



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 02:45 AM GMT

PDB ID : 2W2Q  
Title : PCSK9-DELTAC D374H MUTANT BOUND TO WT EGF-A OF LDLR  
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Deposited on : 2008-11-03  
Resolution : 2.33 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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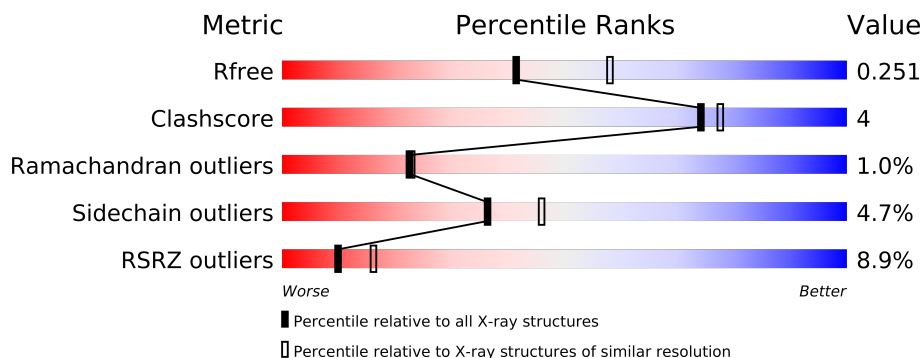
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.33 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	4049 (2.38-2.30)
Clashscore	79885	1094 (2.36-2.32)
Ramachandran outliers	78287	1080 (2.36-2.32)
Sidechain outliers	78261	1081 (2.36-2.32)
RSRZ outliers	66119	4050 (2.38-2.30)

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 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	312	
2	E	107	
3	P	114	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3360 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 PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	3	0
			2049	1280	360	398	11			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	374	HIS	ASP	ENGINEERED MUTATION	UNP Q8NBP7

- Molecule 2 is a protein called LOW-DENSITY LIPOPROTEIN RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	47	Total	C	N	O	S	0	0	0
			357	217	63	70	7			

- Molecule 3 is a protein called PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 9.

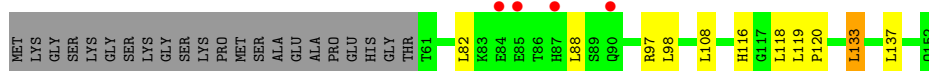
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	92	Total	C	N	O	S	0	3	0
			757	486	137	132	2			

- 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	E	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	117	Total 117	O 117	0	0
5	E	33	Total 33	O 33	0	0
5	P	45	Total 45	O 45	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.37Å 88.37Å 218.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.33 39.52 – 2.33	Depositor EDS
% Data completeness (in resolution range)	99.0 (40.00-2.33) 99.0 (39.52-2.33)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.33 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.219 , 0.253 0.216 , 0.251	Depositor DCC
$R_{free}$ test set	1872 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.6	Xtriage
Anisotropy	0.574	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 34.4	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	0 of 37527 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3360	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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: 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	A	0.41	0/2092	0.53	0/2848
2	E	0.50	0/362	0.59	0/486
3	P	0.38	0/783	0.59	1/1056 (0.1%)
All	All	0.41	0/3237	0.55	1/4390 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	133	LEU	CA-CB-CG	5.45	127.84	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	2049	0	2039	17	0
2	E	357	0	323	6	0
3	P	757	0	781	4	0
4	A	1	0	0	0	0
4	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	117	0	0	2	0
5	E	33	0	0	0	0
5	P	45	0	0	0	0
All	All	3360	0	3143	26	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 4.

All (26) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:E:291:ALA:O	2:E:292:MET:HB2	1.64	0.92
1:A:186:ASP:OD2	1:A:288:PRO:HG2	1.98	0.62
1:A:193:HIS:HD2	1:A:195:GLU:H	1.48	0.60
1:A:200:VAL:HG22	1:A:247:MET:HB2	1.86	0.58
1:A:304:LEU:HD13	3:P:118:LEU:HD21	1.87	0.57
2:E:290:GLY:O	2:E:291:ALA:HB2	2.05	0.56
1:A:184:LEU:HD13	1:A:286:LEU:HD23	1.91	0.53
3:P:82:LEU:HB2	3:P:120:PRO:HB2	1.92	0.52
2:E:309:ASN:HB2	2:E:318:LEU:HD22	1.93	0.51
1:A:192:ASP:HA	1:A:197:GLU:HG3	1.93	0.50
2:E:290:GLY:O	2:E:291:ALA:CB	2.61	0.48
2:E:291:ALA:O	2:E:292:MET:CB	2.49	0.48
3:P:88:LEU:HD13	3:P:116:HIS:HB3	1.97	0.47
1:A:349:GLY:HA2	5:A:2083:HOH:O	2.16	0.46
1:A:205:PHE:HE1	1:A:266:ILE:HG22	1.82	0.45
1:A:272:ARG:HE	1:A:303:ARG:HH21	1.63	0.44
2:E:330:ARG:NH2	2:E:332:GLU:OE2	2.50	0.44
1:A:317:ASN:HB3	1:A:348:LEU:HD13	2.00	0.43
1:A:346:VAL:HG12	1:A:348:LEU:HG	1.99	0.43
1:A:193:HIS:CD2	1:A:195:GLU:H	2.32	0.42
1:A:205:PHE:CE1	1:A:266:ILE:HG22	2.54	0.42
1:A:178:SER:N	1:A:401:SER:HG	2.16	0.42
1:A:403:GLU:OE1	1:A:414:ARG:NH1	2.53	0.42
1:A:211:GLU:OE2	1:A:254:ASN:HB2	2.20	0.41
3:P:98:LEU:HB2	3:P:137:LEU:HD11	2.02	0.41
1:A:423:VAL:HG12	5:A:2112:HOH:O	2.20	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	272/312 (87%)	261 (96%)	9 (3%)	2 (1%)	30	33
2	E	45/107 (42%)	37 (82%)	6 (13%)	2 (4%)	4	1
3	P	93/114 (82%)	91 (98%)	2 (2%)	0	100	100
All	All	410/533 (77%)	389 (95%)	17 (4%)	4 (1%)	22	23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	291	ALA
2	E	292	MET
1	A	245	ALA
1	A	280	VAL

### 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	224/247 (91%)	215 (96%)	9 (4%)	42	55
2	E	39/95 (41%)	36 (92%)	3 (8%)	18	19
3	P	82/95 (86%)	78 (95%)	4 (5%)	35	43
All	All	345/437 (79%)	329 (95%)	16 (5%)	36	47

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	ILE
1	A	199	ARG

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Mol	Chain	Res	Type
1	A	201	MET
1	A	224	ASP
1	A	283	LEU
1	A	376	SER
1	A	401	SER
1	A	414	ARG
1	A	423	VAL
2	E	309	ASN
2	E	312	LYS
2	E	318	LEU
3	P	97	ARG
3	P	108	LEU
3	P	119	LEU
3	P	133	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	190	GLN
1	A	193	HIS
2	E	309	ASN
3	P	113	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 ⓘ

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.

## 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	275/312 (88%)	0.64	27 (9%) 8 13	27, 35, 52, 60	0
2	E	47/107 (43%)	0.53	6 (12%) 4 7	32, 37, 48, 49	1 (2%)
3	P	92/114 (80%)	0.04	4 (4%) 34 45	24, 34, 46, 49	0
All	All	414/533 (77%)	0.49	37 (8%) 10 16	24, 35, 50, 60	1 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	447	SER	8.3
1	A	277	VAL	6.0
1	A	280	VAL	5.9
2	E	323	PHE	4.5
1	A	165	ARG	4.3
1	A	164	PRO	3.9
1	A	153	SER	3.9
2	E	322	GLY	3.8
1	A	446	PRO	3.7
1	A	279	PRO	3.7
3	P	84	GLU	3.4
1	A	178	SER	3.4
2	E	320	PRO	3.4
1	A	278	GLN	3.3
1	A	179	LEU	3.2
2	E	292	MET	3.1
1	A	286	LEU	3.1
1	A	445	PRO	2.9
1	A	314	ALA	2.8
1	A	388	ALA	2.8
1	A	210	GLU	2.8
3	P	87	HIS	2.7
1	A	389	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	281	GLY	2.5
1	A	386	SER	2.4
1	A	390	ALA	2.3
1	A	406	LEU	2.3
2	E	324	GLN	2.3
3	P	85	GLU	2.3
1	A	392	VAL	2.2
3	P	90	GLN	2.2
1	A	402	ALA	2.2
1	A	313	THR	2.1
1	A	418	PHE	2.1
2	E	290	GLY	2.0
1	A	335	THR	2.0
1	A	350	THR	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 ⓘ

There are no carbohydrates in this entry.

## 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
4	CA	A	1448	1/1	0.12	-1.04	86,86,86,86	0
4	CA	E	1333	1/1	0.05	-1.93	52,52,52,52	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.