



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 2, 2021 – 05:13 PM EDT

PDB ID : 3H42  
Title : Crystal structure of PCSK9 in complex with Fab from LDLR competitive antibody  
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Deposited on : 2009-04-17  
Resolution : 2.30 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

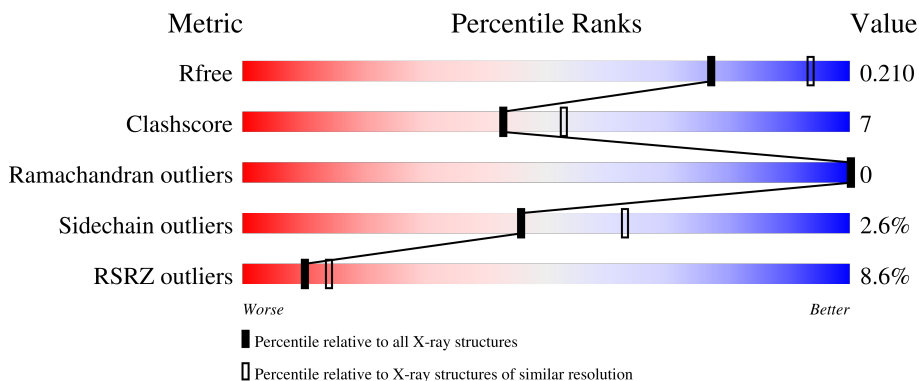
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	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)
RSRZ outliers	127900	4938 (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  $\geq 3$ , 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  $\leq 5\%$ . 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	A	126	 3% 58% 14% 27%
2	B	540	 13% 76% 14% 9%
3	L	217	 4% 87% 12%
4	H	238	 3% 82% 11% 7%

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8196 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	A	92	Total	C	N	O	S	0	0	0
			740	474	133	131	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	GLY	-	expression tag	UNP Q8NBP7
A	28	ALA	-	expression tag	UNP Q8NBP7
A	29	MET	-	expression tag	UNP Q8NBP7
A	30	GLY	-	expression tag	UNP Q8NBP7

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	492	Total	C	N	O	S	0	0	0
			3659	2261	676	690	32			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	533	ALA	ASN	engineered mutation	UNP Q8NBP7
B	620	GLY	GLU	SEE REMARK 999	UNP Q8NBP7

- Molecule 3 is a protein called Fab from LDLR competitive antibody: Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total	C	N	O	S	0	0	0
			1568	975	263	326	4			

- Molecule 4 is a protein called Fab from LDLR competitive antibody: Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	221	Total	C	N	O	S	0	0	0
			1660	1051	274	328	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	233	HIS	-	expression tag	PDB 3H42
H	234	HIS	-	expression tag	PDB 3H42
H	235	HIS	-	expression tag	PDB 3H42
H	236	HIS	-	expression tag	PDB 3H42
H	237	HIS	-	expression tag	PDB 3H42
H	238	HIS	-	expression tag	PDB 3H42

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		

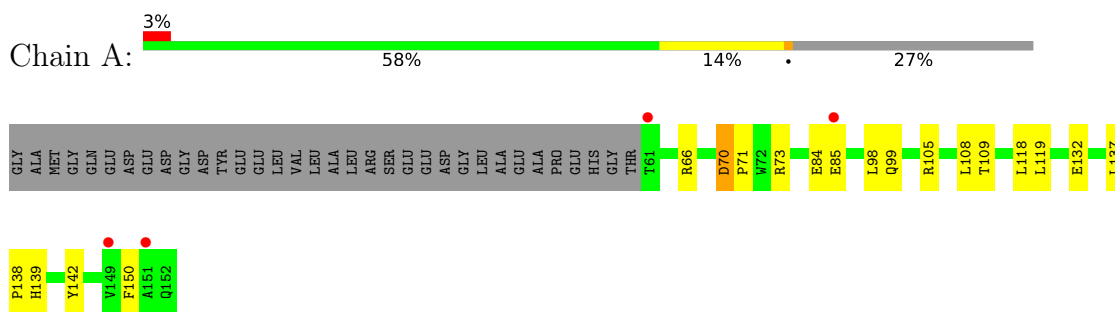
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	76	Total	O	0	0
			76	76		
6	B	178	Total	O	0	0
			178	178		
6	L	159	Total	O	0	0
			159	159		
6	H	155	Total	O	0	0
			155	155		

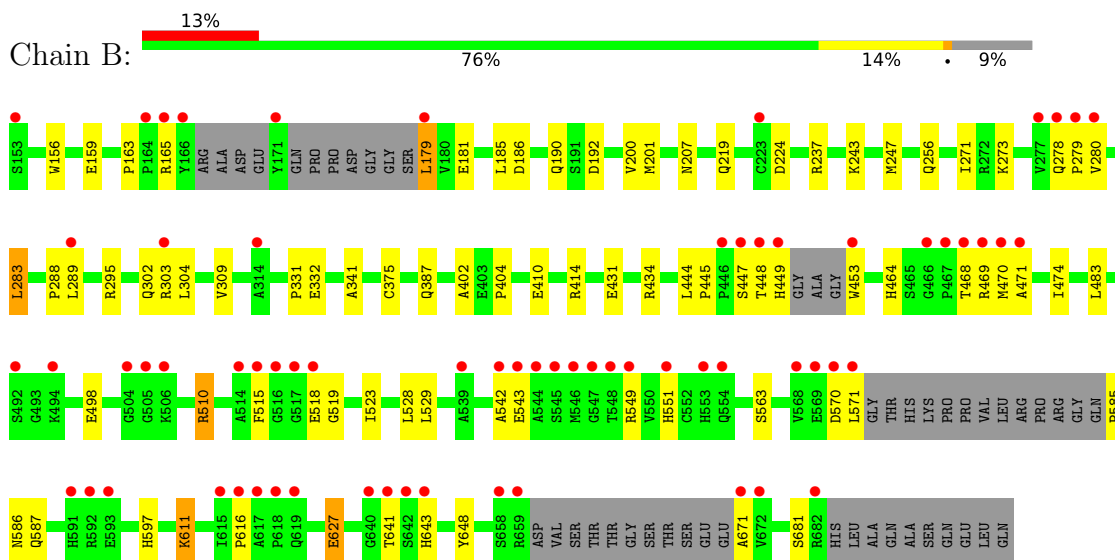
### 3 Residue-property plots [i](#)

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.

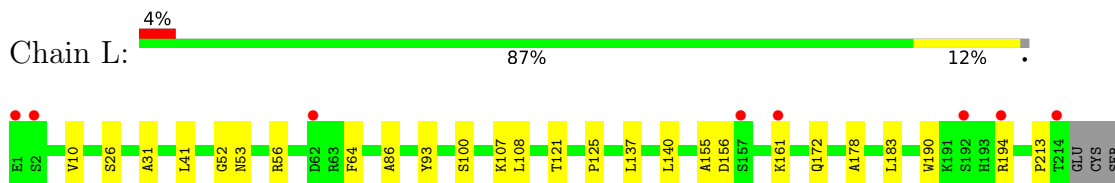
- Molecule 1: Proprotein convertase subtilisin/kexin type 9



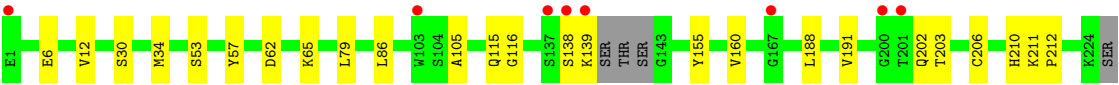
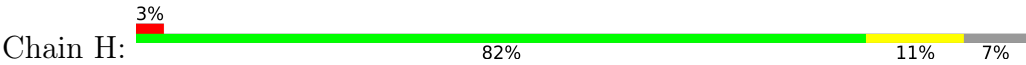
- Molecule 2: Proprotein convertase subtilisin/kexin type 9



- Molecule 3: Fab from LDLR competitive antibody: Light chain



- Molecule 4: Fab from LDLR competitive antibody: Heavy chain



CYS
ALA
ALA
ASP
GLU
VAL
ASP
HIS
HIS
HIS
HIS
HIS
HIS

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	264.72Å 137.35Å 69.89Å 90.00° 102.84° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 38.29 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.00-2.30) 99.8 (38.29-2.30)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.53 (at 2.29Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.191 , 0.209 0.191 , 0.210	Depositor DCC
$R_{free}$ test set	5376 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.0	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 49.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h-2*k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8196	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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

### 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	0.31	0/757	0.43	0/1023
2	B	0.26	0/3729	0.47	0/5064
3	L	0.30	0/1605	0.49	0/2192
4	H	0.32	0/1701	0.49	0/2313
All	All	0.29	0/7792	0.47	0/10592

There are no bond length outliers.

There are no bond angle outliers.

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	740	0	750	15	0
2	B	3659	0	3572	56	0
3	L	1568	0	1518	18	0
4	H	1660	0	1610	18	0
5	B	1	0	0	0	0
6	A	76	0	0	2	0
6	B	178	0	0	1	0
6	H	155	0	0	1	0
6	L	159	0	0	2	0
All	All	8196	0	7450	103	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 7.

The worst 5 of 103 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:B:474:ILE:HD11	2:B:510:ARG:HH21	1.40	0.84
2:B:200:VAL:HG12	2:B:247:MET:HB2	1.60	0.82
1:A:66:ARG:HH21	1:A:73:ARG:HD2	1.43	0.81
2:B:474:ILE:HD11	2:B:510:ARG:NH2	1.97	0.80
2:B:402:ALA:HB1	2:B:448:THR:HG23	1.65	0.77

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	90/126 (71%)	87 (97%)	3 (3%)	0	100	100
2	B	481/540 (89%)	466 (97%)	15 (3%)	0	100	100
3	L	212/217 (98%)	207 (98%)	5 (2%)	0	100	100
4	H	217/238 (91%)	216 (100%)	1 (0%)	0	100	100
All	All	1000/1121 (89%)	976 (98%)	24 (2%)	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	79/104 (76%)	78 (99%)	1 (1%)	69	82
2	B	392/429 (91%)	375 (96%)	17 (4%)	29	40
3	L	177/180 (98%)	175 (99%)	2 (1%)	73	86
4	H	186/201 (92%)	184 (99%)	2 (1%)	73	86
All	All	834/914 (91%)	812 (97%)	22 (3%)	46	63

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	518	GLU
2	B	627	GLU
2	B	611	LYS
3	L	107	LYS
2	B	207	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	553	HIS
2	B	587	GLN
4	H	202	GLN
4	H	3	GLN
2	B	382	GLN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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 [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	A	92/126 (73%)	0.07	4 (4%) 35 42	22, 39, 56, 69	0
2	B	492/540 (91%)	0.79	68 (13%) 2 4	23, 48, 93, 116	0
3	L	214/217 (98%)	-0.07	8 (3%) 41 48	23, 36, 61, 75	0
4	H	221/238 (92%)	0.10	8 (3%) 42 49	23, 38, 57, 91	0
All	All	1019/1121 (90%)	0.40	88 (8%) 10 14	22, 41, 83, 116	0

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	546	MET	10.1
2	B	515	PHE	8.4
2	B	453	TRP	7.2
2	B	545	SER	7.1
2	B	643	HIS	6.5

### 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 monosaccharides 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NA	B	1	1/1	0.86	0.66	62,62,62,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.