W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report ⓘ

Sep 29, 2022 – 01:24 am BST

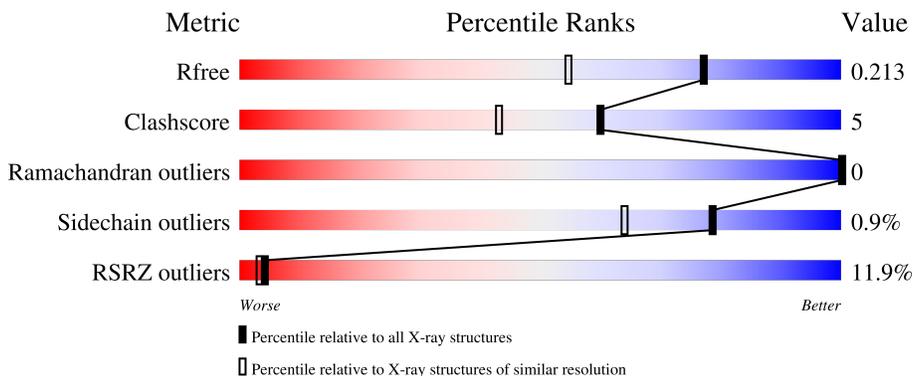|		
PDB ID	:	6RPX
Title	:	Cytokine receptor-like factor 3 C-terminus residues 174-442: native
Authors	:	Mifsud, R.W.; Yan, Y.; Bennett, C.; Read, R.J.
Deposited on	:	2019-05-15
Resolution	:	1.61 Å(reported)

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 1.61 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		0.213
Clashscore		5
Ramachandran outliers		0
Sidechain outliers		0.9%
RSRZ outliers		11.9%

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	4693 (1.64-1.60)
Clashscore	141614	5002 (1.64-1.60)
Ramachandran outliers	138981	4888 (1.64-1.60)
Sidechain outliers	138945	4887 (1.64-1.60)
RSRZ outliers	127900	4609 (1.64-1.60)

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% 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	269	11% / 84% / 10% / 6%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4009 atoms, of which 1882 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 Cytokine receptor-like factor 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	252	Total 3901	C 1273	H 1882	N 349	O 388	S 9	0	2	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	108	Total 108	O 108	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 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: Cytokine receptor-like factor 3
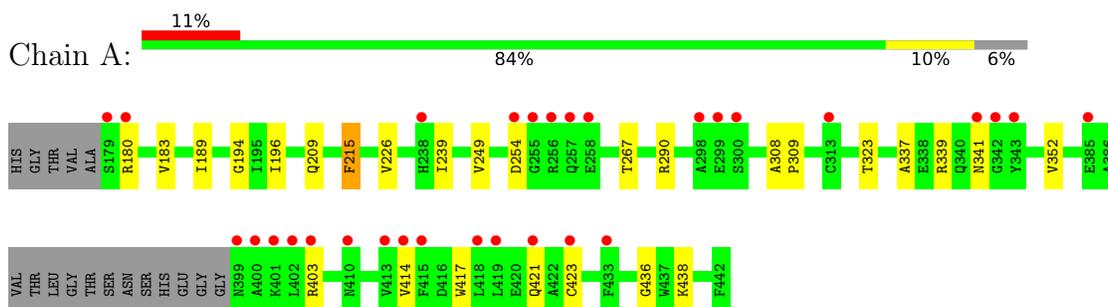
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	88.03Å 40.38Å 76.53Å 90.00° 99.94° 90.00°	Depositor
Resolution (Å)	37.69 – 1.61 37.69 – 1.61	Depositor EDS
% Data completeness (in resolution range)	96.3 (37.69-1.61) 96.3 (37.69-1.61)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.78 (at 1.61Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.177 , 0.201 0.191 , 0.213	Depositor DCC
R_{free} test set	1613 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å^2)	21.3	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4009	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.31% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

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	0.50	0/2069	0.66	1/2813 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	339	ARG	NE-CZ-NH1	-5.54	117.53	120.30

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	2019	1882	1917	18	1
2	A	108	0	0	4	0
All	All	2127	1882	1917	18	1

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 5.

All (18) 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:180:ARG:NH1	2:A:502:HOH:O	2.11	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:GLN:OE1	1:A:254:ASP:HA	1.81	0.79
1:A:323:THR:HG23	1:A:436:GLY:O	1.84	0.78
1:A:267[B]:THR:HG23	2:A:586:HOH:O	1.99	0.63
1:A:323:THR:HG22	1:A:438:LYS:HB3	1.85	0.57
1:A:341:ASN:ND2	2:A:501:HOH:O	1.67	0.57
1:A:403:ARG:CZ	1:A:414:VAL:HG11	2.35	0.56
1:A:403:ARG:NH2	1:A:414:VAL:HG11	2.20	0.56
1:A:337:ALA:HB1	1:A:421:GLN:OE1	2.06	0.56
1:A:323:THR:HG22	1:A:438:LYS:CB	2.38	0.53
1:A:267[A]:THR:HG22	2:A:575:HOH:O	2.13	0.49
1:A:194:GLY:HA2	1:A:239:ILE:HD11	1.96	0.46
1:A:183[B]:VAL:HG13	1:A:249:VAL:HG13	1.99	0.45
1:A:215:PHE:CD1	1:A:226:VAL:CG1	3.01	0.44
1:A:189:ILE:HB	1:A:196:ILE:HB	2.01	0.42
1:A:352:VAL:HG23	1:A:417:TRP:CE2	2.55	0.42
1:A:403:ARG:CZ	1:A:414:VAL:CG1	2.98	0.40
1:A:308:ALA:HB1	1:A:309:PRO:HD2	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:ARG:HH21	1:A:290:ARG:HD2[2_757]	1.26	0.34

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	250/269 (93%)	241 (96%)	9 (4%)	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	222/232 (96%)	220 (99%)	2 (1%)	78	64

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	215	PHE
1	A	423	CYS

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

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 (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(Å²)	Q<0.9
1	A	252/269 (93%)	0.57	30 (11%)	4	3	16, 29, 64, 103	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	255	GLY	8.1
1	A	399	ASN	8.0
1	A	418	LEU	7.3
1	A	401	LYS	5.7
1	A	400	ALA	5.5
1	A	341	ASN	4.9
1	A	421	GLN	4.8
1	A	257	GLN	4.3
1	A	254	ASP	4.0
1	A	403	ARG	3.9
1	A	258	GLU	3.7
1	A	179	SER	3.6
1	A	180	ARG	3.5
1	A	256	ARG	3.4
1	A	414	VAL	3.3
1	A	433	PHE	3.0
1	A	419	LEU	3.0
1	A	343	TYR	2.7
1	A	413	VAL	2.6
1	A	402	LEU	2.6
1	A	423	CYS	2.5
1	A	298	ALA	2.5
1	A	300	SER	2.4
1	A	342	GLY	2.3
1	A	299	GLU	2.3
1	A	313	CYS	2.3
1	A	238	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	415	PHE	2.2
1	A	385	GLU	2.0
1	A	410	ASN	2.0

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.