



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2017 – 01:56 AM EDT

PDB ID : 3P5B  
Title : The structure of the LDLR/PCSK9 complex reveals the receptor in an extended conformation  
Authors : Lo Surdo, P.; Bottomley, M.J.; Calzetta, A.; Settembre, E.C.; Cirillo, A.; Pandit, S.; Ni, Y.; Hubbard, B.; Sitlani, A.; Carfi, A.  
Deposited on : unknown  
Resolution : 3.30 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

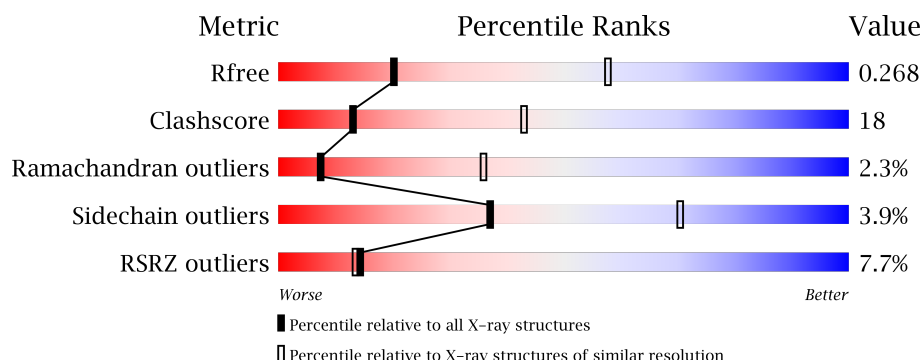
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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))
$R_{free}$	100719	1034 (3.36-3.24)
Clashscore	112137	1100 (3.36-3.24)
Ramachandran outliers	110173	1081 (3.36-3.24)
Sidechain outliers	110143	1080 (3.36-3.24)
RSRZ outliers	101464	1039 (3.36-3.24)

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. 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  $\leq 5\%$ . 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	P	92	<div> <div>0.1%</div> <div>92%</div> <div>7%</div> <div>0.1%</div> </div>
2	A	540	<div> <div>5%</div> <div>74%</div> <div>15%</div> <div>9%</div> <div>0.1%</div> </div>
3	L	400	<div> <div>12%</div> <div>70%</div> <div>23%</div> <div>5%</div> <div>0.1%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7464 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 Proprotein convertase subtilisin/kexin type 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	92	Total	C	N	O	S	0	0	0
			740	474	133	131	2			

- Molecule 2 is a protein called Proprotein convertase subtilisin/kexin type 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	493	Total	C	N	O	S	0	0	0
			3637	2243	668	694	32			

- Molecule 3 is a protein called Low density lipoprotein receptor variant.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	394	Total	C	N	O	S	0	0	0
			3084	1931	535	593	25			

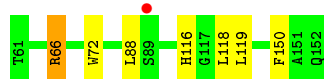
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	L	2	Total	Ca	0	0
			2	2		

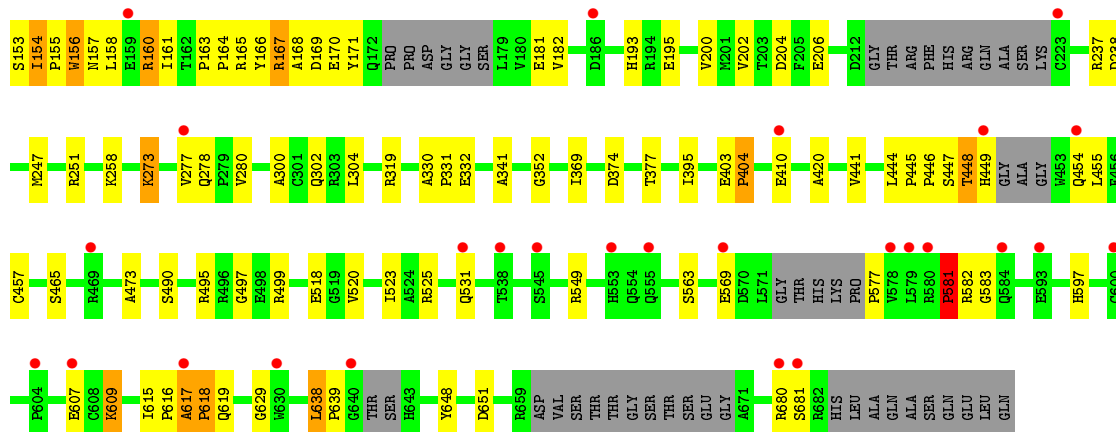
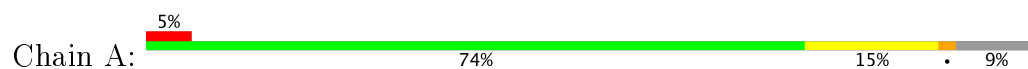
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

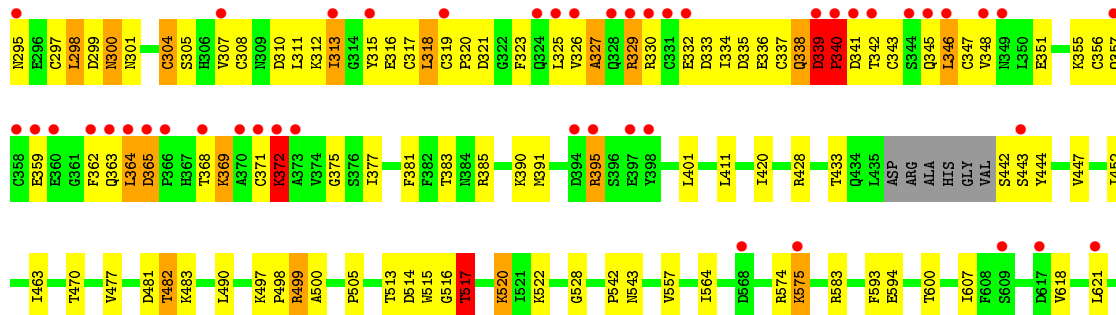
- Molecule 1: Proprotein convertase subtilisin/kexin type 9



- Molecule 2: Proprotein convertase subtilisin/kexin type 9



- Molecule 3: Low density lipoprotein receptor variant





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.00Å 109.70Å 178.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.30 47.07 – 3.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.30) 98.3 (47.07-3.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 3.33Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.271 , 0.298 0.274 , 0.268	Depositor DCC
$R_{free}$ test set	1158 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	66.3	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 40.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	7464	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	P	0.31	0/757	0.46	0/1023
2	A	0.31	0/3702	0.47	2/5030 (0.0%)
3	L	0.44	0/3149	0.66	4/4279 (0.1%)
All	All	0.37	0/7608	0.56	6/10332 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	L	0	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	517	THR	C-N-CD	13.73	157.24	128.40
3	L	517	THR	C-N-CA	-10.60	77.48	122.00
3	L	517	THR	CA-C-N	7.04	136.82	117.10
2	A	581	PRO	N-CA-CB	5.68	110.12	103.30
3	L	339	ASP	N-CA-C	5.24	125.16	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	L	517	THR	Peptide

## 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	P	740	0	750	7	0
2	A	3637	0	3512	78	3
3	L	3084	0	2990	191	0
4	A	1	0	0	0	0
4	L	2	0	0	0	0
All	All	7464	0	7252	269	3

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 18.

The worst 5 of 269 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)
2:A:447:SER:OG	2:A:449:HIS:HD2	1.23	1.20
3:L:339:ASP:HB3	3:L:340:PRO:HD2	1.19	1.14
3:L:299:ASP:O	3:L:300:ASN:ND2	1.81	1.14
3:L:339:ASP:HB3	3:L:340:PRO:CD	1.76	1.14
2:A:447:SER:OG	2:A:449:HIS:CD2	2.01	1.12

All (3) 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)
2:A:237:ARG:CZ	2:A:569:GLU:OE1[3_644]	1.85	0.35
2:A:237:ARG:NH1	2:A:569:GLU:OE1[3_644]	1.96	0.24
2:A:237:ARG:NH2	2:A:569:GLU:CD[3_644]	2.09	0.11

## 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	P	90/92 (98%)	86 (96%)	4 (4%)	0	100	100
2	A	479/540 (89%)	437 (91%)	34 (7%)	8 (2%)	11	42
3	L	390/400 (98%)	327 (84%)	49 (13%)	14 (4%)	4	26
All	All	959/1032 (93%)	850 (89%)	87 (9%)	22 (2%)	7	36

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	448	THR
2	A	581	PRO
2	A	618	PRO
3	L	327	ALA
3	L	339	ASP

### 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	P	79/79 (100%)	78 (99%)	1 (1%)	73	86
2	A	386/430 (90%)	374 (97%)	12 (3%)	45	75
3	L	347/352 (99%)	328 (94%)	19 (6%)	25	61
All	All	812/861 (94%)	780 (96%)	32 (4%)	37	70

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	313	ILE
3	L	333	ASP
3	L	520	LYS
3	L	329	ARG
3	L	335	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	295	ASN
3	L	636	ASN
3	L	309	ASN
2	A	464	HIS
3	L	300	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 [i](#)

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	P	92/92 (100%)	0.33	1 (1%) 80 79	37, 56, 81, 86	0
2	A	493/540 (91%)	0.49	27 (5%) 26 24	34, 68, 96, 110	0
3	L	394/400 (98%)	0.67	47 (11%) 5 4	25, 63, 98, 116	0
All	All	979/1032 (94%)	0.55	75 (7%) 14 13	25, 65, 97, 116	0

The worst 5 of 75 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	341	ASP	5.7
3	L	364	LEU	4.3
3	L	357	GLN	3.9
3	L	358	CYS	3.9
3	L	360	GLU	3.9

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	CA	A	2	1/1	0.92	0.17	-1.76	78,78,78,78	0
4	CA	L	3	1/1	0.82	0.16	-3.11	117,117,117,117	0
4	CA	L	1	1/1	0.81	0.07	-4.97	64,64,64,64	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.