A:518:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:LEU:HD23	1:A:539:LEU:HA	1.90	0.40
1:A:28:PRO:HB2	1:A:105:TYR:HB3	2.02	0.40
1:A:138:LEU:HB3	1:A:146:LEU:HD21	2.03	0.40
1:A:159:LEU:HD23	1:A:159:LEU:C	2.46	0.40
1:A:317:ASN:ND2	1:A:417:ARG:HE	2.20	0.40
1:A:290:PRO:HB2	1:A:291:GLN:OE1	2.22	0.40
1:A:370:ALA:HB1	1:A:374:ALA:HB3	2.03	0.40
1:A:380:LEU:C	1:A:380:LEU:HD23	2.46	0.40
1:A:439:TRP:HB3	1:A:440:PRO:HD2	2.03	0.40
1:A:36:PRO:HB2	1:A:53:LYS:HD3	2.04	0.40
1:A:117:TRP:CE3	1:A:200:PHE:CE2	3.09	0.40
1:A:187:ILE:HD12	1:A:187:ILE:HA	1.95	0.40
1:A:114:VAL:C	1:A:115:LEU:HD12	2.47	0.40
1:A:243:GLU:OE1	1:A:247:ARG:NE	2.55	0.40
1:A:283:ASP:HB3	1:A:284:HIS:HD2	1.87	0.40
1:A:289:LEU:HD12	1:A:289:LEU:HA	1.74	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	529/543 (97%)	458 (87%)	56 (11%)	15 (3%)	4	25
2	F	59/61 (97%)	52 (88%)	6 (10%)	1 (2%)	7	35
All	All	588/604 (97%)	510 (87%)	62 (10%)	16 (3%)	4	25

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	PRO
1	A	323	ASP

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Mol	Chain	Res	Type
1	A	372	ASP
1	A	13	ARG
1	A	492	PRO
1	A	523	GLY
1	A	121	GLY
1	A	196	SER
1	A	219	ARG
1	A	332	LYS
1	A	186	ASN
1	A	290	PRO
1	A	162	PRO
1	A	256	GLY
1	A	497	SER
2	F	56	PRO

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	430/443 (97%)	389 (90%)	41 (10%)	8	32
2	F	54/55 (98%)	52 (96%)	2 (4%)	30	63
All	All	484/498 (97%)	441 (91%)	43 (9%)	9	34

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	12	VAL
1	A	33	LEU
1	A	60	LEU
1	A	110	SER
1	A	149	MET
1	A	161	LEU
1	A	178	LEU
1	A	180	LEU

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Mol	Chain	Res	Type
1	A	195	MET
1	A	199	LEU
1	A	216	LEU
1	A	266	ASP
1	A	275	THR
1	A	289	LEU
1	A	309	SER
1	A	322	GLN
1	A	324	LEU
1	A	327	LEU
1	A	328	VAL
1	A	353	LEU
1	A	380	LEU
1	A	386	LEU
1	A	395	ARG
1	A	399	SER
1	A	408	VAL
1	A	417	ARG
1	A	418	LEU
1	A	421	GLN
1	A	437	LEU
1	A	438	THR
1	A	468	GLU
1	A	474	GLN
1	A	476	LEU
1	A	478	LYS
1	A	499	GLN
1	A	524	LEU
1	A	527	GLN
1	A	536	LEU
1	A	539	LEU
1	A	540	LEU
2	F	8	THR
2	F	48	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	87	ASN
1	A	140	GLN
1	A	181	GLN

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Mol	Chain	Res	Type
1	A	184	GLN
1	A	212	HIS
1	A	228	GLN
1	A	284	HIS
1	A	317	ASN
1	A	322	GLN
1	A	413	GLN
1	A	432	HIS
1	A	474	GLN
1	A	482	ASN
1	A	533	ASN
2	F	6	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	NAG	A	544	1	14,14,15	0.76	0	17,19,21	0.79	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
3	NAG	A	544	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	544	NAG	C1-C2-N2-C7
3	A	544	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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.