



wwPDB X-ray Structure Validation Summary Report i

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PDB ID : 3S8V
Title : Crystal structure of LRP6-Dkk1 complex
Authors : Cheng, Z.; Xu, W.
Deposited on : 2011-05-31
Resolution : 3.10 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

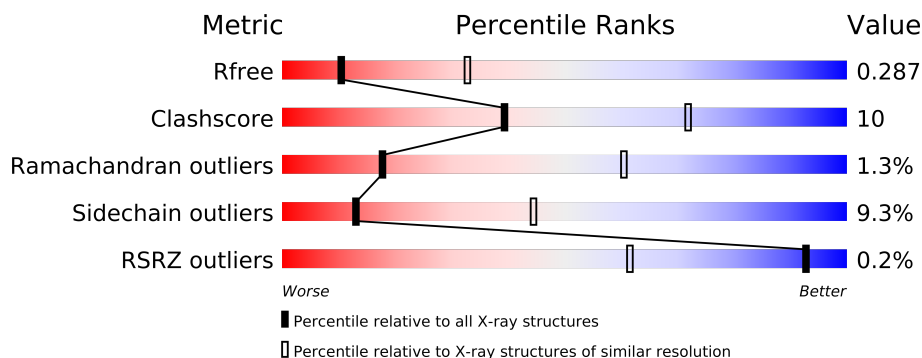
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.10 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}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	623	<div><div></div><div><div></div><div></div><div></div><div></div><div></div></div></div>
1	B	623	<div><div></div><div><div></div><div></div><div></div><div></div><div></div></div></div>
2	X	88	<div><div></div><div><div></div><div></div><div></div><div></div><div></div></div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10177 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Low-density lipoprotein receptor-related protein 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	600	Total	C	N	O	S	0	0	0
			4790	3011	846	908	25			
1	B	604	Total	C	N	O	S	0	0	0
			4818	3025	854	914	25			

There are 18 discrepancies between the modelled and reference sequences:

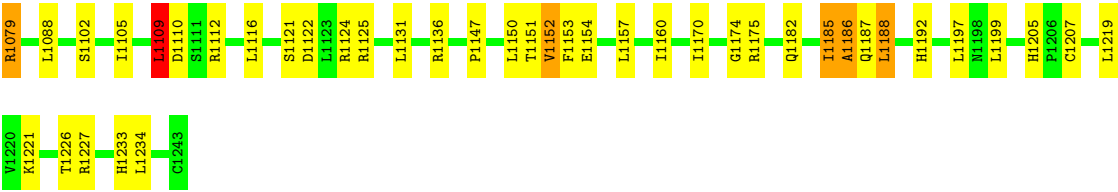
Chain	Residue	Modelled	Actual	Comment	Reference
A	621	HIS	-	EXPRESSION TAG	UNP O75581
A	622	HIS	-	EXPRESSION TAG	UNP O75581
A	623	HIS	-	EXPRESSION TAG	UNP O75581
A	624	HIS	-	EXPRESSION TAG	UNP O75581
A	625	HIS	-	EXPRESSION TAG	UNP O75581
A	626	HIS	-	EXPRESSION TAG	UNP O75581
A	627	HIS	-	EXPRESSION TAG	UNP O75581
A	628	HIS	-	EXPRESSION TAG	UNP O75581
A	1062	ILE	VAL	CONFLICT	UNP O75581
B	621	HIS	-	EXPRESSION TAG	UNP O75581
B	622	HIS	-	EXPRESSION TAG	UNP O75581
B	623	HIS	-	EXPRESSION TAG	UNP O75581
B	624	HIS	-	EXPRESSION TAG	UNP O75581
B	625	HIS	-	EXPRESSION TAG	UNP O75581
B	626	HIS	-	EXPRESSION TAG	UNP O75581
B	627	HIS	-	EXPRESSION TAG	UNP O75581
B	628	HIS	-	EXPRESSION TAG	UNP O75581
B	1062	ILE	VAL	CONFLICT	UNP O75581

- Molecule 2 is a protein called Dickkopf-related protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	X	73	Total	C	N	O	S	0	0	0
			569	345	116	98	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	179	GLY	-	EXPRESSION TAG	UNP O94907
X	180	PRO	-	EXPRESSION TAG	UNP O94907
X	181	GLY	-	EXPRESSION TAG	UNP O94907
X	182	SER	-	EXPRESSION TAG	UNP O94907



• Molecule 2: Dickkopf-related protein 1

Chain X:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	94.38Å 105.05Å 161.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.10 29.63 – 3.05	Depositor EDS
% Data completeness (in resolution range)	98.2 (30.00-3.10) 97.4 (29.63-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.240 , 0.292 0.239 , 0.287	Depositor DCC
R_{free} test set	1534 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	71.7	Xtriage
Anisotropy	0.612	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 32.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 30357 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10177	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.36	0/4889	0.57	0/6630
1	B	0.36	0/4919	0.55	1/6674 (0.0%)
2	X	0.37	0/577	0.55	0/766
All	All	0.36	0/10385	0.56	1/14070 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1109	LEU	CA-CB-CG	5.38	127.66	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4790	0	4676	94	0
1	B	4818	0	4705	88	0
2	X	569	0	558	14	0
All	All	10177	0	9939	194	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

The worst 5 of 194 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1031:THR:HG23	1:A:1062:ILE:HD11	1.19	1.12
1:B:1031:THR:HG23	1:B:1062:ILE:HD11	1.36	1.03
1:A:679:THR:HG21	1:A:707:PRO:O	1.63	0.99
1:B:1031:THR:HG23	1:B:1062:ILE:CD1	1.94	0.97
1:A:1019:LEU:HD12	1:A:1028:ILE:HD11	1.44	0.97

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	590/623 (95%)	529 (90%)	50 (8%)	11 (2%)	12	51
1	B	600/623 (96%)	540 (90%)	55 (9%)	5 (1%)	27	74
2	X	69/88 (78%)	65 (94%)	4 (6%)	0	100	100
All	All	1259/1334 (94%)	1134 (90%)	109 (9%)	16 (1%)	18	60

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1174	GLY
1	A	878	ASP
1	A	879	ILE
1	B	926	ASN
1	B	986	GLN

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	525/546 (96%)	473 (90%)	52 (10%)	11	39
1	B	527/546 (96%)	479 (91%)	48 (9%)	14	45
2	X	64/75 (85%)	60 (94%)	4 (6%)	25	66
All	All	1116/1167 (96%)	1012 (91%)	104 (9%)	13	44

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1188	LEU
1	B	748	ASP
1	B	1188	LEU
1	A	1203	ARG
1	B	641	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1155	ASN
1	A	1211	ASN
2	X	223	HIS
1	A	1205	HIS
1	A	1216	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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 ⓘ

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	600/623 (96%)	-0.24	0	100 100	45, 80, 113, 143	0
1	B	604/623 (96%)	-0.16	1 (0%)	93 61	45, 90, 113, 141	0
2	X	73/88 (82%)	-0.14	1 (1%)	72 17	65, 86, 107, 122	0
All	All	1277/1334 (95%)	-0.20	2 (0%)	93 61	45, 86, 113, 143	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	899	HIS	2.6
2	X	241	GLU	2.6

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 carbohydrates 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.