



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 03:38 PM GMT

PDB ID : 2ON6
Title : Crystal structure of human purine nucleoside phosphorylase mutant H257F with Imm-H
Authors : Rinaldo-Matthis, A.; Murkin, A.S.; Almo, S.C.; Schramm, V.L.
Deposited on : 2007-01-23
Resolution : 2.50 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

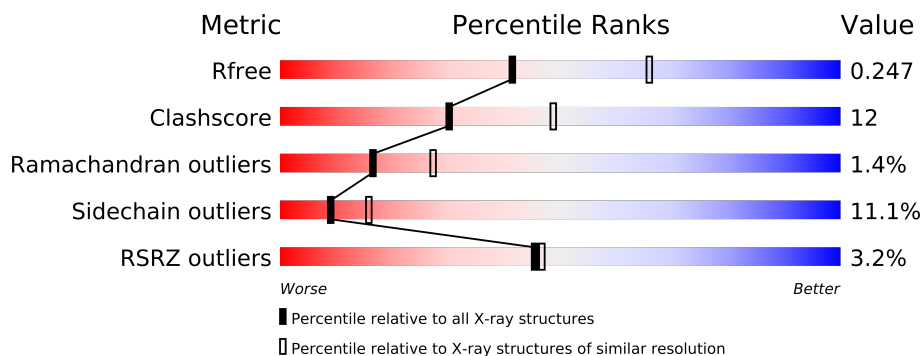
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.50 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	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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. 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	289	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	IMH	A	300	-	X

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 2297 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.

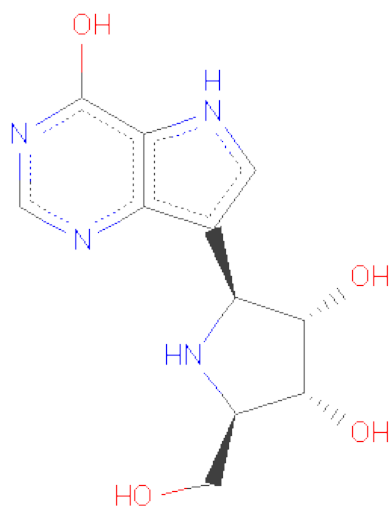
- Molecule 1 is a protein called Purine nucleoside phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	2214	1409	385	404	16	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	SER	GLY	CONFLICT	UNP P00491
A	257	PHE	HIS	ENGINEERED	UNP P00491

- Molecule 2 is 1,4-DIDEOXY-4-AZA-1-(S)-(9-DEAZAHYPOXANTHIN-9-YL)-D-RIBITOL (three-letter code: IMH) (formula: C₁₁H₁₄N₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	19	11	4	4	0	0

- Molecule 3 is water.

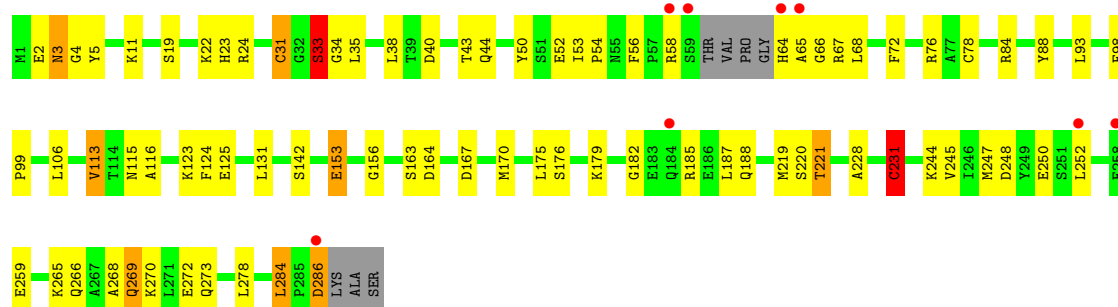
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	64	Total 64	O 64	0	0

3 Residue-property plots

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: Purine nucleoside phosphorylase

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	142.86Å 142.86Å 168.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.53 – 2.50 29.52 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.5 (29.53-2.50) 94.5 (29.52-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.201 , 0.245 0.203 , 0.247	Depositor DCC
R_{free} test set	1114 reflections (5.43%)	DCC
Wilson B-factor (Å ²)	62.8	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.2	EDS
Estimated twinning fraction	0.018 for -2/3*h-1/3*k+2/3*l,-1/3*h-2/3*k-2/3*l,2/3*h-2/3*k+1/3*l 0.016 for -h,1/3*h-1/3*k+2/3*l,2/3*h+4/3*k+1/3*l 0.007 for -1/3*h+1/3*k-2/3*l,-k,-4/3*h-2/3*k+1/3*l	Xtriage
L-test for twinning	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 21629 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2297	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: IMH

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	1.17	5/2264 (0.2%)	1.00	5/3060 (0.2%)

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	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	286	ASP	CG-OD2	13.32	1.55	1.25
1	A	286	ASP	CG-OD1	12.87	1.54	1.25
1	A	231	CYS	CB-SG	-11.45	1.62	1.82
1	A	78	CYS	CB-SG	-8.41	1.68	1.82
1	A	52	GLU	CG-CD	5.22	1.59	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	286	ASP	OD1-CG-OD2	-7.16	109.69	123.30
1	A	286	ASP	CB-CG-OD1	-6.54	112.42	118.30
1	A	231	CYS	CB-CA-C	-5.33	99.74	110.40
1	A	113	VAL	CB-CA-C	-5.16	101.59	111.40
1	A	142	SER	CB-CA-C	-5.00	100.59	110.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	286	ASP	Sidechain
1	A	34	GLY	Peptide

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	2214	0	2187	52	0
2	A	19	0	13	6	0
3	A	64	0	0	11	0
All	All	2297	0	2200	53	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 12.

All (53) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:220:SER:OG	2:A:300:IMH:H5'2	1.33	1.23
1:A:153:GLU:CD	1:A:153:GLU:H	1.69	0.95
1:A:220:SER:OG	2:A:300:IMH:C5'	2.22	0.85
1:A:125:GLU:HG3	3:A:325:HOH:O	1.86	0.75
1:A:113:VAL:HG23	1:A:113:VAL:O	1.86	0.74
1:A:67:ARG:HD3	3:A:350:HOH:O	1.89	0.71
1:A:3:ASN:ND2	1:A:5:TYR:H	1.90	0.70
1:A:265:LYS:HE3	3:A:324:HOH:O	1.96	0.66
1:A:153:GLU:N	1:A:153:GLU:CD	2.45	0.66
2:A:300:IMH:H5'1	3:A:311:HOH:O	1.94	0.66
1:A:247:MET:HE2	3:A:353:HOH:O	1.97	0.65
1:A:269:GLN:HA	1:A:269:GLN:NE2	2.17	0.59
1:A:23:HIS:O	1:A:24:ARG:HD3	2.03	0.58
1:A:219:MET:HG3	2:A:300:IMH:H1'	1.86	0.57
1:A:220:SER:CB	2:A:300:IMH:H5'2	2.35	0.56
1:A:113:VAL:CG2	1:A:113:VAL:O	2.53	0.56
1:A:268:ALA:O	1:A:272:GLU:HG3	2.06	0.55
1:A:124:PHE:O	1:A:244:LYS:HE2	2.08	0.53
1:A:179:LYS:HE2	1:A:179:LYS:HA	1.92	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:125:GLU:CG	3:A:325:HOH:O	2.51	0.51
1:A:123:LYS:HD2	3:A:338:HOH:O	2.11	0.51
1:A:247:MET:CE	3:A:353:HOH:O	2.58	0.51
1:A:228:ALA:O	1:A:231:CYS:HB2	2.11	0.51
1:A:67:ARG:CD	3:A:350:HOH:O	2.53	0.49
1:A:220:SER:O	1:A:221:THR:HB	2.11	0.49
1:A:50:TYR:CD2	1:A:66:GLY:HA3	2.47	0.49
1:A:3:ASN:HD22	1:A:4:GLY:N	2.12	0.48
1:A:43:THR:O	1:A:44:GLN:HB2	2.15	0.47
1:A:269:GLN:HA	1:A:269:GLN:HE21	1.79	0.47
1:A:167:ASP:HB3	1:A:170:MET:HB2	1.97	0.47
1:A:98:PHE:HB3	1:A:99:PRO:HD3	1.98	0.46
1:A:64:HIS:O	1:A:66:GLY:N	2.44	0.45
1:A:68:LEU:HA	1:A:68:LEU:HD12	1.74	0.45
1:A:38:LEU:HA	1:A:38:LEU:HD23	1.70	0.45
1:A:131:LEU:HD13	1:A:187:LEU:HD21	1.99	0.45
1:A:31:CYS:HB3	1:A:35:LEU:HB2	1.98	0.44
1:A:88:TYR:CE2	1:A:219:MET:HE3	2.53	0.44
1:A:3:ASN:HD22	1:A:5:TYR:H	1.65	0.43
1:A:98:PHE:N	1:A:99:PRO:CD	2.82	0.43
1:A:22:LYS:HA	1:A:22:LYS:HD3	1.77	0.43
1:A:219:MET:HE2	1:A:219:MET:HB2	1.89	0.42
1:A:115:ASN:HB2	2:A:300:IMH:H5'1	2.02	0.42
1:A:164:ASP:OD1	1:A:164:ASP:N	2.42	0.42
1:A:175:LEU:O	1:A:176:SER:C	2.59	0.41
1:A:284:LEU:CD1	3:A:364:HOH:O	2.68	0.41
1:A:153:GLU:HA	1:A:156:GLY:O	2.20	0.41
1:A:72:PHE:HA	1:A:76:ARG:O	2.20	0.41
1:A:106:LEU:HD23	1:A:106:LEU:HA	1.91	0.41
1:A:35:LEU:HA	1:A:35:LEU:HD23	1.94	0.41
1:A:284:LEU:HD12	3:A:364:HOH:O	2.21	0.41
1:A:33:SER:HB2	1:A:116:ALA:HB2	2.03	0.41
1:A:93:LEU:HD23	1:A:93:LEU:HA	1.85	0.41
1:A:53:ILE:O	1:A:54:PRO:C	2.55	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	278/289 (96%)	260 (94%)	14 (5%)	4 (1%)	16	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	SER
1	A	65	ALA
1	A	221	THR
1	A	182	GLY

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	235/240 (98%)	209 (89%)	26 (11%)	9	16

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	3	ASN
1	A	11	LYS
1	A	19	SER
1	A	31	CYS
1	A	33	SER
1	A	40	ASP
1	A	56	PHE
1	A	58	ARG
1	A	84	ARG

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Mol	Chain	Res	Type
1	A	153	GLU
1	A	163	SER
1	A	185	ARG
1	A	188	GLN
1	A	231	CYS
1	A	245	VAL
1	A	248	ASP
1	A	250	GLU
1	A	252	LEU
1	A	259	GLU
1	A	266	GLN
1	A	269	GLN
1	A	270	LYS
1	A	273	GLN
1	A	278	LEU
1	A	284	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	23	HIS
1	A	44	GLN
1	A	55	ASN
1	A	82	GLN
1	A	188	GLN
1	A	269	GLN
1	A	273	GLN

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 ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	IMH	A	300	-	21,21,21	1.17	2 (9%)	26,31,31	2.92	10 (38%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IMH	A	300	-	-	0/2/22/22	0/1/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	IMH	C6-C5	2.66	1.48	1.43
2	A	300	IMH	C2'-C1'	2.20	1.56	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	IMH	N3-C2-N1	-8.47	121.63	128.71
2	A	300	IMH	C9-C1'-N4'	7.48	124.85	113.28
2	A	300	IMH	C2-N3-C4	5.86	119.86	115.13
2	A	300	IMH	O2'-C2'-C1'	2.93	116.37	109.26
2	A	300	IMH	C3'-C2'-C1'	2.72	106.90	103.37
2	A	300	IMH	C5'-C4'-C3'	-2.49	109.55	114.07
2	A	300	IMH	C5-C4-N3	-2.34	122.82	125.25
2	A	300	IMH	O6-C6-C5	2.32	121.89	116.79
2	A	300	IMH	C4-C5-N7	2.30	107.94	106.07
2	A	300	IMH	C8-N7-C5	2.20	111.53	107.66

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, 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	282/289 (97%)	-0.02	8 (2%) 50 53	42, 62, 90, 101	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	184	GLN	3.6
1	A	65	ALA	3.1
1	A	64	HIS	3.1
1	A	286	ASP	2.9
1	A	252	LEU	2.9
1	A	58	ARG	2.6
1	A	59	SER	2.5
1	A	258	GLU	2.3

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, 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	IMH	A	300	19/19	0.87	15.34	55,58,63,64	19

6.5 Other polymers ⓘ

There are no such residues in this entry.