Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 12:03 AM EST

PDB ID	:	3EWI
Title	:	Structural analysis of the C-terminal domain of murine CMP-Sialic acid Synthetase
Authors	:	Oschlies, M.; Dickmanns, A.; Stummeyer, K.; Gerardy-Schahn, R.; Ficner, R.; Muenster-Kuehnel, A.K.
Deposited on	:	2008-10-15
Resolution	:	1.90 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 (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 (1)) were used in the production of this report:

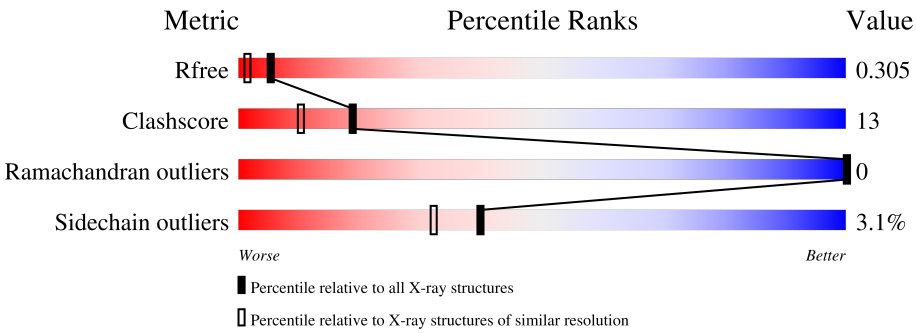
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 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%

Mol	Chain	Length	Quality of chain
1	A	168	76% 16% • 7%
1	B	168	73% 18% • • 6%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2575 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 N-acylneuraminate cytidylyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	157	1192	746	202	232	12	0	3	0
1	B	158	1202	749	205	237	11	0	3	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q99KK2
A	2	SER	-	expression tag	UNP Q99KK2
B	1	GLY	-	expression tag	UNP Q99KK2
B	2	SER	-	expression tag	UNP Q99KK2

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	105	105	105	0	0
2	B	76	76	76	0	0

3 Residue-property plots (i)

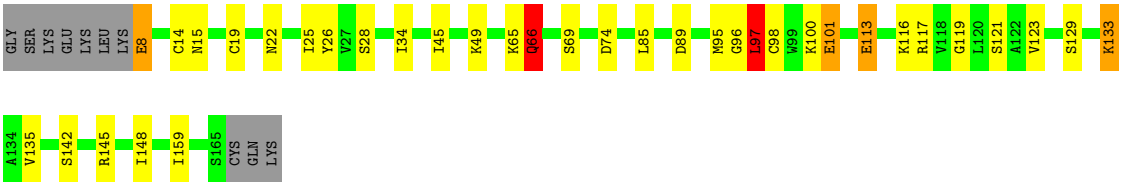
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

- Molecule 1: N-acylneuraminate cytidylyltransferase

Chain A:

- Molecule 1: N-acylneuraminate cytidylyltransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	121.09Å 37.49Å 78.83Å 90.00° 116.30° 90.00°	Depositor
Resolution (Å)	27.43 – 1.90 27.43 – 1.89	Depositor EDS
% Data completeness (in resolution range)	95.2 (27.43-1.90) 95.2 (27.43-1.89)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	3.75 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.206 , 0.250 0.278 , 0.305	Depositor DCC
R_{free} test set	1256 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å^2)	30.3	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 49.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	2575	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.19% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.59	0/1210	0.67	1/1627 (0.1%)
1	B	0.83	5/1220 (0.4%)	0.66	0/1643
All	All	0.72	5/2430 (0.2%)	0.67	1/3270 (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
1	B	0	2
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	96	GLY	C-O	11.83	1.42	1.23
1	B	101	GLU	CD-OE2	6.63	1.32	1.25
1	B	97	LEU	C-O	6.53	1.35	1.23
1	B	89	ASP	C-O	6.46	1.35	1.23
1	B	101	GLU	CD-OE1	6.42	1.32	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	30	ASP	CB-CG-OD1	-5.12	113.70	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	31	GLN	Peptide
1	B	66	GLN	Peptide
1	B	8	GLU	Peptide

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	1192	0	1198	31	0
1	B	1202	0	1200	36	0
2	A	105	0	0	0	0
2	B	76	0	0	0	0
All	All	2575	0	2398	63	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 13.

All (63) 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:B:66:GLN:HG3	1:B:69:SER:OG	1.63	0.99
1:B:97:LEU:HD21	1:B:101:GLU:HB2	1.49	0.93
1:B:97:LEU:CD2	1:B:101:GLU:HB2	2.05	0.86
1:B:65:LYS:O	1:B:66:GLN:OE1	1.93	0.85
1:B:66:GLN:OE1	1:B:66:GLN:HA	1.80	0.80
1:B:129:SER:O	1:B:133:LYS:HE2	1.84	0.76
1:B:8:GLU:HB3	1:B:101:GLU:HG2	1.69	0.75
1:A:156:PHE:O	1:A:159:ILE:HG22	1.88	0.73
1:A:39:VAL:CG2	1:B:25:ILE:HD11	2.20	0.72
1:B:66:GLN:HE21	1:B:69:SER:HB3	1.55	0.71
1:A:106:GLY:O	1:A:123:VAL:HG12	1.94	0.68
1:B:85:LEU:HD11	1:B:117:ARG:HD3	1.76	0.67
1:B:142:SER:HB2	1:B:145[B]:ARG:HD2	1.76	0.66
1:A:107:ASN:ND2	1:A:108:GLU:HG3	2.12	0.64
1:A:29:GLY:C	1:A:31:GLN:H	2.00	0.64
1:B:121:SER:HB2	1:B:135:VAL:HG12	1.80	0.63
1:B:113:GLU:N	1:B:113:GLU:OE1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:LEU:HB2	1:B:113:GLU:HG2	1.81	0.62
1:A:78:GLU:HG3	1:A:91:TRP:HZ2	1.65	0.62
1:A:63:CYS:HB3	1:A:79:VAL:HG11	1.80	0.62
1:B:66:GLN:OE1	1:B:66:GLN:CA	2.39	0.62
1:B:97:LEU:HD23	1:B:98:CYS:H	1.66	0.61
1:A:27:VAL:HA	1:A:31:GLN:HG2	1.82	0.60
1:A:29:GLY:H	1:A:31:GLN:HB2	1.67	0.60
1:A:28:SER:OG	1:A:30:ASP:OD1	2.20	0.60
1:A:29:GLY:C	1:A:31:GLN:N	2.54	0.60
1:A:64:SER:O	1:A:67:THR:HG22	2.02	0.59
1:B:66:GLN:CG	1:B:69:SER:OG	2.48	0.57
1:A:39:VAL:CG2	1:B:25:ILE:CD1	2.82	0.57
1:A:15:ASN:O	1:A:19[A]:CYS:HB3	2.06	0.55
1:B:49:LYS:NZ	1:B:74:ASP:O	2.39	0.55
1:A:15:ASN:ND2	1:A:107:ASN:OD1	2.37	0.54
1:A:64:SER:HB3	1:A:67:THR:HG22	1.89	0.54
1:B:66:GLN:HE21	1:B:69:SER:CB	2.22	0.52
1:B:45:ILE:O	1:B:49:LYS:HG3	2.08	0.52
1:A:99:TRP:CD2	1:A:117:ARG:HG2	2.45	0.52
1:B:97:LEU:HD23	1:B:101:GLU:HB2	1.91	0.52
1:B:95:MET:HG3	1:B:97:LEU:HD12	1.93	0.50
1:B:97:LEU:HD21	1:B:101:GLU:CB	2.31	0.50
1:B:8:GLU:HG2	1:B:101:GLU:HB3	1.92	0.50
1:B:97:LEU:HD23	1:B:98:CYS:N	2.26	0.50
1:A:39:VAL:HG23	1:B:25:ILE:CD1	2.41	0.49
1:A:78:GLU:CG	1:A:91:TRP:HZ2	2.26	0.48
1:B:15:ASN:O	1:B:19:CYS:HB2	2.14	0.48
1:A:64:SER:HB3	1:A:67:THR:CG2	2.43	0.48
1:A:78:GLU:HG3	1:A:91:TRP:CZ2	2.46	0.47
1:B:85:LEU:HD22	1:B:113:GLU:HB2	1.96	0.47
1:B:65:LYS:C	1:B:66:GLN:OE1	2.53	0.46
1:A:26:TYR:HB2	1:A:34:ILE:HB	1.96	0.46
1:A:123:VAL:HG13	1:A:135:VAL:HG11	1.98	0.45
1:B:14[A]:CYS:SG	1:B:148:ILE:HD11	2.57	0.45
1:A:149:ARG:O	1:A:153:GLU:HG2	2.17	0.44
1:A:15:ASN:O	1:A:19[B]:CYS:HB2	2.17	0.44
1:A:39:VAL:HG22	1:B:25:ILE:HD11	1.97	0.43
1:A:109:VAL:HG12	1:A:112:GLU:OE2	2.18	0.43
1:A:19[A]:CYS:SG	1:A:105:LEU:HG	2.59	0.42
1:B:100:LYS:HA	1:B:119:GLY:HA3	2.02	0.42
1:A:30:ASP:OD1	1:A:30:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:ASN:HB2	1:B:145[B]:ARG:NH2	2.36	0.41
1:A:27:VAL:HA	1:A:31:GLN:CG	2.51	0.41
1:B:123:VAL:HG13	1:B:135:VAL:HG11	2.03	0.41
1:A:29:GLY:N	1:A:31:GLN:HB2	2.34	0.40
1:B:26:TYR:HB2	1:B:34:ILE: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	158/168 (94%)	150 (95%)	8 (5%)	0	100	100
1	B	159/168 (95%)	151 (95%)	8 (5%)	0	100	100
All	All	317/336 (94%)	301 (95%)	16 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	129/142 (91%)	128 (99%)	1 (1%)	81	82
1	B	131/142 (92%)	124 (95%)	7 (5%)	22	13
All	All	260/284 (92%)	252 (97%)	8 (3%)	40	32

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

Mol	Chain	Res	Type
1	A	117	ARG
1	B	28	SER
1	B	66	GLN
1	B	97	LEU
1	B	113	GLU
1	B	116	LYS
1	B	133	LYS
1	B	159	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	132	GLN

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 monosaccharides 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 (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.