



wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 08:01 am BST

PDB ID : 2F8X
Title : Crystal structure of activated Notch, CSL and MAML on HES-1 promoter DNA sequence
Authors : Nam, Y.; Sliz, P.; Blacklow, S.C.
Deposited on : 2005-12-04
Resolution : 3.25 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

<https://www.wwpdb.org/validation/2017/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)	:	1.13
EDS	:	2.11
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)	:	2.11

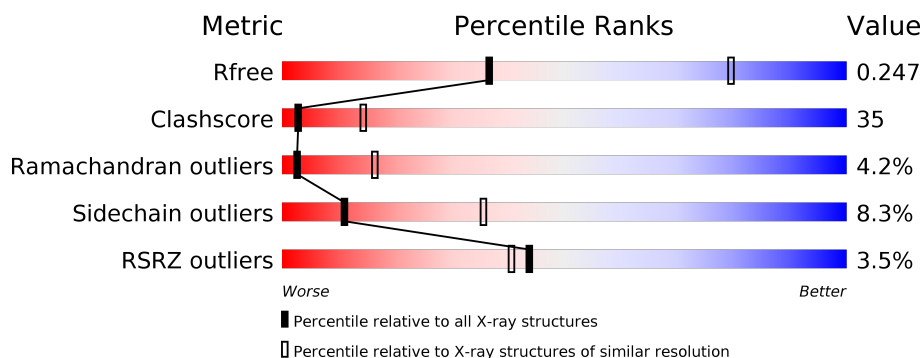
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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 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	X	18	<div> <div>6%</div> <div>6% 67% 22% 6%</div> </div>
2	Y	18	<div> <div>6%</div> <div>94% 6%</div> </div>
3	C	434	<div> <div>3%</div> <div>42% 47% 9%</div> </div>
4	K	256	<div> <div>4%</div> <div>50% 32% 15%</div> </div>
5	M	63	<div> <div>3%</div> <div>48% 30% 10% 13%</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6236 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 DNA chain called 5'-D(*GP*TP*TP*AP*CP*TP*GP*TP*GP*GP*GP*A P*AP*AP*GP*AP*AP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	18	Total	C	N	O	P	0	0	0
			375	179	76	103	17			

- Molecule 2 is a DNA chain called 5'-D(*TP*TP*TP*CP*TP*TP*TP*CP*CP*CP*AP*CP *AP*GP*TP*AP*AP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Y	18	Total	C	N	O	P	0	0	0
			357	174	57	109	17			

- Molecule 3 is a protein called Recombining binding protein suppressor of hairless, isoform 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	424	Total	C	N	O	S	0	0	0
			3369	2133	580	631	25			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	8	MET	-	INITIATING METHIONINE	UNP Q06330
C	436	HIS	-	EXPRESSION TAG	UNP Q06330
C	437	HIS	-	EXPRESSION TAG	UNP Q06330
C	438	HIS	-	EXPRESSION TAG	UNP Q06330
C	439	HIS	-	EXPRESSION TAG	UNP Q06330
C	440	HIS	-	EXPRESSION TAG	UNP Q06330
C	441	HIS	-	EXPRESSION TAG	UNP Q06330

- Molecule 4 is a protein called Neurogenic locus notch homolog protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	K	218	Total	C	N	O	S	0	0	0
			1658	1014	312	324	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1872	GLY	-	CLONING ARTIFACT	UNP P46531

- Molecule 5 is a protein called Mastermind-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	M	55	Total	C	N	O	S	0	0	0
			467	282	103	78	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	12	GLY	-	CLONING ARTIFACT	UNP Q92585

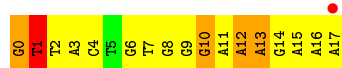
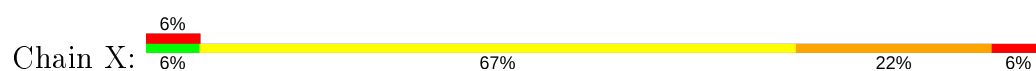
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	4	Total	O	0	0
			4	4		
6	K	4	Total	O	0	0
			4	4		
6	M	2	Total	O	0	0
			2	2		

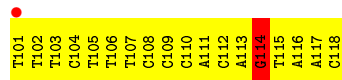
3 Residue-property plots [i](#)

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.

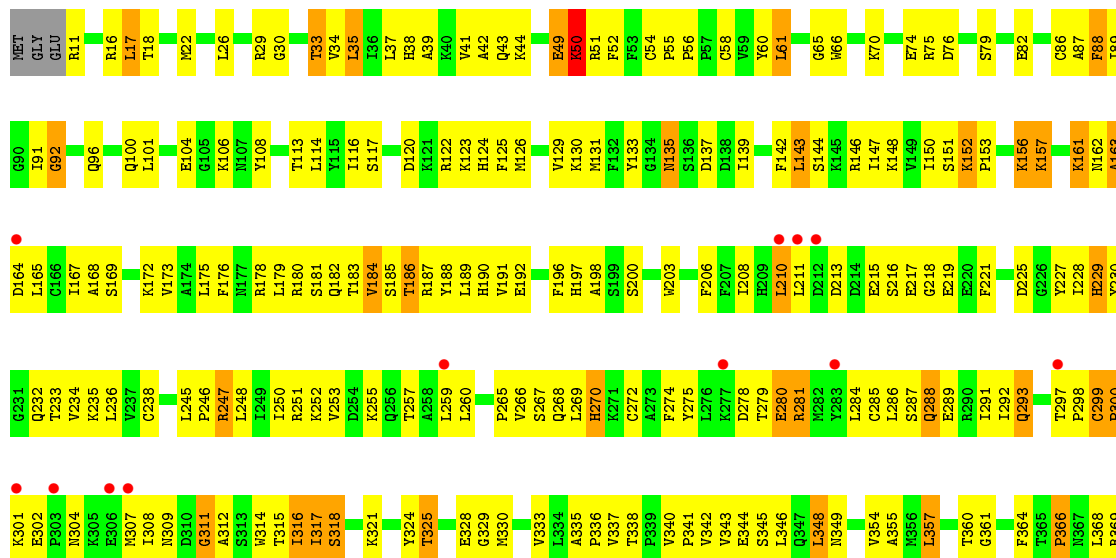
- Molecule 1: 5'-D(*GP*TP*TP*AP*CP*TP*GP*TP*GP*GP*GP*AP*AP*AP*GP*AP*AP*A)-3'



- Molecule 2: 5'-D(*TP*TP*TP*CP*TP*TP*TP*CP*CP*CP*AP*CP*AP*GP*TP*AP*AP*C)-3'

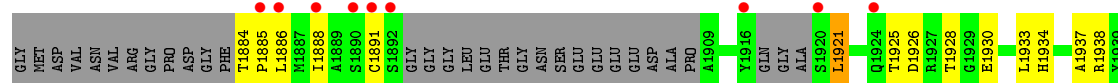


- Molecule 3: Recombining binding protein suppressor of hairless, isoform 4

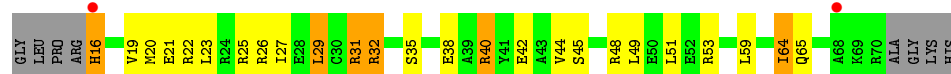




• Molecule 4: Neurogenic locus notch homolog protein 1



• Molecule 5: Mastermind-like protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	273.87Å 273.87Å 121.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.82 – 3.25 44.82 – 3.25	Depositor EDS
% Data completeness (in resolution range)	91.1 (44.82-3.25) 97.6 (44.82-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 3.25Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.222 , 0.257 0.220 , 0.247	Depositor DCC
R_{free} test set	3688 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	83.1	Xtriage
Anisotropy	0.464	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6236	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.18% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	X	0.79	0/423	1.01	2/653 (0.3%)
2	Y	0.82	0/397	1.00	1/609 (0.2%)
3	C	0.49	0/3444	0.73	0/4655
4	K	0.52	0/1678	0.78	0/2275
5	M	0.55	0/474	0.67	0/631
All	All	0.55	0/6416	0.78	3/8823 (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	X	0	4
2	Y	0	1
All	All	0	5

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	1	DT	N1-C1'-C2'	5.33	122.73	112.60
1	X	10	DG	O4'-C1'-N9	5.05	111.54	108.00
2	Y	114	DG	O5'-P-OP2	-5.02	101.18	105.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	0	DG	Sidechain
1	X	1	DT	Sidechain
1	X	12	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	X	13	DA	Sidechain
2	Y	114	DG	Sidechain

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	X	375	0	204	18	0
2	Y	357	0	207	29	0
3	C	3369	0	3348	280	0
4	K	1658	0	1606	85	0
5	M	467	0	472	26	0
6	C	4	0	0	0	0
6	K	4	0	0	0	0
6	M	2	0	0	0	0
All	All	6236	0	5837	424	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 35.

The worst 5 of 424 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:C:299:CYS:H	3:C:300:PRO:HD2	1.19	1.05
2:Y:112:DC:H2''	2:Y:113:DA:H5'	1.39	1.04
3:C:157:LYS:HD2	3:C:157:LYS:H	1.34	0.92
3:C:41:VAL:HG21	3:C:268:GLN:HG2	1.52	0.91
3:C:401:TRP:H	3:C:401:TRP:HD1	1.17	0.91

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	
3	C	422/434 (97%)	329 (78%)	66 (16%)	27 (6%)	1	9
4	K	212/256 (83%)	195 (92%)	15 (7%)	2 (1%)	17	50
5	M	53/63 (84%)	53 (100%)	0	0	100	100
All	All	687/753 (91%)	577 (84%)	81 (12%)	29 (4%)	3	16

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	219	GLU
3	C	225	ASP
3	C	247	ARG
3	C	299	CYS
3	C	329	GLY

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	
3	C	374/382 (98%)	345 (92%)	29 (8%)	12	38
4	K	170/204 (83%)	161 (95%)	9 (5%)	22	53
5	M	49/54 (91%)	38 (78%)	11 (22%)	1	3
All	All	593/640 (93%)	544 (92%)	49 (8%)	11	36

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	318	SER
3	C	370	VAL
5	M	40	ARG
3	C	338	THR
3	C	421	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	304	ASN
3	C	349	ASN
4	K	2060	ASN
3	C	182	GLN
3	C	288	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](#)

There are no ligands in this entry.

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	X	18/18 (100%)	0.26	1 (5%) 24 22	69, 100, 192, 200	0
2	Y	18/18 (100%)	0.29	1 (5%) 24 22	61, 98, 201, 201	0
3	C	424/434 (97%)	0.01	13 (3%) 49 47	19, 81, 196, 201	1 (0%)
4	K	218/256 (85%)	-0.21	9 (4%) 37 34	21, 54, 179, 201	0
5	M	55/63 (87%)	-0.10	2 (3%) 42 39	24, 68, 182, 201	0
All	All	733/789 (92%)	-0.05	26 (3%) 44 40	19, 71, 194, 201	1 (0%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	K	1891	CYS	5.6
4	K	1920	SER	5.2
4	K	1890	SER	5.1
3	C	211	LEU	3.7
3	C	307	MET	3.2

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.