



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Mar 2, 2017 – 12:24 pm GMT

PDB ID : 5FN4
EMDB ID: : EMD-3239
Title : Cryo-EM structure of gamma secretase in class 2 of the apo- state ensemble
Authors : Bai, X.C.; Rajendra, E.; Yang, G.H.; Shi, Y.G.; Scheres, S.H.W.
Deposited on : 2015-11-10
Resolution : 4.00 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

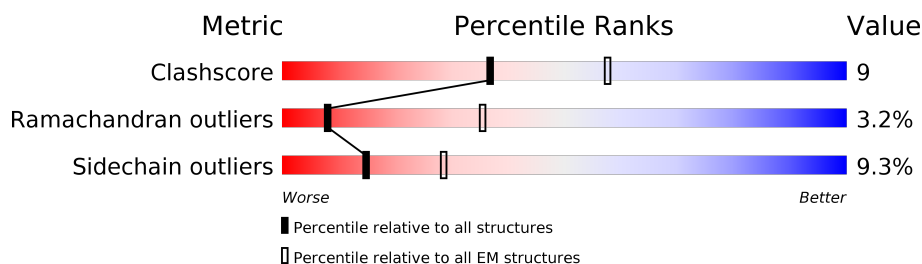
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	709	67% 24% • 6%
2	B	467	27% 17% • 54%
3	C	265	67% 22% • 8%
4	D	101	82% 14% • •
5	G	25	84% 8% 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9776 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 NICASTRIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	665	Total	C	N	O	S	0	0
			5222	3312	888	1001	21		

- Molecule 2 is a protein called PRESENILIN-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	217	Total	C	N	O	S	0	0
			1714	1180	251	274	9		

- Molecule 3 is a protein called GAMMA-SECRETASE SUBUNIT APH-1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	243	Total	C	N	O	S	0	0
			1868	1252	299	313	4		

- Molecule 4 is a protein called GAMMA-SECRETASE SUBUNIT PEN-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	100	Total	C	N	O	S	0	0
			847	579	133	134	1		

- Molecule 5 is a protein called POLY ALA CHAIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	25	Total	C	N	O	0	0
			125	75	25	25		

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	79263	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	35714	Depositor
Image detector	GATAN K2 QUANTUM (4K X 4K)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.47	0/5345	0.77	1/7284 (0.0%)
2	B	0.57	0/1759	0.89	1/2399 (0.0%)
3	C	0.58	1/1920 (0.1%)	0.87	0/2619
4	D	0.64	0/880	0.89	1/1201 (0.1%)
5	G	0.58	0/124	1.20	2/172 (1.2%)
All	All	0.52	1/10028 (0.0%)	0.83	5/13675 (0.0%)

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	A	0	1
2	B	0	1
5	G	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	244	LEU	C-O	7.93	1.38	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	22	ALA	O-C-N	-8.12	109.70	122.70
5	G	21	ALA	O-C-N	-8.11	109.73	122.70
1	A	312	LEU	CA-CB-CG	5.83	128.70	115.30
2	B	173	LEU	CA-CB-CG	5.33	127.56	115.30
4	D	36	TRP	CB-CA-C	-5.11	100.17	110.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	PHE	Peptide
2	B	435	LEU	Peptide
5	G	21	ALA	Mainchain
5	G	22	ALA	Mainchain

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	5222	0	5120	93	0
2	B	1714	0	1810	59	0
3	C	1868	0	1907	46	0
4	D	847	0	836	8	0
5	G	125	0	127	5	0
All	All	9776	0	9800	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 9.

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:260:LEU:HD11	1:A:318:VAL:HG13	1.63	0.80
2:B:174:LEU:HG	2:B:229:ILE:HD11	1.65	0.78
2:B:96:VAL:HG21	2:B:390:SER:HB3	1.65	0.77
1:A:672:THR:HG23	3:C:158:LEU:HD13	1.69	0.73
3:C:170:LEU:HD21	3:C:200:THR:HG21	1.71	0.69
3:C:17:ALA:HB2	3:C:168:ILE:HG21	1.73	0.68
2:B:406:THR:HA	2:B:449:THR:HG21	1.75	0.68
2:B:387:ILE:O	2:B:391:VAL:HG23	1.95	0.66
1:A:162:ILE:HD11	1:A:164:TRP:CE2	2.30	0.66
3:C:40:PHE:O	3:C:44:VAL:HG23	1.97	0.64
1:A:181:PHE:CD1	1:A:217:LEU:HD21	2.32	0.64
4:D:98:LEU:O	4:D:100:THR:N	2.30	0.63
2:B:104:SER:O	2:B:106:TYR:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:LEU:HD11	1:A:439:VAL:HG21	1.82	0.62
2:B:176:PHE:CZ	5:G:17:ALA:HB1	2.36	0.61
2:B:234:ALA:HA	2:B:391:VAL:HG22	1.82	0.61
1:A:516:GLN:O	1:A:519:THR:HG22	2.00	0.61
2:B:208:VAL:O	2:B:211:ILE:HG13	2.01	0.61
1:A:225:ILE:HG21	1:A:229:THR:HG21	1.82	0.60
3:C:179:PHE:O	3:C:182:CYS:SG	2.60	0.60
2:B:176:PHE:CZ	5:G:17:ALA:CB	2.84	0.60
1:A:299:VAL:HA	1:A:302:PHE:CE2	2.38	0.58
1:A:280:THR:HG21	1:A:302:PHE:HA	1.84	0.58
1:A:121:LEU:HD23	1:A:178:PHE:CE1	2.38	0.58
3:C:24:THR:HG21	3:C:119:TYR:CE1	2.38	0.58
1:A:47:THR:HG22	1:A:183:LEU:HD22	1.86	0.58
1:A:683:SER:HB2	3:C:16:PRO:HA	1.86	0.58
1:A:249:ASP:HB3	1:A:557:VAL:HG11	1.86	0.58
2:B:408:ILE:HD13	3:C:131:VAL:HG11	1.86	0.58
1:A:73:ILE:HD13	1:A:660:ILE:HD11	1.85	0.57
3:C:174:TRP:CZ2	3:C:197:HIS:HA	2.39	0.57
1:A:36:VAL:HG21	3:C:137:ILE:HG22	1.85	0.57
1:A:362:PHE:CD1	1:A:427:LEU:HD13	2.39	0.57
1:A:111:LEU:HG	1:A:118:ILE:HD13	1.85	0.57
1:A:371:ARG:NH2	1:A:486:ALA:HB1	2.19	0.57
1:A:54:LEU:HD11	1:A:223:ALA:HB1	1.87	0.57
1:A:124:SER:OG	1:A:189:THR:HG21	2.05	0.57
1:A:256:VAL:HG21	1:A:567:VAL:HG12	1.84	0.57
1:A:222:HIS:HB2	1:A:247:VAL:HG23	1.87	0.56
1:A:260:LEU:HD13	1:A:312:LEU:CD1	2.35	0.56
2:B:198:VAL:HG21	4:D:94:PHE:CD2	2.41	0.56
2:B:223:GLN:O	2:B:227:ILE:HG23	2.06	0.56
4:D:81:TYR:O	4:D:85:TRP:N	2.38	0.56
3:C:25:VAL:HG12	3:C:32:VAL:HG22	1.87	0.55
1:A:534:PHE:CE2	1:A:566:VAL:HG11	2.40	0.55
1:A:683:SER:CB	3:C:16:PRO:HA	2.37	0.55
1:A:210:PHE:CE1	1:A:212:LEU:HD12	2.41	0.55
1:A:422:LEU:HD22	1:A:428:GLN:HB3	1.88	0.55
1:A:307:ALA:HB2	1:A:518:VAL:HG22	1.88	0.54
3:C:192:LEU:HD13	3:C:227:TRP:HH2	1.72	0.54
1:A:111:LEU:HD23	1:A:118:ILE:HG21	1.90	0.54
1:A:54:LEU:HD11	1:A:223:ALA:CB	2.38	0.53
3:C:159:THR:HG21	3:C:210:TYR:CE1	2.43	0.53
1:A:679:ILE:HG21	3:C:12:VAL:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:406:THR:HG23	2:B:449:THR:HB	1.91	0.53
1:A:463:ILE:HG23	1:A:465:VAL:HG23	1.91	0.52
3:C:116:GLN:O	3:C:120:VAL:HG13	2.08	0.52
1:A:385:GLN:O	1:A:391:ARG:HB2	2.10	0.52
2:B:448:ALA:HB1	3:C:47:LEU:HD21	1.91	0.52
2:B:402:GLY:N	2:B:454:GLN:HG3	2.25	0.52
2:B:250:LEU:HB3	2:B:443:LEU:HD11	1.92	0.52
1:A:282:LEU:HD13	1:A:329:PHE:HB3	1.92	0.52
2:B:106:TYR:CE1	2:B:235:LEU:HB3	2.44	0.51
1:A:101:LYS:HG3	1:A:126:THR:HG21	1.92	0.51
1:A:56:ALA:HA	1:A:227:THR:HG22	1.92	0.51
1:A:370:LEU:N	1:A:443:ASP:OD2	2.44	0.51
2:B:207:VAL:HB	4:D:26:LEU:HD21	1.92	0.51
1:A:121:LEU:CB	1:A:180:ILE:HG23	2.42	0.50
1:A:258:SER:HB2	1:A:571:LEU:HD21	1.92	0.50
1:A:684:LEU:O	1:A:688:TYR:HB2	2.11	0.50
2:B:174:LEU:HD22	2:B:206:GLY:HA2	1.94	0.50
3:C:216:PRO:O	3:C:220:VAL:HG23	2.11	0.50
1:A:365:LEU:N	1:A:365:LEU:HD12	2.26	0.50
1:A:635:PHE:CZ	1:A:649:THR:HG23	2.47	0.50
3:C:215:LEU:HB3	3:C:216:PRO:HD3	1.94	0.50
1:A:192:ILE:HG12	1:A:660:ILE:HD13	1.94	0.50
2:B:92:CYS:O	2:B:96:VAL:HG23	2.11	0.50
2:B:91:LEU:HD13	2:B:227:ILE:HD13	1.94	0.49
1:A:121:LEU:HB3	1:A:180:ILE:HG23	1.95	0.49
1:A:376:LEU:HD22	1:A:490:VAL:HG13	1.95	0.49
2:B:244:TRP:CE3	2:B:244:TRP:HA	2.48	0.49
3:C:35:LEU:O	3:C:124:SER:OG	2.13	0.48
1:A:309:ALA:HA	1:A:327:PHE:CZ	2.47	0.48
1:A:390:VAL:O	1:A:394:VAL:HG23	2.12	0.48
1:A:277:VAL:HG23	1:A:359:VAL:HG13	1.94	0.48
1:A:73:ILE:HG21	1:A:660:ILE:HD11	1.96	0.48
1:A:376:LEU:CD2	1:A:490:VAL:HG13	2.44	0.48
2:B:250:LEU:HD13	2:B:443:LEU:HD21	1.94	0.48
3:C:123:LEU:HD22	3:C:127:ILE:CD1	2.44	0.48
2:B:459:GLN:HG2	3:C:72:LEU:HD11	1.95	0.48
3:C:176:VAL:HG11	3:C:228:ALA:HB1	1.96	0.48
2:B:106:TYR:CD2	2:B:235:LEU:HD22	2.49	0.48
3:C:174:TRP:CH2	3:C:197:HIS:HA	2.49	0.48
1:A:335:PHE:O	1:A:338:ILE:HG23	2.14	0.48
1:A:303:VAL:HG21	1:A:522:LEU:HD12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:122:GLY:HA3	3:C:172:THR:HA	1.94	0.47
1:A:279:ALA:O	1:A:305:GLN:NE2	2.47	0.47
1:A:111:LEU:CG	1:A:118:ILE:HD13	2.43	0.47
2:B:421:THR:HG21	2:B:434:ALA:HA	1.96	0.47
2:B:466:TYR:CE2	3:C:163:LEU:HD23	2.49	0.47
2:B:390:SER:O	2:B:393:VAL:HG12	2.15	0.47
2:B:218:PRO:HG3	4:D:36:TRP:CZ2	2.50	0.47
5:G:22:ALA:O	5:G:23:ALA:C	2.51	0.47
1:A:96:VAL:HG23	1:A:121:LEU:HD13	1.97	0.47
1:A:365:LEU:HD11	1:A:494:LEU:CD1	2.45	0.47
1:A:653:TRP:CD1	1:A:656:ILE:HG23	2.49	0.47
3:C:137:ILE:HD11	3:C:160:SER:HB3	1.95	0.47
1:A:303:VAL:HG11	1:A:522:LEU:HD13	1.96	0.47
1:A:111:LEU:CD2	1:A:118:ILE:HG21	2.44	0.47
1:A:126:THR:HG22	1:A:128:PRO:HD2	1.96	0.47
5:G:21:ALA:O	5:G:22:ALA:C	2.51	0.47
1:A:300:ALA:O	1:A:304:THR:HG23	2.15	0.47
2:B:411:PHE:O	2:B:415:LEU:HD13	2.14	0.47
1:A:72:VAL:HG13	1:A:94:TYR:CE1	2.49	0.47
2:B:452:LEU:HD13	3:C:51:VAL:HG22	1.97	0.46
2:B:181:TYR:O	2:B:185:VAL:HG23	2.14	0.46
1:A:368:VAL:HG13	1:A:376:LEU:HD13	1.97	0.46
3:C:196:SER:O	3:C:200:THR:HG23	2.15	0.46
2:B:402:GLY:O	2:B:404:TRP:N	2.48	0.46
2:B:410:CYS:SG	2:B:446:TYR:HB2	2.55	0.46
1:A:42:ILE:HD11	3:C:150:HIS:CD2	2.51	0.46
2:B:227:ILE:HG13	2:B:228:MET:N	2.29	0.46
2:B:453:VAL:HA	3:C:50:SER:HB2	1.97	0.46
1:A:371:ARG:N	1:A:443:ASP:OD2	2.48	0.46
2:B:173:LEU:HA	2:B:177:PHE:CD2	2.51	0.46
2:B:417:GLY:HA3	2:B:438:SER:HA	1.98	0.46
2:B:432:LEU:N	2:B:433:PRO:CD	2.79	0.46
1:A:529:ALA:HB2	1:A:551:LEU:HG	1.98	0.45
1:A:365:LEU:HD11	1:A:494:LEU:HD11	1.98	0.45
2:B:408:ILE:O	2:B:412:VAL:HG23	2.15	0.45
1:A:36:VAL:HG21	3:C:137:ILE:CG2	2.47	0.45
2:B:420:LEU:O	2:B:424:LEU:HG	2.16	0.45
1:A:237:GLN:O	1:A:244:PRO:HB3	2.17	0.45
4:D:66:PHE:O	4:D:69:ILE:HG22	2.16	0.45
2:B:182:LEU:HD23	2:B:198:VAL:HG13	1.97	0.45
1:A:40:ILE:HD11	3:C:157:PHE:HZ	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LEU:HA	1:A:122:ALA:HB3	1.98	0.45
2:B:466:TYR:CD2	3:C:163:LEU:HD23	2.52	0.45
3:C:197:HIS:O	3:C:200:THR:OG1	2.25	0.45
2:B:176:PHE:CZ	5:G:17:ALA:HB2	2.52	0.44
1:A:538:LEU:HD23	1:A:569:TYR:CG	2.52	0.44
1:A:492:THR:HG23	1:A:512:GLN:HA	2.00	0.44
3:C:147:VAL:HG12	3:C:148:GLY:N	2.33	0.44
1:A:275:VAL:HG12	1:A:324:ASN:HB3	1.99	0.44
1:A:427:LEU:HD11	1:A:438:GLY:HA3	2.00	0.44
2:B:103:VAL:O	2:B:104:SER:CB	2.66	0.44
3:C:134:VAL:O	3:C:137:ILE:N	2.47	0.44
1:A:74:HIS:HA	1:A:196:TYR:CE1	2.54	0.43
2:B:211:ILE:HD12	2:B:212:SER:N	2.34	0.43
2:B:244:TRP:HA	2:B:244:TRP:HE3	1.83	0.43
1:A:162:ILE:HD12	1:A:163:GLN:N	2.33	0.42
1:A:542:LEU:HD21	1:A:565:TYR:CD1	2.54	0.42
1:A:54:LEU:HD13	1:A:226:SER:O	2.20	0.42
1:A:282:LEU:HD11	1:A:567:VAL:HG21	2.01	0.42
3:C:134:VAL:HG22	3:C:138:LEU:CD1	2.49	0.42
3:C:192:LEU:HD13	3:C:227:TRP:CH2	2.53	0.42
2:B:449:THR:HA	2:B:453:VAL:HB	2.00	0.42
3:C:73:ILE:HG23	3:C:205:PHE:CE2	2.54	0.42
2:B:230:SER:HA	2:B:387:ILE:HG12	2.01	0.42
1:A:673:LEU:C	1:A:673:LEU:HD23	2.41	0.42
2:B:200:LEU:HD23	2:B:201:LEU:N	2.35	0.42
1:A:42:ILE:HD12	3:C:149:ILE:HG12	2.02	0.42
3:C:42:TRP:CZ3	3:C:43:LEU:HD23	2.54	0.42
2:B:204:ASN:O	2:B:208:VAL:HG22	2.19	0.42
2:B:424:LEU:O	2:B:428:PHE:N	2.52	0.41
1:A:42:ILE:HG13	3:C:149:ILE:HG21	2.01	0.41
2:B:209:GLY:O	2:B:213:ILE:HG12	2.20	0.41
1:A:328:VAL:C	1:A:329:PHE:CD1	2.94	0.41
2:B:182:LEU:HG	2:B:186:PHE:CE2	2.56	0.41
1:A:259:MET:SD	1:A:326:MET:HA	2.61	0.41
1:A:662:LEU:HD13	3:C:149:ILE:N	2.34	0.41
2:B:171:LEU:HD23	2:B:172:LEU:N	2.36	0.41
2:B:257:ASP:O	2:B:261:VAL:HG23	2.21	0.41
1:A:162:ILE:HD11	1:A:164:TRP:CD2	2.56	0.40
4:D:98:LEU:N	4:D:98:LEU:CD1	2.83	0.40
1:A:278:ALA:O	1:A:305:GLN:NE2	2.54	0.40
2:B:99:THR:CG2	2:B:235:LEU:HD21	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:211:ILE:HD13	4:D:18:TYR:OH	2.21	0.40
3:C:141:ALA:HB2	3:C:157:PHE:CE1	2.57	0.40
1:A:385:GLN:HE22	1:A:394:VAL:HB	1.87	0.40
1:A:534:PHE:CD2	1:A:566:VAL:HG11	2.56	0.40
2:B:96:VAL:O	2:B:99:THR:HG22	2.22	0.40
1:A:261:LYS:HB2	1:A:324:ASN:HD21	1.87	0.40
1:A:40:ILE:HD11	3:C:157:PHE:CZ	2.56	0.40
1:A:442:ALA:HB1	1:A:444:HIS:CE1	2.57	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 PDB entries followed by that with respect to all EM entries.

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	663/709 (94%)	525 (79%)	108 (16%)	30 (4%)	3	31
2	B	210/467 (45%)	191 (91%)	12 (6%)	7 (3%)	4	39
3	C	241/265 (91%)	218 (90%)	21 (9%)	2 (1%)	22	66
4	D	98/101 (97%)	90 (92%)	7 (7%)	1 (1%)	18	61
5	G	23/25 (92%)	23 (100%)	0	0	100	100
All	All	1235/1567 (79%)	1047 (85%)	148 (12%)	40 (3%)	8	39

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	289	TRP
1	A	333	GLU
1	A	473	PRO
2	B	104	SER
2	B	105	PHE
3	C	156	TYR

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Mol	Chain	Res	Type
4	D	99	GLY
1	A	159	CYS
1	A	211	PRO
1	A	322	PRO
1	A	372	THR
1	A	421	PRO
1	A	472	SER
2	B	403	ASP
1	A	103	PHE
1	A	294	GLY
1	A	298	ALA
1	A	358	ASN
1	A	436	ILE
1	A	655	ASP
2	B	216	LYS
1	A	185	ASP
1	A	559	SER
1	A	630	ALA
2	B	107	THR
1	A	163	GLN
1	A	332	GLY
1	A	632	SER
2	B	215	TRP
1	A	129	SER
1	A	416	PRO
1	A	593	PRO
3	C	207	ASN
1	A	113	GLY
1	A	316	PRO
1	A	318	VAL
1	A	359	VAL
1	A	511	VAL
1	A	40	ILE
2	B	432	LEU

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 PDB entries followed by that with respect to all EM entries.

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	583/612 (95%)	535 (92%)	48 (8%)	13	47
2	B	185/408 (45%)	158 (85%)	27 (15%)	3	24
3	C	192/214 (90%)	178 (93%)	14 (7%)	16	52
4	D	87/89 (98%)	79 (91%)	8 (9%)	11	42
All	All	1047/1323 (79%)	950 (91%)	97 (9%)	15	42

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LYS
1	A	83	GLN
1	A	100	SER
1	A	107	LEU
1	A	139	GLN
1	A	140	CYS
1	A	151	SER
1	A	163	GLN
1	A	167	LEU
1	A	174	GLU
1	A	210	PHE
1	A	218	PHE
1	A	224	VAL
1	A	237	GLN
1	A	249	ASP
1	A	257	TRP
1	A	264	ASN
1	A	269	LEU
1	A	285	ARG
1	A	301	SER
1	A	302	PHE
1	A	312	LEU
1	A	331	GLN
1	A	333	GLU
1	A	343	MET
1	A	347	MET
1	A	370	LEU
1	A	378	MET
1	A	413	LEU
1	A	431	LEU
1	A	450	ASN
1	A	457	TYR
1	A	459	THR

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Mol	Chain	Res	Type
1	A	463	ILE
1	A	472	SER
1	A	474	GLU
1	A	481	THR
1	A	561	THR
1	A	565	TYR
1	A	573	ASN
1	A	574	LEU
1	A	586	CYS
1	A	588	ASP
1	A	604	TRP
1	A	610	HIS
1	A	644	GLU
1	A	649	THR
1	A	670	LEU
2	B	81	HIS
2	B	91	LEU
2	B	167	ILE
2	B	171	LEU
2	B	174	LEU
2	B	184	GLU
2	B	200	LEU
2	B	201	LEU
2	B	202	ILE
2	B	211	ILE
2	B	230	SER
2	B	241	LEU
2	B	244	TRP
2	B	248	LEU
2	B	255	VAL
2	B	381	LEU
2	B	383	LEU
2	B	385	ASP
2	B	386	PHE
2	B	392	LEU
2	B	419	CYS
2	B	425	LEU
2	B	429	LYS
2	B	438	SER
2	B	445	PHE
2	B	458	ASP
2	B	459	GLN

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Mol	Chain	Res	Type
3	C	46	LEU
3	C	68	GLN
3	C	93	LEU
3	C	112	ILE
3	C	114	ILE
3	C	120	VAL
3	C	123	LEU
3	C	127	ILE
3	C	131	VAL
3	C	134	VAL
3	C	135	ILE
3	C	137	ILE
3	C	192	LEU
3	C	218	TYR
4	D	9	GLU
4	D	14	LEU
4	D	40	GLU
4	D	47	TYR
4	D	58	TRP
4	D	66	PHE
4	D	75	ILE
4	D	85	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	HIS
1	A	163	GLN
1	A	305	GLN
1	A	417	ASN
1	A	478	ASN
1	A	587	GLN
3	C	68	GLN
4	D	50	GLN

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 carbohydrates 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.