wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 06:08 AM GMT

PDB ID	:	2W2M
Title	:	WT PCSK9-DELTAC BOUND TO WT EGF-A OF LDLR
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Deposited on	:	2008-11-03
Resolution	:	2.40 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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

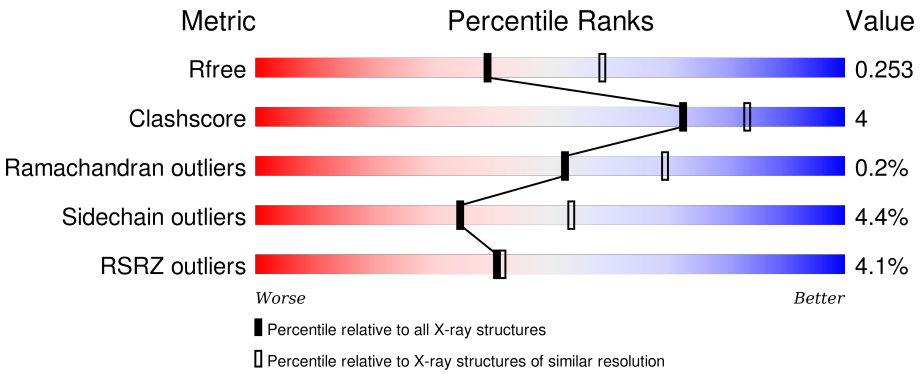
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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 <=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	4%, 80%, 8%, •, 11%
2	E	107	5%, 39%, 7%, 54%
3	P	114	69%, 10%, ••, 19%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3408 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
			Total	C	N	O	S			
1	A	277	2054	1281	360	402	11	0	3	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	452	ALA	-	EXPRESSION TAG	UNP Q8NBP7
A	453	GLY	-	EXPRESSION TAG	UNP Q8NBP7
A	454	THR	-	EXPRESSION TAG	UNP Q8NBP7
A	455	ALA	-	EXPRESSION TAG	UNP Q8NBP7
A	456	ALA	-	EXPRESSION TAG	UNP Q8NBP7
A	457	ALA	-	EXPRESSION TAG	UNP Q8NBP7
A	458	SER	-	EXPRESSION TAG	UNP Q8NBP7
A	459	HIS	-	EXPRESSION TAG	UNP Q8NBP7
A	460	HIS	-	EXPRESSION TAG	UNP Q8NBP7
A	461	HIS	-	EXPRESSION TAG	UNP Q8NBP7
A	462	HIS	-	EXPRESSION TAG	UNP Q8NBP7
A	463	HIS	-	EXPRESSION TAG	UNP Q8NBP7
A	464	HIS	-	EXPRESSION TAG	UNP Q8NBP7

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	49	373	227	66	73	7	0	1	0

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	266	MET	-	EXPRESSION TAG	UNP P01130
E	267	LYS	-	EXPRESSION TAG	UNP P01130

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Chain	Residue	Modelled	Actual	Comment	Reference
E	268	HIS	-	EXPRESSION TAG	UNP P01130
E	269	HIS	-	EXPRESSION TAG	UNP P01130
E	270	HIS	-	EXPRESSION TAG	UNP P01130
E	271	HIS	-	EXPRESSION TAG	UNP P01130
E	272	HIS	-	EXPRESSION TAG	UNP P01130
E	273	HIS	-	EXPRESSION TAG	UNP P01130
E	274	PRO	-	EXPRESSION TAG	UNP P01130
E	275	MET	-	EXPRESSION TAG	UNP P01130
E	276	SER	-	EXPRESSION TAG	UNP P01130
E	277	ASP	-	EXPRESSION TAG	UNP P01130
E	278	TYR	-	EXPRESSION TAG	UNP P01130
E	279	ASP	-	EXPRESSION TAG	UNP P01130
E	280	ILE	-	EXPRESSION TAG	UNP P01130
E	281	PRO	-	EXPRESSION TAG	UNP P01130
E	282	THR	-	EXPRESSION TAG	UNP P01130
E	283	THR	-	EXPRESSION TAG	UNP P01130
E	284	GLU	-	EXPRESSION TAG	UNP P01130
E	285	ASN	-	EXPRESSION TAG	UNP P01130
E	286	LEU	-	EXPRESSION TAG	UNP P01130
E	287	TYR	-	EXPRESSION TAG	UNP P01130
E	288	PHE	-	EXPRESSION TAG	UNP P01130
E	289	GLN	-	EXPRESSION TAG	UNP P01130
E	290	GLY	-	EXPRESSION TAG	UNP P01130
E	291	ALA	-	EXPRESSION TAG	UNP P01130
E	292	MET	-	EXPRESSION TAG	UNP P01130

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	P	92	763	491	138	132	2	0	4	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	39	MET	-	EXPRESSION TAG	UNP Q8NBP7
P	40	LYS	-	EXPRESSION TAG	UNP Q8NBP7
P	41	GLY	-	EXPRESSION TAG	UNP Q8NBP7
P	42	SER	-	EXPRESSION TAG	UNP Q8NBP7
P	43	LYS	-	EXPRESSION TAG	UNP Q8NBP7
P	44	GLY	-	EXPRESSION TAG	UNP Q8NBP7

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Chain	Residue	Modelled	Actual	Comment	Reference
P	45	SER	-	EXPRESSION TAG	UNP Q8NBP7
P	46	LYS	-	EXPRESSION TAG	UNP Q8NBP7
P	47	GLY	-	EXPRESSION TAG	UNP Q8NBP7
P	48	SER	-	EXPRESSION TAG	UNP Q8NBP7
P	49	LYS	-	EXPRESSION TAG	UNP Q8NBP7
P	50	PRO	-	EXPRESSION TAG	UNP Q8NBP7
P	51	MET	-	EXPRESSION TAG	UNP Q8NBP7
P	52	SER	-	EXPRESSION TAG	UNP Q8NBP7

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

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

- Molecule 5 is water.

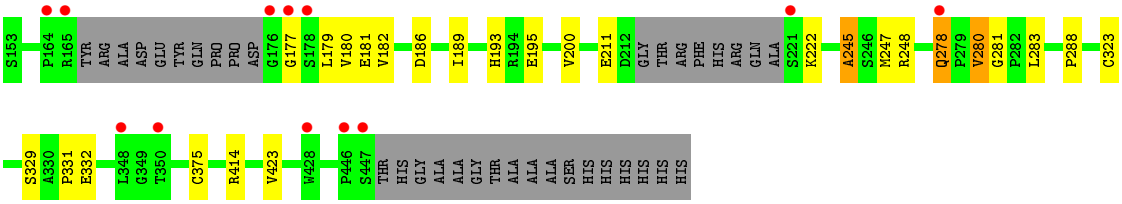
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	117	Total O 117 117	0	0
5	E	41	Total O 41 41	0	0
5	P	57	Total O 57 57	0	0

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 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.

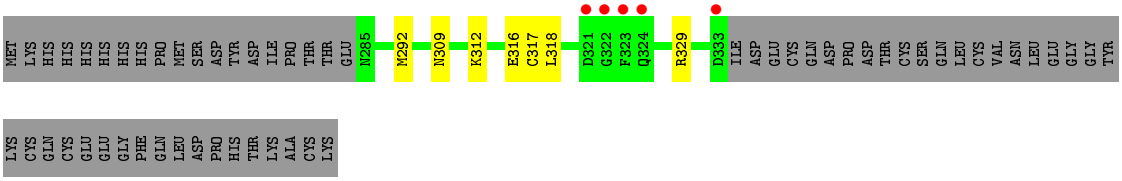
- Molecule 1: PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 9

Chain A:



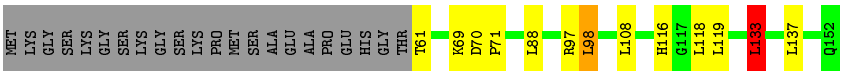
- Molecule 2: LOW-DENSITY LIPOPROTEIN RECEPTOR

Chain E:



- Molecule 3: PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 9

Chain P:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	83.00Å 83.00Å 211.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 2.40 45.11 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.00-2.40) 99.9 (45.11-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.78 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.215 , 0.254 0.213 , 0.253	Depositor DCC
R_{free} test set	1512 reflections (5.34%)	DCC
Wilson B-factor (Å^2)	35.2	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 46.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	1 of 29811 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3408	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	A	0.38	0/2096	0.54	0/2853
2	E	0.51	0/381	0.55	0/512
3	P	0.38	0/792	0.58	1/1067 (0.1%)
All	All	0.40	0/3269	0.55	1/4432 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	133	LEU	CA-CB-CG	5.07	126.97	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2054	0	2040	15	0
2	E	373	0	335	6	0
3	P	763	0	794	6	0
4	A	1	0	0	0	0
4	E	2	0	0	0	0
5	A	117	0	0	0	0
5	E	41	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	P	57	0	0	0	0
All	All	3408	0	3169	27	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 4.

The worst 5 of 27 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:69[B]:LYS:HG3	3:P:71:PRO:HD2	1.73	0.70
2:E:316:GLU:HG3	2:E:318:LEU:CD1	2.26	0.66
1:A:177:GLY:HA3	1:A:245:ALA:HA	1.79	0.64
1:A:186:ASP:OD2	1:A:288:PRO:HG2	2.02	0.60
3:P:98:LEU:HB2	3:P:137:LEU:HD11	1.86	0.57

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	274/312 (88%)	262 (96%)	11 (4%)	1 (0%)	39 56
2	E	48/107 (45%)	44 (92%)	4 (8%)	0	100 100
3	P	94/114 (82%)	90 (96%)	4 (4%)	0	100 100
All	All	416/533 (78%)	396 (95%)	19 (5%)	1 (0%)	52 69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	245	ALA

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%)	215 (96%)	9 (4%)	38	58
2	E	40/95 (42%)	40 (100%)	0	100	100
3	P	83/95 (87%)	77 (93%)	6 (7%)	18	28
All	All	347/437 (79%)	332 (96%)	15 (4%)	35	55

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	375	CYS
1	A	414	ARG
3	P	108	LEU
1	A	283	LEU
3	P	98	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	193	HIS
1	A	278	GLN
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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

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, 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	277/312 (88%)	0.01	12 (4%) 39 40	16, 24, 38, 50	0
2	E	49/107 (45%)	-0.02	5 (10%) 9 8	24, 27, 39, 41	0
3	P	92/114 (80%)	-0.48	0 100 100	15, 24, 31, 35	0
All	All	418/533 (78%)	-0.10	17 (4%) 41 42	15, 25, 38, 50	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	178	SER	10.1
1	A	447	SER	7.1
1	A	221	SER	5.0
1	A	446	PRO	4.5
1	A	164	PRO	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, 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(Å^2)	Q<0.9
4	CA	A	1448	1/1	0.93	0.17	1.76	61,61,61,61	0
4	CA	E	1334	1/1	0.95	0.06	-3.11	30,30,30,30	0
4	CA	E	1335	1/1	0.71	0.06	-	92,92,92,92	0

6.5 Other polymers (i)

There are no such residues in this entry.