wwPDB X-ray Structure Validation Summary Report (i)

Mar 28, 2022 – 01:04 pm BST

PDB ID	:	7P3I
Title	:	Crystal structure of human CD40/TNFRSF5 in complex with the anti-CD40 DARPin protein
Authors	:	Malvezzi, F.; Mangold, S.; Hospodarsch, T.; Reichen, C.; Iss, C.; Lammens, A.; Krapp, S.; Domke, C.
Deposited on	:	2021-07-07
Resolution	:	2.29 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see references (1)) were used in the production of this report:

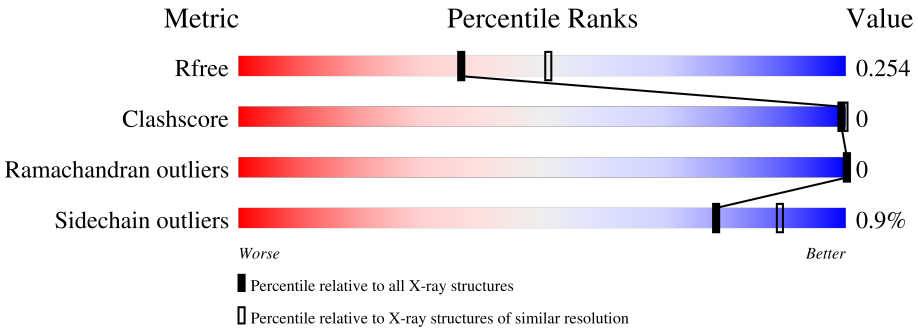
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.27
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 2.29 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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	177	92% · 5%
1	C	177	90% · 7%
2	B	159	96% · ·
2	D	159	98% ·

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5104 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 Tumor necrosis factor receptor superfamily member 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	S	11	0	0
			1282	780	219	263	20			
1	C	165	Total	C	N	O	S	55	1	0
			1267	771	217	259	20			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	194	LEU	-	expression tag	UNP P25942
A	195	VAL	-	expression tag	UNP P25942
A	196	PRO	-	expression tag	UNP P25942
A	197	ARG	-	expression tag	UNP P25942
C	194	LEU	-	expression tag	UNP P25942
C	195	VAL	-	expression tag	UNP P25942
C	196	PRO	-	expression tag	UNP P25942
C	197	ARG	-	expression tag	UNP P25942

- Molecule 2 is a protein called Darpin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	159	Total	C	N	O	22	0	0
			1180	742	215	223			
2	D	156	Total	C	N	O	172	0	0
			1165	734	212	219			

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	C	1	Total	Na	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	78	Total O 78 78	0	0
4	B	76	Total O 76 76	0	0
4	C	49	Total O 49 49	0	0
4	D	5	Total O 5 5	0	0

3 Residue-property plots (i)

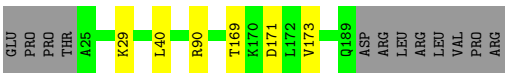
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Tumor necrosis factor receptor superfamily member 5

Chain A:

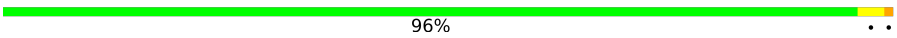
• Molecule 1: Tumor necrosis factor receptor superfamily member 5

Chain C:



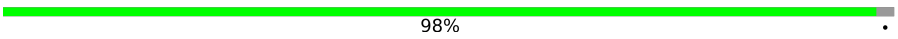
• Molecule 2: Darpin

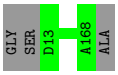
Chain B:



• Molecule 2: Darpin

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	193.67Å 59.56Å 81.84Å 90.00° 106.99° 90.00°	Depositor
Resolution (Å)	92.61 – 2.29 78.27 – 2.29	Depositor EDS
% Data completeness (in resolution range)	97.8 (92.61-2.29) 97.8 (78.27-2.29)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	1.77 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.220 , 0.253 0.223 , 0.254	Depositor DCC
R_{free} test set	1962 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	52.7	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5104	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA

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	0.70	0/1310	0.84	3/1779 (0.2%)
1	C	0.67	1/1294 (0.1%)	0.81	2/1757 (0.1%)
2	B	0.81	2/1199 (0.2%)	0.95	4/1625 (0.2%)
2	D	0.64	0/1184	0.79	0/1605
All	All	0.71	3/4987 (0.1%)	0.85	9/6766 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	29	GLU	CG-CD	-9.38	1.37	1.51
2	B	32	GLU	CG-CD	6.41	1.61	1.51
1	C	169	THR	CB-OG1	-5.99	1.31	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	73	ARG	NE-CZ-NH2	-8.77	115.92	120.30
2	B	160	ASP	CB-CG-OD1	7.29	124.86	118.30
1	A	73	ARG	NE-CZ-NH1	6.89	123.75	120.30
1	C	173	VAL	CA-CB-CG2	5.84	119.66	110.90
1	A	27	ARG	NE-CZ-NH1	5.50	123.05	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	1282	0	1173	0	0
1	C	1267	0	1160	1	0
2	B	1180	0	1193	0	0
2	D	1165	0	1180	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	78	0	0	0	0
4	B	76	0	0	0	0
4	C	49	0	0	0	0
4	D	5	0	0	0	0
All	All	5104	0	4706	1	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 0.

All (1) 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:C:29:LYS:HA	1:C:40:LEU:HD12	2.03	0.41

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	166/177 (94%)	165 (99%)	1 (1%)	0	100	100
1	C	164/177 (93%)	164 (100%)	0	0	100	100
2	B	157/159 (99%)	157 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	154/159 (97%)	154 (100%)	0	0	100	100
All	All	641/672 (95%)	640 (100%)	1 (0%)	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	152/161 (94%)	149 (98%)	3 (2%)	55	72
1	C	150/161 (93%)	149 (99%)	1 (1%)	84	92
2	B	116/116 (100%)	115 (99%)	1 (1%)	78	89
2	D	115/116 (99%)	115 (100%)	0	100	100
All	All	533/554 (96%)	528 (99%)	5 (1%)	78	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	THR
1	A	51	CYS
1	A	68	LEU
2	B	32	GLU
1	C	171	ASP

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

Mol	Chain	Res	Type
1	A	42	GLN

5.3.3 RNA (i)

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

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.