Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 09:48 pm GMT

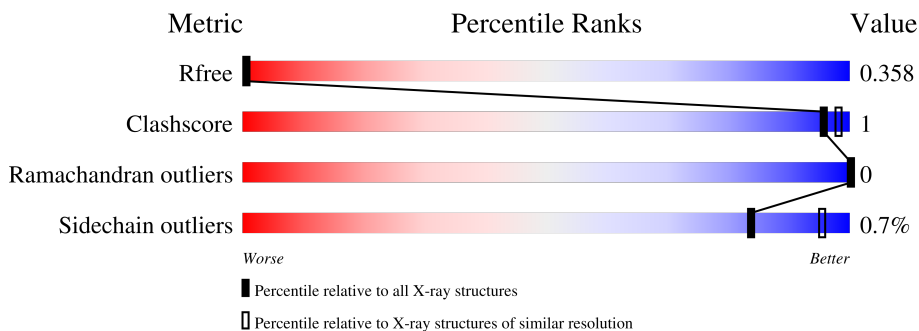|		
PDB ID	:	4CNU
Title	:	CRYSTAL STRUCTURE OF WT HUMAN CRMP-4 from lattice translocation
Authors	:	Ponnusamy, R.; Lebedev, A.; Lohkamp, B.
Deposited on	:	2014-01-24
Resolution	:	2.80 Å(reported)

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 2.80 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	Percentile Ranks	Value
Rfree		0.358
Clashscore		1
Ramachandran outliers		0
Sidechain outliers		0.7%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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	570	83% • 14%
1	B	570	82% • 14%

2 Entry composition ⓘ

There is only 1 type of molecule in this entry. The entry contains 7512 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 DIHYDROPYRIMIDINASE-LIKE 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	488	Total	C	N	O	S	0	0	0
			3756	2373	635	725	23			
1	B	488	Total	C	N	O	S	0	0	0
			3756	2373	635	725	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	76	TYR	PHE	conflict	UNP Q14195
B	76	TYR	PHE	conflict	UNP Q14195

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.

- Molecule 1: DIHYDROPYRIMIDINASE-LIKE 3

- Molecule 1: DIHYDROPYRIMIDINASE-LIKE 3

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	96.24Å 108.22Å 118.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.43 – 2.80 39.40 – 2.80	Depositor EDS
% Data completeness (in resolution range)	93.0 (39.43-2.80) 93.1 (39.40-2.80)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.74 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.255 , 0.295 0.322 , 0.358	Depositor DCC
R_{free} test set	1465 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	41.5	Xtriage
Anisotropy	0.570	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 25.4	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	7512	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.08 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6339e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.31	0/3835	0.50	0/5201
1	B	0.31	0/3835	0.50	0/5201
All	All	0.31	0/7670	0.50	0/10402

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 ⓘ

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	3756	0	3700	8	0
1	B	3756	0	3700	9	0
All	All	7512	0	7400	17	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 1.

All (17) 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:76:TYR:CE1	1:B:92:GLY:HA3	2.43	0.53
1:A:76:TYR:CE1	1:A:92:GLY:HA3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:HIS:O	1:A:227:ARG:HG3	2.11	0.51
1:B:223:HIS:O	1:B:227:ARG:HG3	2.13	0.49
1:B:77:GLN:OE1	1:B:88:ASP:HB2	2.14	0.48
1:A:77:GLN:OE1	1:A:88:ASP:HB2	2.14	0.47
1:A:253:THR:C	1:A:254:LYS:HG2	2.36	0.45
1:B:110:PRO:HG3	1:B:116:LEU:HG	1.99	0.45
1:A:110:PRO:HG3	1:A:116:LEU:HG	1.99	0.45
1:B:281:ALA:HB1	1:B:307:LEU:HD11	1.98	0.45
1:A:281:ALA:HB1	1:A:307:LEU:HD11	1.99	0.44
1:B:253:THR:C	1:B:254:LYS:HG2	2.39	0.42
1:A:72:VAL:HG11	1:A:328:LEU:HD12	2.02	0.42
1:B:72:VAL:HG11	1:B:328:LEU:HD12	2.02	0.41
1:A:254:LYS:CE	1:A:304:SER:O	2.68	0.41
1:B:76:TYR:OH	1:B:358:VAL:HG21	2.20	0.41
1:B:254:LYS:CE	1:B:304:SER:O	2.69	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	486/570 (85%)	461 (95%)	25 (5%)	0	100	100
1	B	486/570 (85%)	463 (95%)	23 (5%)	0	100	100
All	All	972/1140 (85%)	924 (95%)	48 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	404/471 (86%)	401 (99%)	3 (1%)	84	95
1	B	404/471 (86%)	401 (99%)	3 (1%)	84	95
All	All	808/942 (86%)	802 (99%)	6 (1%)	84	95

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	TRP
1	A	227	ARG
1	A	425	HIS
1	B	123	TRP
1	B	227	ARG
1	B	425	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	B	29	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

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

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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