Full wwPDB X-ray Structure Validation Report (i)

Jun 11, 2024 – 11:51 PM EDT

PDB ID	:	2QDD
Title	:	Crystal structure of a member of enolase superfamily from Roseovarius nubinhibens ISM
Authors	:	Patskovsky, Y.; Bonanno, J.; Sauder, J.M.; Gilmore, J.M.; Iizuka, M.; Groshong, C.; Gheyi, T.; Sojitra, S.; Wasserman, S.R.; Koss, J.; Gerlt, J.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on	:	2007-06-20
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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

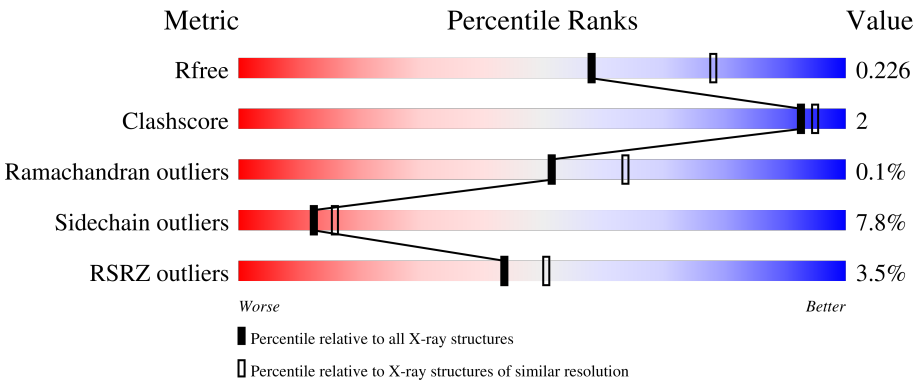
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

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 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 of 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 <=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	378	4%, 89%, 8%, •
1	B	378	3%, 87%, 10%, • •

Validation Pipeline (wwPDB-VP) : 2.36.2

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5975 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.

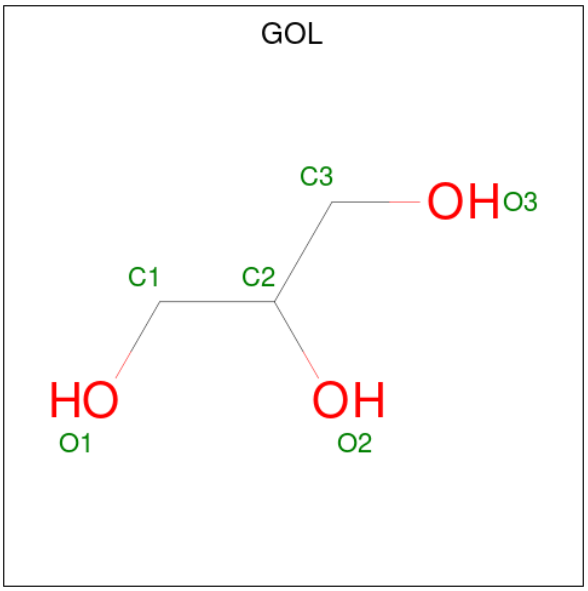
- Molecule 1 is a protein called Mandelate racemase/muconate lactonizing enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	368	2803	1763	510	519	11	0	6	0
1	B	368	2837	1777	527	522	11	0	10	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	cloning artifact	UNP A3SNF7
A	0	SER	-	cloning artifact	UNP A3SNF7
A	1	LEU	-	cloning artifact	UNP A3SNF7
A	369	GLU	-	cloning artifact	UNP A3SNF7
A	370	GLY	-	cloning artifact	UNP A3SNF7
A	371	HIS	-	cloning artifact	UNP A3SNF7
A	372	HIS	-	cloning artifact	UNP A3SNF7
A	373	HIS	-	cloning artifact	UNP A3SNF7
A	374	HIS	-	cloning artifact	UNP A3SNF7
A	375	HIS	-	cloning artifact	UNP A3SNF7
A	376	HIS	-	cloning artifact	UNP A3SNF7
B	-1	MET	-	cloning artifact	UNP A3SNF7
B	0	SER	-	cloning artifact	UNP A3SNF7
B	1	LEU	-	cloning artifact	UNP A3SNF7
B	369	GLU	-	cloning artifact	UNP A3SNF7
B	370	GLY	-	cloning artifact	UNP A3SNF7
B	371	HIS	-	cloning artifact	UNP A3SNF7
B	372	HIS	-	cloning artifact	UNP A3SNF7
B	373	HIS	-	cloning artifact	UNP A3SNF7
B	374	HIS	-	cloning artifact	UNP A3SNF7
B	375	HIS	-	cloning artifact	UNP A3SNF7
B	376	HIS	-	cloning artifact	UNP A3SNF7

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	6	3	3	0	0
			Total	C	O		
2	B	1	6	3	3	0	0

- Molecule 3 is water.

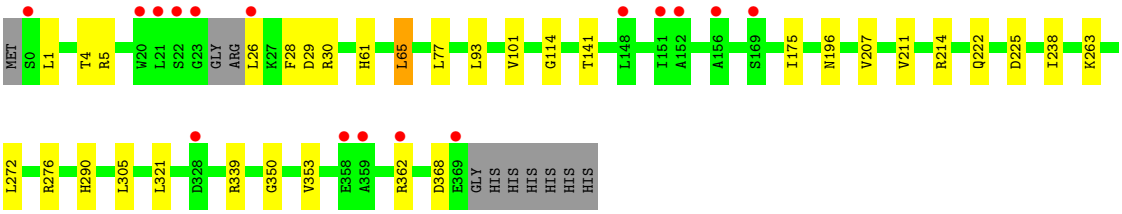
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	157	157	157	0	0
			Total	O		
3	B	166	166	166	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

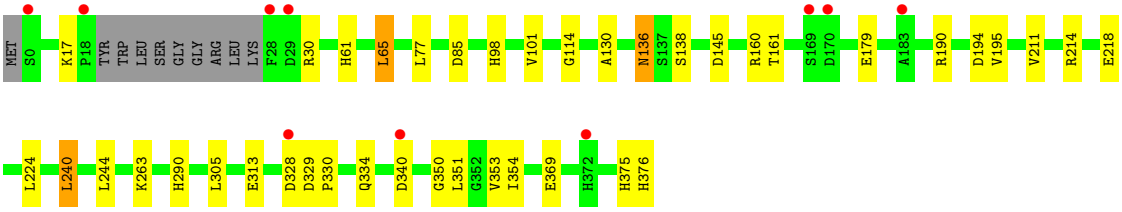
• Molecule 1: Mandelate racemase/muconate lactonizing enzyme

Chain A:



• Molecule 1: Mandelate racemase/muconate lactonizing enzyme

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α, β, γ	126.84Å 126.84Å 96.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 30.86 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (20.00-2.30) 99.3 (30.86-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.67 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.3.0034	Depositor
R, R_{free}	0.182 , 0.228 0.178 , 0.226	Depositor DCC
R_{free} test set	1099 reflections (3.13%)	wwPDB-VP
Wilson B-factor (Å^2)	36.6	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 44.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5975	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: GOL

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	0.34	0/2893	0.57	0/3953
1	B	0.35	0/2940	0.56	0/4014
All	All	0.34	0/5833	0.56	0/7967

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	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	28	PHE	Peptide

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	2803	0	2769	5	0
1	B	2837	0	2785	12	0
2	A	6	0	8	1	0
2	B	6	0	8	0	0
3	A	157	0	0	1	0
3	B	166	0	0	0	0
All	All	5975	0	5570	17	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 2.

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)
1:B:334:GLN:HE22	1:B:354:ILE:H	1.53	0.55
1:A:263:LYS:HG2	1:A:290:HIS:HB2	1.90	0.54
1:A:114:GLY:HA3	1:A:350:GLY:HA2	1.96	0.48
1:B:263:LYS:HG2	1:B:290:HIS:HB2	1.95	0.47
1:A:214:ARG:NH2	3:A:525:HOH:O	2.48	0.47
1:B:194:ASP:HA	1:B:218:GLU:HB3	1.98	0.45
2:A:377:GOL:C3	1:B:98:HIS:H	2.31	0.44
1:B:179[A]:GLU:HG2	1:B:211:VAL:HG22	2.00	0.44
1:B:65:LEU:HA	1:B:101:VAL:HG22	1.99	0.43
1:B:240:LEU:HB3	1:B:244:LEU:HD11	2.00	0.43
1:B:211:VAL:O	1:B:214:ARG:NH1	2.52	0.43
1:A:175:ILE:HG13	1:A:207:VAL:HB	2.02	0.41
1:B:375:HIS:ND1	1:B:376:HIS:OXT	2.53	0.41
1:B:329:ASP:HA	1:B:330:PRO:HD3	1.89	0.41
1:B:114:GLY:HA3	1:B:350:GLY:HA2	2.03	0.41
1:B:136[A]:ASN:HB3	1:B:161:THR:HB	2.03	0.41
1:A:65:LEU:HA	1:A:101:VAL:HG22	2.04	0.40

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	370/378 (98%)	363 (98%)	7 (2%)	0	100	100
1	B	374/378 (99%)	364 (97%)	9 (2%)	1 (0%)	41	50
All	All	744/756 (98%)	727 (98%)	16 (2%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	130	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	293/295 (99%)	266 (91%)	27 (9%)	9	11
1	B	297/295 (101%)	275 (93%)	22 (7%)	13	17
All	All	590/590 (100%)	541 (92%)	49 (8%)	12	14

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	LEU
1	A	4	THR
1	A	5[A]	ARG
1	A	5[B]	ARG
1	A	26	LEU
1	A	29	ASP
1	A	30	ARG
1	A	61	HIS
1	A	65	LEU
1	A	77	LEU
1	A	93	LEU
1	A	141	THR

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Mol	Chain	Res	Type
1	A	196[A]	ASN
1	A	196[B]	ASN
1	A	211	VAL
1	A	222	GLN
1	A	225	ASP
1	A	238[A]	ILE
1	A	238[B]	ILE
1	A	272	LEU
1	A	276	ARG
1	A	305	LEU
1	A	321	LEU
1	A	339	ARG
1	A	353	VAL
1	A	362	ARG
1	A	368	ASP
1	B	17	LYS
1	B	30	ARG
1	B	61	HIS
1	B	65	LEU
1	B	77	LEU
1	B	85	ASP
1	B	136[A]	ASN
1	B	136[B]	ASN
1	B	138	SER
1	B	145	ASP
1	B	160	ARG
1	B	190	ARG
1	B	195	VAL
1	B	224	LEU
1	B	240	LEU
1	B	305	LEU
1	B	313	GLU
1	B	328	ASP
1	B	340	ASP
1	B	351	LEU
1	B	353	VAL
1	B	369	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	267	ASN

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Mol	Chain	Res	Type
1	A	277	GLN
1	B	94	GLN
1	B	123	GLN
1	B	267	ASN
1	B	277	GLN
1	B	334	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are 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	GOL	A	377	-	5,5,5	0.42	0	5,5,5	0.61	0
2	GOL	B	377	-	5,5,5	0.40	0	5,5,5	0.22	0

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	GOL	A	377	-	-	4/4/4/4	-
2	GOL	B	377	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	377	GOL	C1-C2-C3-O3
2	B	377	GOL	O2-C2-C3-O3
2	A	377	GOL	O1-C1-C2-C3
2	A	377	GOL	C1-C2-C3-O3
2	A	377	GOL	O1-C1-C2-O2
2	A	377	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	377	GOL	1	0

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	368/378 (97%)	-0.14	16 (4%)	35	42	19, 36, 70, 103	0
1	B	368/378 (97%)	-0.17	10 (2%)	54	62	17, 35, 71, 87	0
All	All	736/756 (97%)	-0.15	26 (3%)	44	51	17, 36, 71, 103	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	22	SER	4.4
1	B	169	SER	4.2
1	A	152	ALA	4.2
1	B	372[A]	HIS	4.1
1	A	156	ALA	3.6
1	A	369	GLU	3.6
1	A	26	LEU	3.4
1	B	28	PHE	3.3
1	A	358	GLU	3.2
1	A	328	ASP	3.2
1	B	170	ASP	3.2
1	A	169	SER	2.9
1	A	20	TRP	2.8
1	B	29	ASP	2.8
1	A	23	GLY	2.7
1	B	183	ALA	2.6
1	A	362	ARG	2.6
1	A	0	SER	2.5
1	A	359	ALA	2.4
1	B	328	ASP	2.3
1	B	18	PRO	2.3
1	A	151	ILE	2.3
1	B	0	SER	2.1
1	A	148	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	21	LEU	2.1
1	B	340	ASP	2.1

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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
2	GOL	B	377	6/6	0.92	0.42	68,77,78,87	0
2	GOL	A	377	6/6	0.94	0.18	44,48,53,64	0

6.5 Other polymers (i)

There are no such residues in this entry.