



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 07:32 PM GMT

PDB ID : 3S8Z  
Title : Crystal structure of LRP6-E3E4  
Authors : Cheng, Z.; Xu, W.  
Deposited on : 2011-05-31  
Resolution : 2.80 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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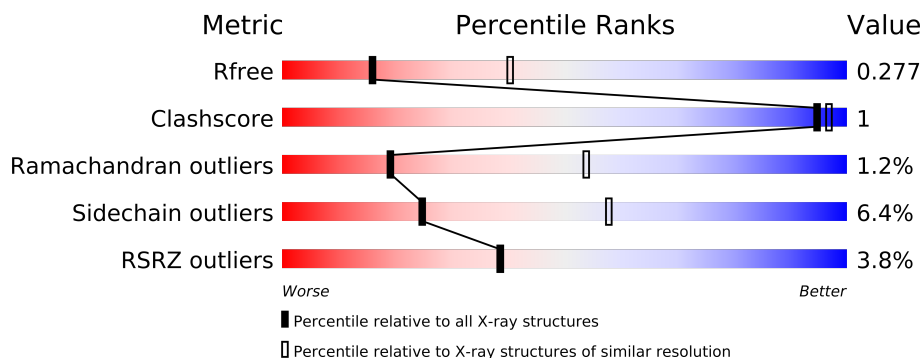
The following versions of software and data (see [references](#)) were used in the production of this report:

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 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	NAG	A	1248	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4903 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
			Total	C	N	O	S			
1	A	606	4833	3035	856	917	25	0	0	0

There are 9 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	VARIANT	UNP O75581

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

There are 9 discrepancies between the modelled and reference sequences:

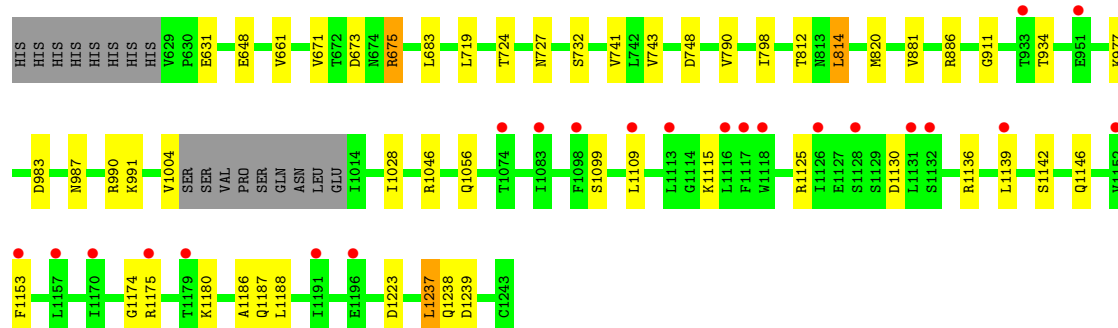
Chain	Residue	Modelled	Actual	Comment	Reference
A	621	HIS	-	EXPRESSION TAG	UNP O75581
A	622	HIS	-	EXPRESSION TAG	UNP O75581
A	623	HIS	-	EXPRESSION TAG	UNP O75581
A	624	HIS	-	EXPRESSION TAG	UNP O75581
A	625	HIS	-	EXPRESSION TAG	UNP O75581
A	626	HIS	-	EXPRESSION TAG	UNP O75581
A	627	HIS	-	EXPRESSION TAG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

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Low-density lipoprotein receptor-related protein 6

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.60Å 83.75Å 166.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 52.96 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-2.80) 99.9 (52.96-2.75)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.45 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.257 , 0.282 0.256 , 0.277	Depositor DCC
$R_{free}$ test set	1309 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	69.6	Xtriage
Anisotropy	0.547	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 73.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 25672 reflections (0.012%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4903	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.34	0/4935	0.56	1/6696 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	814	LEU	CA-CB-CG	5.10	127.03	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	4833	0	0	7	0
2	A	42	0	0	0	0
3	A	28	0	0	0	0
All	All	4903	0	0	7	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 1.

All (7) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:727:ASN:ND2	1:A:748:ASP:O	2.36	0.58
1:A:1099:SER:O	1:A:1136:ARG:NH2	2.40	0.55
1:A:798:ILE:O	1:A:886:ARG:NH2	2.41	0.53
1:A:1237:LEU:O	1:A:1239:ASP:N	2.49	0.45
1:A:719:LEU:N	1:A:732:SER:O	2.51	0.44
1:A:673:ASP:OD2	1:A:675:ARG:NE	2.54	0.41
1:A:724:THR:O	1:A:727:ASN:ND2	2.54	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	602/623 (97%)	550 (91%)	45 (8%)	7 (1%)	19 54

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	911	GLY
1	A	1186	ALA
1	A	648	GLU
1	A	1153	PHE
1	A	987	ASN
1	A	1142	SER
1	A	1174	GLY

### 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	529/546 (97%)	495 (94%)	34 (6%)	25	58

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	631	GLU
1	A	661	VAL
1	A	671	VAL
1	A	675	ARG
1	A	683	LEU
1	A	741	VAL
1	A	743	VAL
1	A	790	VAL
1	A	812	THR
1	A	814	LEU
1	A	820	MET
1	A	881	VAL
1	A	934	THR
1	A	977	LYS
1	A	983	ASP
1	A	990	ARG
1	A	991	LYS
1	A	1004	VAL
1	A	1028	ILE
1	A	1046	ARG
1	A	1056	GLN
1	A	1109	LEU
1	A	1115	LYS
1	A	1125	ARG
1	A	1130	ASP
1	A	1139	LEU
1	A	1146	GLN
1	A	1175	ARG
1	A	1180	LYS
1	A	1187	GLN
1	A	1188	LEU
1	A	1223	ASP
1	A	1237	LEU
1	A	1238	GLN

Some 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 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 ⓘ

2 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	NAG	A	1245	1,3	12,14,15	0.66	0	15,19,21	1.06	1 (6%)
3	NAG	A	1246	3	12,14,15	0.55	0	15,19,21	0.87	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	1245	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1246	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1245	NAG	C3-C2-N2	-2.80	107.50	111.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NAG	A	1244	1	12,14,15	0.70	1 (8%)	15,19,21	1.19	2 (13%)
2	NAG	A	1247	1	12,14,15	0.58	0	15,19,21	0.95	0
2	NAG	A	1248	1	12,14,15	0.67	0	15,19,21	1.03	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1244	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	A	1247	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1248	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1244	NAG	O5-C5	-2.01	1.41	1.45

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1244	NAG	O5-C5-C4	-2.41	107.60	110.65
2	A	1244	NAG	O5-C5-C6	2.30	109.39	106.98
2	A	1248	NAG	O5-C5-C6	2.29	109.39	106.98

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1244	NAG	C1

There are no torsion outliers.

There are no ring outliers.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	606/623 (97%)	0.36	23 (3%) 38 38	74, 110, 171, 210	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1131	LEU	5.6
1	A	1132	SER	5.1
1	A	1139	LEU	4.7
1	A	1113	LEU	3.8
1	A	1153	PHE	3.4
1	A	1157	LEU	3.3
1	A	1152	VAL	3.1
1	A	1118	TRP	3.1
1	A	1117	PHE	3.0
1	A	1109	LEU	2.6
1	A	1098	PHE	2.6
1	A	1116	LEU	2.6
1	A	933	THR	2.5
1	A	951	GLU	2.5
1	A	1179	THR	2.4
1	A	1126	ILE	2.4
1	A	1128	SER	2.3
1	A	1191	ILE	2.2
1	A	1175	ARG	2.1
1	A	1074	THR	2.1
1	A	1196	GLU	2.1
1	A	1170	ILE	2.1
1	A	1083	ILE	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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	A	1245	14/15	0.26	1.19	147,148,149,149	0
3	NAG	A	1246	14/15	0.26	0.69	163,165,166,166	0

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	A	1248	14/15	0.27	4.25	172,173,173,174	0
2	NAG	A	1244	14/15	0.18	1.69	170,172,175,176	0
2	NAG	A	1247	14/15	0.19	-0.93	178,180,181,181	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.