Full wwPDB Geometry-Only Validation Report (i)

Feb 10, 2024 – 08:44 PM EST

PDB ID	:	2QFG
Title	:	Solution Structure of the N-terminal SCR-1/5 fragment of Complement Factor H.
Authors	:	Okemefuna, A.I.; Gilbert, H.E.; Griggs, K.M.; Ormsby, R.J.; Gordon, D.L.; Perkins, S.J.
Deposited on	:	2007-06-27
Resolution	:	Not provided

This is a Full wwPDB Geometry-Only 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 (i) 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 (i)) were used in the production of this report:

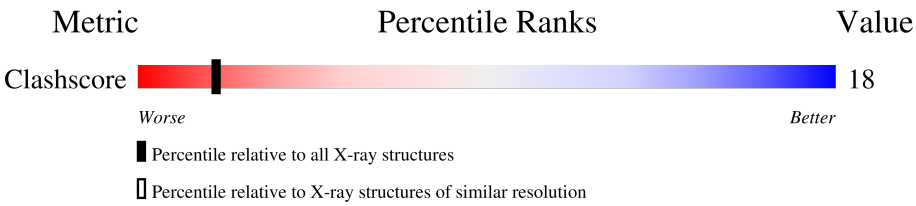
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION SCATTERING

The reported resolution of this entry is unknown.

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	141614	-

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1-A	312	97% .
1	10-A	312	96% .
1	11-A	312	98% .
1	12-A	312	98% .
1	2-A	312	96% .
1	3-A	312	97% .
1	4-A	312	97% .
1	5-A	312	97% .
1	6-A	312	96% .
1	7-A	312	97% .

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Mol	Chain	Length	Quality of chain
1	8-A	312	96%
1	9-A	312	94% 6%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 3744 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 Complement factor H.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	1-A	312	Total C 312 312	0	0	312
1	2-A	312	Total C 312 312	0	0	312
1	3-A	312	Total C 312 312	0	0	312
1	4-A	312	Total C 312 312	0	0	312
1	5-A	312	Total C 312 312	0	0	312
1	6-A	312	Total C 312 312	0	0	312
1	7-A	312	Total C 312 312	0	0	312
1	8-A	312	Total C 312 312	0	0	312
1	9-A	312	Total C 312 312	0	0	312
1	10-A	312	Total C 312 312	0	0	312
1	11-A	312	Total C 312 312	0	0	312
1	12-A	312	Total C 312 312	0	0	312

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLU	-	expression tag	UNP P08603
A	18	PHE	-	expression tag	UNP P08603
A	323	HIS	-	expression tag	UNP P08603
A	324	HIS	-	expression tag	UNP P08603
A	325	HIS	-	expression tag	UNP P08603

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Chain	Residue	Modelled	Actual	Comment	Reference
A	326	HIS	-	expression tag	UNP P08603
A	327	HIS	-	expression tag	UNP P08603
A	328	HIS	-	expression tag	UNP P08603

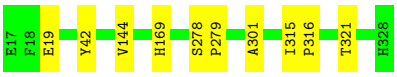
3 Residue-property plots (i)

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: Complement factor H

Chain 1-A: 97%



• Molecule 1: Complement factor H

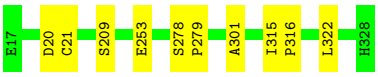
Chain 2-A: 96%

• Molecule 1: Complement factor H

Chain 3-A: 97%

• Molecule 1: Complement factor H

Chain 4-A: 97%



• Molecule 1: Complement factor H

Chain 5-A: 97%

• Molecule 1: Complement factor H

Chain 6-A: 96%

E17 E207 I208 E229 N230 S278 P279 A301 I315 P316 T321 L322 H328

• Molecule 1: Complement factor H

Chain 7-A: 97%

E17 G117 D194 S209 E229 S266 S278 P279 R285 I315 P316 H328

• Molecule 1: Complement factor H

Chain 8-A: 96%

E17 V144 F170 I208 S209 E229 K265 S278 P279 T286 I315 P316 H328

• Molecule 1: Complement factor H

Chain 9-A: 94% 6%

E17 D20 G69 R83 E105 Y106 V144 D194 S209 E242 E253 E263 E264 S278 P279 A301 I315 P316 L322 H328

• Molecule 1: Complement factor H

Chain 10-A: 96%

E17 F18 E19 T41 E153 N154 V206 E207 I208 S209 E253 S278 P279 I315 P316 H328

• Molecule 1: Complement factor H

Chain 11-A: 98%

E17 I208 E253 S278 P279 I315 P316 H328

• Molecule 1: Complement factor H

Chain 12-A: 98%

E17 Y182 V206 S278 P279 I315 P316 H328

4 Model quality (i)

4.1 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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

4.2 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	1-A	312	0	0	5	0
1	2-A	312	0	0	8	0
1	3-A	312	0	0	4	0
1	4-A	312	0	0	5	0
1	5-A	312	0	0	5	0
1	6-A	312	0	0	6	0
1	7-A	312	0	0	5	0
1	8-A	312	0	0	6	0
1	9-A	312	0	0	10	0
1	10-A	312	0	0	7	0
1	11-A	312	0	0	3	0
1	12-A	312	0	0	3	0
All	All	3744	0	0	67	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 18.

All (67) 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:20:ASP:CA	1:A:69:GLY:CA	1.87	1.51
1:A:153:GLU:CA	1:A:207:GLU:CA	1.87	1.50
1:A:301:ALA:CA	1:A:322:LEU:CA	1.91	1.49
1:A:83:ARG:CA	1:A:106:TYR:CA	1.94	1.45
1:A:83:ARG:CA	1:A:105:GLU:CA	1.97	1.41
1:A:19:GLU:CA	1:A:42:TYR:CA	1.97	1.39
1:A:242:GLU:CA	1:A:264:GLU:CA	2.14	1.26
1:A:29:ASN:CA	1:A:82:LYS:CA	2.13	1.26
1:A:83:ARG:CA	1:A:105:GLU:CA	2.14	1.25
1:A:83:ARG:CA	1:A:106:TYR:CA	2.23	1.17
1:A:301:ALA:CA	1:A:321:THR:CA	2.25	1.14
1:A:209:SER:CA	1:A:253:GLU:CA	2.26	1.14
1:A:144:VAL:CA	1:A:194:ASP:CA	2.28	1.11
1:A:208:ILE:CA	1:A:253:GLU:CA	2.31	1.08
1:A:209:SER:CA	1:A:253:GLU:CA	2.36	1.02
1:A:301:ALA:CA	1:A:322:LEU:CA	2.37	1.01
1:A:209:SER:CA	1:A:253:GLU:CA	2.38	1.01
1:A:209:SER:CA	1:A:229:GLU:CA	2.39	1.00
1:A:242:GLU:CA	1:A:263:GLU:CA	2.40	0.99
1:A:20:ASP:CA	1:A:69:GLY:CA	2.45	0.93
1:A:144:VAL:CA	1:A:169:HIS:CA	2.49	0.91
1:A:207:GLU:CA	1:A:230:ASN:CA	2.49	0.91
1:A:208:ILE:CA	1:A:229:GLU:CA	2.63	0.76
1:A:181:GLY:CA	1:A:208:ILE:CA	2.63	0.76
1:A:144:VAL:CA	1:A:194:ASP:CA	2.66	0.73
1:A:144:VAL:CA	1:A:170:PHE:CA	0.72	0.71
1:A:154:ASN:CA	1:A:206:VAL:CA	2.69	0.71
1:A:117:GLY:CA	1:A:194:ASP:CA	2.70	0.68
1:A:265:LYS:CA	1:A:286:THR:CA	2.76	0.64
1:A:208:ILE:CA	1:A:253:GLU:CA	2.76	0.63
1:A:266:SER:CA	1:A:285:ARG:CA	2.78	0.62
1:A:209:SER:CA	1:A:253:GLU:CA	2.78	0.62
1:A:301:ALA:CA	1:A:322:LEU:CA	2.80	0.60
1:A:183:LYS:CA	1:A:207:GLU:CA	2.79	0.60
1:A:208:ILE:CA	1:A:229:GLU:CA	2.83	0.57
1:A:208:ILE:CA	1:A:253:GLU:CA	2.85	0.55
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.53
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.53
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.53
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.53
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.53
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.53
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.52
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.52
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:315:ILE:CA	1:A:316:PRO:CA	2.87	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.52
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.51
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.51
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.51
1:A:278:SER:CA	1:A:279:PRO:CA	2.88	0.51
1:A:301:ALA:CA	1:A:321:THR:CA	2.90	0.49
1:A:182:TYR:CA	1:A:206:VAL:CA	2.91	0.49
1:A:19:GLU:CA	1:A:41:THR:CA	2.93	0.46
1:A:265:LYS:CA	1:A:286:THR:CA	2.94	0.45
1:A:20:ASP:CA	1:A:21:CYS:CA	2.97	0.42
1:A:209:SER:CA	1:A:229:GLU:CA	2.97	0.41
1:A:207:GLU:CA	1:A:230:ASN:CA	2.99	0.41

There are no symmetry-related clashes.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

4.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

4.3.3 RNA (i)

There are no RNA molecules in this entry.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.