



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:08 AM GMT

PDB ID : 2W2N
Title : WT PCSK9-DELTAC BOUND TO EGF-A H306Y MUTANT OF LDLR
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Deposited on : 2008-11-03
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

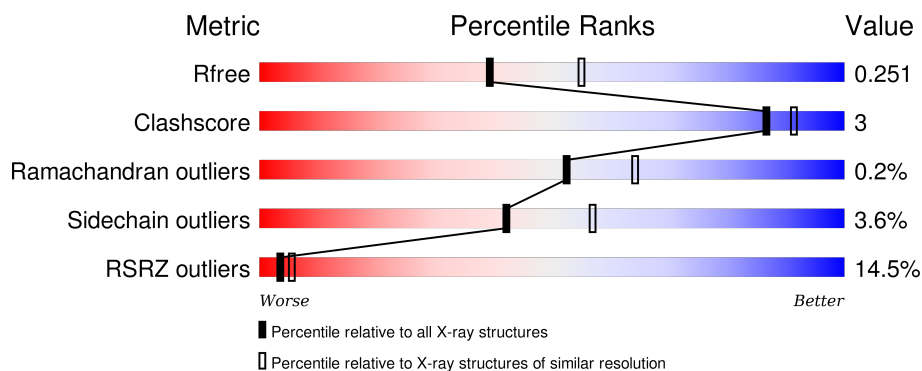
1 Overall quality at a glance

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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	A	312	<div> <div>14%</div> <div> <div></div> <div>80%</div> <div>7%</div> <div>13%</div> </div> </div>
2	E	107	<div> <div>9%</div> <div> <div></div> <div>40%</div> <div>6%</div> <div>54%</div> </div> </div>
3	P	114	<div> <div>6%</div> <div> <div></div> <div>73%</div> <div>7%</div> <div>•</div> <div>18%</div> </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3365 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	273	Total	C	N	O	S	0	7	0
			2050	1281	357	401	11			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	49	Total	C	N	O	S	0	0	0
			372	227	63	75	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	306	TYR	HIS	ENGINEERED MUTATION	UNP P01130

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	93	Total	C	N	O	S	0	3	0
			765	490	139	134	2			

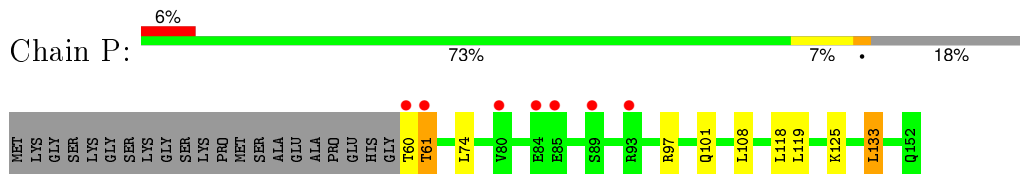
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	99	Total 99	O 99	0	0
5	E	27	Total 27	O 27	0	0
5	P	49	Total 49	O 49	0	0

- Molecule 1: PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 9



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	83.94Å 83.94Å 209.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 25.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.4 (40.00-2.30) 97.5 (25.98-2.30)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.213 , 0.254 0.215 , 0.251	Depositor DCC
R_{free} test set	1691 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 33386 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3365	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.39	0/2104	0.56	1/2863 (0.0%)
2	E	0.53	0/377	0.55	0/507
3	P	0.37	0/792	0.57	0/1070
All	All	0.41	0/3273	0.56	1/4440 (0.0%)

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
1	A	1	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	280	VAL	N-CA-C	5.64	126.23	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	280	VAL	CA

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	2050	0	2038	9	0
2	E	372	0	331	3	0
3	P	765	0	782	7	0
4	A	1	0	0	0	0
4	E	2	0	0	0	0
5	A	99	0	0	0	0
5	E	27	0	0	0	1
5	P	49	0	0	1	1
All	All	3365	0	3151	17	1

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 3.

All (17) 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)
3:P:60:THR:N	3:P:61:THR:HA	1.91	0.86
2:E:285:ASN:N	2:E:286:LEU:HA	2.03	0.73
1:A:304:LEU:HD13	3:P:118:LEU:HD21	1.74	0.68
1:A:275:GLN:O	1:A:279:PRO:HB3	2.05	0.56
3:P:133:LEU:HD12	3:P:133:LEU:C	2.26	0.56
1:A:201:MET:CE	1:A:203:THR:HG22	2.37	0.55
1:A:367[B]:ASP:HA	1:A:381[B]:SER:OG	2.06	0.55
3:P:125:LYS:NZ	5:P:2030:HOH:O	2.40	0.54
3:P:60:THR:N	3:P:61:THR:CA	2.71	0.51
3:P:101:GLN:OE1	3:P:133:LEU:HD13	2.12	0.48
2:E:285:ASN:N	2:E:286:LEU:CA	2.76	0.46
2:E:332:GLU:O	2:E:333:ASP:HB3	2.16	0.46
1:A:260:THR:HG22	3:P:74:LEU:CD1	2.48	0.44
1:A:357:ARG:HB3	1:A:436:LEU:HB3	2.01	0.42
1:A:189:ILE:HD13	1:A:200:VAL:HG21	2.00	0.42
1:A:184:LEU:HD13	1:A:286:LEU:HD23	2.02	0.41
1:A:186:ASP:OD2	1:A:288:PRO:HG2	2.20	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:2018:HOH:O	5:P:2032:HOH:O[6_455]	2.11	0.09

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	274/312 (88%)	266 (97%)	7 (3%)	1 (0%)	39	48
2	E	47/107 (44%)	42 (89%)	5 (11%)	0	100	100
3	P	94/114 (82%)	92 (98%)	2 (2%)	0	100	100
All	All	415/533 (78%)	400 (96%)	14 (3%)	1 (0%)	52	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	280	VAL

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	224/247 (91%)	219 (98%)	5 (2%)	60	77
2	E	40/95 (42%)	38 (95%)	2 (5%)	30	41
3	P	83/95 (87%)	78 (94%)	5 (6%)	24	31
All	All	347/437 (79%)	335 (96%)	12 (4%)	42	58

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	199	ARG
1	A	278	GLN
1	A	375	CYS
1	A	414	ARG
1	A	423	VAL
2	E	312	LYS
2	E	318	LEU
3	P	61	THR
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 (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	193	HIS
2	E	300	ASN
2	E	301	ASN
2	E	309	ASN
3	P	99	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 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

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	273/312 (87%)	0.73	43 (15%) 3 4	18, 25, 35, 42	0
2	E	49/107 (45%)	0.65	10 (20%) 1 2	25, 27, 41, 42	1 (2%)
3	P	93/114 (81%)	0.27	7 (7%) 17 24	17, 26, 33, 36	0
All	All	415/533 (77%)	0.62	60 (14%) 3 5	17, 26, 36, 42	1 (0%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	SER	7.3
1	A	277	VAL	6.1
1	A	278	GLN	5.3
3	P	60	THR	5.2
2	E	285	ASN	5.1
1	A	165	ARG	5.1
1	A	212	ASP	5.1
1	A	287	LEU	4.8
1	A	286	LEU	4.5
2	E	332	GLU	4.3
2	E	323	PHE	4.3
1	A	446	PRO	4.2
2	E	322	GLY	4.0
1	A	211	GLU	3.7
1	A	185	LEU	3.6
1	A	164	PRO	3.5
1	A	392	VAL	3.5
1	A	279	PRO	3.5
1	A	348	LEU	3.3
2	E	331	CYS	3.3
1	A	390	ALA	3.3
3	P	61	THR	3.2
3	P	85	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
2	E	333	ASP	3.2
1	A	153	SER	3.1
1	A	184	LEU	3.0
3	P	93[A]	ARG	3.0
1	A	306	ARG	2.9
1	A	204	ASP	2.8
1	A	441	VAL	2.8
3	P	84	GLU	2.7
1	A	265	LEU	2.7
2	E	324	GLN	2.7
1	A	285	VAL	2.7
1	A	268	LEU	2.6
1	A	436	LEU	2.5
3	P	80	VAL	2.5
1	A	402	ALA	2.5
1	A	405	GLU	2.5
1	A	230	LEU	2.5
1	A	234	VAL	2.5
2	E	321	ASP	2.4
1	A	363	ALA	2.4
1	A	389	ALA	2.4
1	A	313	THR	2.4
1	A	289	LEU	2.4
1	A	350	THR	2.3
1	A	201	MET	2.3
1	A	233	VAL	2.2
1	A	288	PRO	2.2
1	A	179	LEU	2.2
1	A	192	ASP	2.1
1	A	413[A]	GLN	2.1
1	A	223	CYS	2.1
1	A	331	PRO	2.1
1	A	280	VAL	2.1
1	A	312	VAL	2.1
2	E	326	VAL	2.1
2	E	286	LEU	2.0
3	P	89	SER	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 [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, 95th 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(\AA^2)	Q<0.9
4	CA	A	1447	1/1	0.87	0.10	-0.60	80,80,80,80	0
4	CA	E	1334	1/1	0.97	0.07	-2.25	35,35,35,35	0
4	CA	E	1335	1/1	0.74	0.08	-	93,93,93,93	0

6.5 Other polymers [i](#)

There are no such residues in this entry.