



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 10:58 pm BST

PDB ID : 4LOT
Title : C1s CUB2-CCP1-CCP2
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Deposited on : 2013-07-13
Resolution : 2.92 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

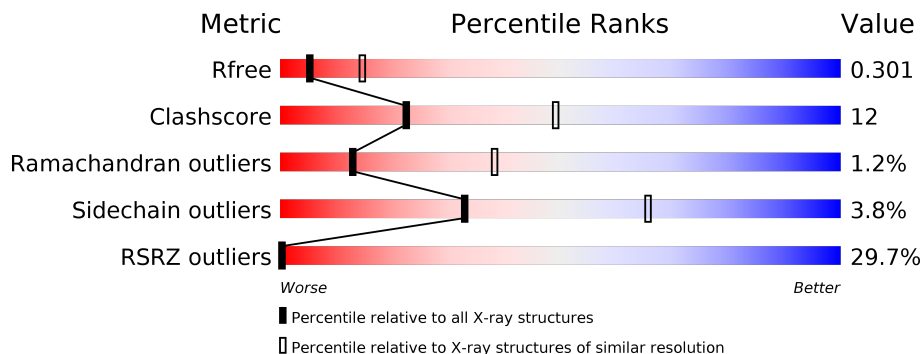
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

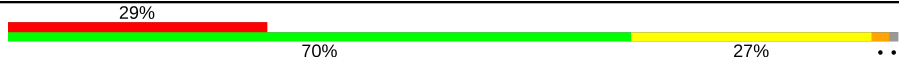
The reported resolution of this entry is 2.92 Å.

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))
R_{free}	130704	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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 on 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	249	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1908 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.

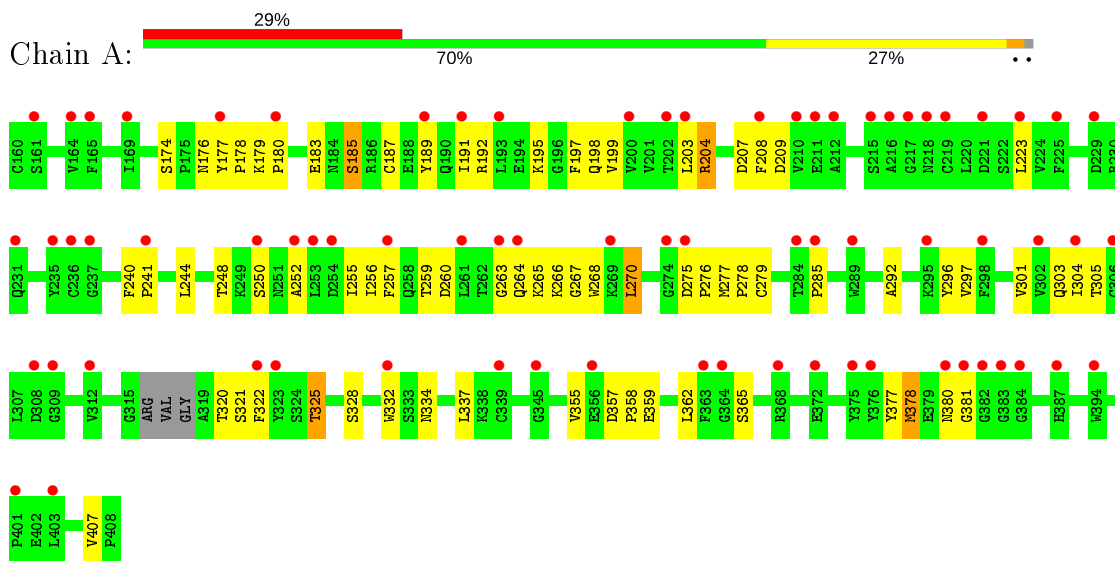
- Molecule 1 is a protein called Complement C1s subcomponent heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	1908	1205	314	375	14	0	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Complement C1s subcomponent heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.04Å 58.59Å 51.21Å 90.00° 91.12° 90.00°	Depositor
Resolution (Å)	54.22 – 2.92 54.22 – 2.85	Depositor EDS
% Data completeness (in resolution range)	92.7 (54.22-2.92) 94.0 (54.22-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.86Å)	Xtrriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.266 , 0.292 0.280 , 0.301	Depositor DCC
R_{free} test set	448 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å ²)	64.5	Xtrriage
Anisotropy	1.039	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 122.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtrriage
Reported twinning fraction	0.050 for -h,-k,l	Depositor
Outliers	3 of 9463 reflections (0.032%)	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1908	wwPDB-VP
Average B, all atoms (Å ²)	132.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [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 >5	RMSZ	# Z >5
1	A	0.28	0/1959	0.50	0/2661

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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	A	1908	0	1791	43	0
All	All	1908	0	1791	43	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 12.

All (43) 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:176:ASN:HB3	1:A:179:LYS:HD2	1.69	0.74
1:A:278:PRO:HA	1:A:297:VAL:HA	1.71	0.73
1:A:203:LEU:HD12	1:A:270:LEU:HB3	1.74	0.70
1:A:203:LEU:HD21	1:A:208:PHE:HB2	1.75	0.69
1:A:263:GLY:O	1:A:265:LYS:N	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:ARG:HB3	1:A:207:ASP:HB2	1.81	0.63
1:A:189:TYR:HB2	1:A:255:ILE:HB	1.83	0.60
1:A:380:ASN:OD1	1:A:381:GLY:N	2.34	0.60
1:A:174:SER:HB3	1:A:268:TRP:H	1.69	0.58
1:A:185:SER:H	1:A:259:THR:HG1	1.53	0.55
1:A:195:LYS:HG2	1:A:328:SER:HB2	1.89	0.55
1:A:187:CYS:HB2	1:A:257:PHE:HB3	1.90	0.53
1:A:199:VAL:O	1:A:248:THR:OG1	2.21	0.53
1:A:359:GLU:OE1	1:A:359:GLU:N	2.41	0.52
1:A:362:LEU:O	1:A:365:SER:OG	2.26	0.51
1:A:197:PHE:HE1	1:A:276:PRO:HG3	1.76	0.51
1:A:378:MET:SD	1:A:380:ASN:ND2	2.84	0.51
1:A:183:GLU:HB2	1:A:260:ASP:O	2.11	0.50
1:A:301:VAL:HG22	1:A:325:THR:HG22	1.94	0.49
1:A:192:ARG:HH21	1:A:252:ALA:HB1	1.77	0.49
1:A:250:SER:OG	1:A:252:ALA:O	2.30	0.48
1:A:198:GLN:HB3	1:A:277:MET:SD	2.53	0.48
1:A:223:LEU:HB2	1:A:257:PHE:HD2	1.78	0.48
1:A:192:ARG:NH2	1:A:252:ALA:HB1	2.29	0.48
1:A:207:ASP:O	1:A:268:TRP:HA	2.15	0.46
1:A:209:ASP:HB3	1:A:267:GLY:H	1.80	0.46
1:A:279:CYS:HB3	1:A:332:TRP:CE2	2.52	0.45
1:A:303:GLN:OE1	1:A:305:THR:OG1	2.34	0.45
1:A:180:PRO:HA	1:A:265:LYS:O	2.17	0.45
1:A:275:ASP:HA	1:A:276:PRO:HD3	1.87	0.45
1:A:191:ILE:O	1:A:192:ARG:HD3	2.18	0.44
1:A:334:ASN:HB3	1:A:337:LEU:HG	2.00	0.44
1:A:223:LEU:HB2	1:A:257:PHE:CD2	2.53	0.43
1:A:177:TYR:CG	1:A:178:PRO:HA	2.53	0.43
1:A:174:SER:O	1:A:177:TYR:HB2	2.19	0.42
1:A:292:ALA:HA	1:A:296:TYR:OH	2.20	0.42
1:A:240:PHE:HA	1:A:241:PRO:HD3	1.68	0.41
1:A:266:LYS:HE2	1:A:266:LYS:HB3	1.79	0.41
1:A:357:ASP:HA	1:A:358:PRO:HD3	1.90	0.41
1:A:304:ILE:HD13	1:A:322:PHE:CE1	2.56	0.41
1:A:377:TYR:N	1:A:407:VAL:O	2.44	0.41
1:A:177:TYR:CD1	1:A:178:PRO:HA	2.56	0.40
1:A:187:CYS:O	1:A:256:ILE:HA	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	242/249 (97%)	216 (89%)	23 (10%)	3 (1%)	13 38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	264	GLN
1	A	285	PRO
1	A	378	MET

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	210/212 (99%)	202 (96%)	8 (4%)	33 65

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	185	SER
1	A	204	ARG
1	A	244	LEU
1	A	270	LEU
1	A	320	THR
1	A	321	SER
1	A	325	THR
1	A	355	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 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.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	246/249 (98%)	1.59	73 (29%) 0 0	78, 128, 193, 263	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	381	GLY	7.1
1	A	263	GLY	6.8
1	A	339	CYS	5.3
1	A	164	VAL	3.8
1	A	309	GLY	3.7
1	A	216	ALA	3.7
1	A	223	LEU	3.7
1	A	189	TYR	3.6
1	A	250	SER	3.5
1	A	382	GLY	3.4
1	A	191	ILE	3.3
1	A	225	PHE	3.3
1	A	363	PHE	3.3
1	A	208	PHE	3.2
1	A	302	VAL	3.2
1	A	375	TYR	3.2
1	A	304	ILE	3.2
1	A	295	LYS	3.1
1	A	323	TYR	3.1
1	A	237	GLY	3.1
1	A	384	GLY	3.1
1	A	312	VAL	3.0
1	A	376	TYR	3.0
1	A	364	GLY	3.0
1	A	368	ARG	3.0
1	A	380	ASN	2.9
1	A	219	CYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	372	GLU	2.8
1	A	322	PHE	2.8
1	A	387	HIS	2.8
1	A	212	ALA	2.8
1	A	394	TRP	2.7
1	A	345	GLY	2.7
1	A	165	PHE	2.6
1	A	275	ASP	2.6
1	A	257	PHE	2.6
1	A	217	GLY	2.6
1	A	169	ILE	2.5
1	A	241	PRO	2.5
1	A	306	CYS	2.5
1	A	289	TRP	2.5
1	A	254	ASP	2.5
1	A	332	TRP	2.4
1	A	261	LEU	2.4
1	A	177	TYR	2.4
1	A	215	SER	2.4
1	A	401	PRO	2.4
1	A	200	VAL	2.4
1	A	218	ASN	2.4
1	A	210	VAL	2.4
1	A	298	PHE	2.4
1	A	308	ASP	2.4
1	A	383	GLY	2.3
1	A	211	GLU	2.3
1	A	284	THR	2.2
1	A	264	GLN	2.2
1	A	356	GLU	2.2
1	A	235	TYR	2.2
1	A	193	LEU	2.2
1	A	202	THR	2.2
1	A	180	PRO	2.2
1	A	403	LEU	2.1
1	A	269	LYS	2.1
1	A	285	PRO	2.1
1	A	161	SER	2.1
1	A	253	LEU	2.1
1	A	252	ALA	2.1
1	A	274	GLY	2.1
1	A	236	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	231	GLN	2.0
1	A	221	ASP	2.0
1	A	203	LEU	2.0
1	A	229	ASP	2.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.