



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 21, 2024 – 05:25 PM EDT

PDB ID : 2QGM  
Title : Crystal structure of succinoglycan biosynthesis protein at the resolution 1.7 Å. Northeast Structural Genomics Consortium target BcR136.  
Authors : Kuzin, A.P.; Abashidze, M.; Jayaraman, S.; Wang, H.; Fang, Y.; Maglaqui, M.; Ma, L.-C.; Xiao, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2007-06-29  
Resolution : 1.70 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) 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	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

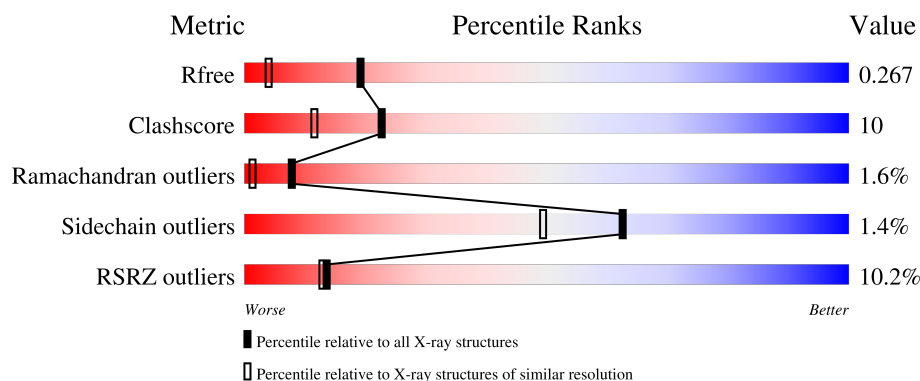
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
$R_{free}$	164625	5161 (1.70-1.70)
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (1.70-1.70)

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  $\geq 3$ , 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	A	445	<div> <div>9%</div> <div>68%</div> <div>18%</div> <div>12%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3436 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 Succinoglycan biosynthesis protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	Se	0	0	0
			3180	2055	524	590	11			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	cloning artifact	UNP Q81BF7
A	6	MSE	MET	cloning artifact	UNP Q81BF7
A	9	MSE	MET	cloning artifact	UNP Q81BF7
A	70	MSE	MET	cloning artifact	UNP Q81BF7
A	92	MSE	MET	cloning artifact	UNP Q81BF7
A	104	MSE	MET	cloning artifact	UNP Q81BF7
A	111	MSE	MET	cloning artifact	UNP Q81BF7
A	148	MSE	MET	cloning artifact	UNP Q81BF7
A	152	MSE	MET	cloning artifact	UNP Q81BF7
A	216	MSE	MET	cloning artifact	UNP Q81BF7
A	269	MSE	MET	cloning artifact	UNP Q81BF7
A	291	MSE	MET	cloning artifact	UNP Q81BF7
A	302	MSE	MET	cloning artifact	UNP Q81BF7
A	385	MSE	MET	cloning artifact	UNP Q81BF7

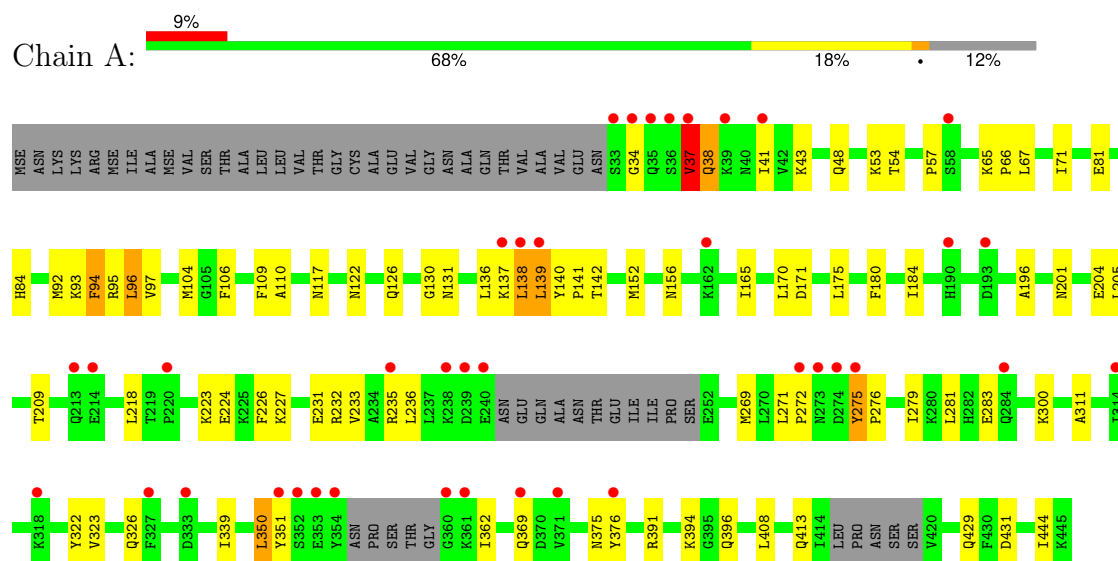
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	256	Total	O	0	0
			256	256		

### 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: Succinoglycan biosynthesis protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.75Å 76.96Å 87.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.59 – 1.70 19.59 – 1.70	Depositor EDS
% Data completeness (in resolution range)	77.8 (19.59-1.70) 81.6 (19.59-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.90 (at 1.70Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.229 , 0.255 0.241 , 0.267	Depositor DCC
$R_{free}$ test set	2148 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.5	Xtriage
Anisotropy	0.242	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 38.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3436	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.00% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0/3240	0.59	0/4347

There are no bond length outliers.

There are no bond angle outliers.

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	3180	0	3200	66	0
2	A	256	0	0	3	0
All	All	3436	0	3200	66	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 10.

All (66) 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:A:201:ASN:HD21	1:A:232:ARG:HE	1.12	0.93
1:A:156:ASN:HD21	1:A:165:ILE:H	1.20	0.85
1:A:92:MSE:HE2	1:A:96:LEU:HD13	1.59	0.83
1:A:48:GLN:HE22	1:A:394:LYS:H	1.25	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:TYR:H	1:A:276:PRO:HD2	1.50	0.76
1:A:110:ALA:HB1	1:A:170:LEU:HD21	1.69	0.74
1:A:37:VAL:HG12	1:A:41:ILE:HD13	1.71	0.72
1:A:122:ASN:O	1:A:126:GLN:HG2	1.90	0.72
1:A:201:ASN:ND2	1:A:232:ARG:HE	1.87	0.71
1:A:322:TYR:HA	1:A:326:GLN:HE22	1.54	0.71
1:A:136:LEU:O	1:A:141:PRO:HG3	1.95	0.65
1:A:81:GLU:OE2	1:A:84:HIS:HD2	1.82	0.63
1:A:323:VAL:H	1:A:326:GLN:NE2	1.99	0.61
1:A:71:ILE:HB	1:A:104:MSE:HE1	1.83	0.60
1:A:322:TYR:HA	1:A:326:GLN:NE2	2.16	0.60
1:A:92:MSE:CE	1:A:96:LEU:HD13	2.31	0.59
1:A:375:ASN:HD21	1:A:408:LEU:H	1.51	0.58
1:A:323:VAL:H	1:A:326:GLN:HE21	1.50	0.58
1:A:138:LEU:O	1:A:139:LEU:HB2	2.04	0.58
1:A:142:THR:HG22	1:A:444:ILE:HD13	1.85	0.57
1:A:283:GLU:HG3	1:A:323:VAL:HA	1.86	0.57
1:A:271:LEU:HB3	1:A:272:PRO:HD3	1.87	0.57
1:A:106:PHE:HA	1:A:300:LYS:HB2	1.87	0.56
1:A:391:ARG:HD3	1:A:431:ASP:HB3	1.87	0.55
1:A:227:LYS:HD2	1:A:271:LEU:HD22	1.89	0.55
1:A:92:MSE:HE3	1:A:95:ARG:HB3	1.89	0.55
1:A:375:ASN:ND2	1:A:408:LEU:H	2.05	0.55
1:A:48:GLN:HE22	1:A:394:LYS:N	2.02	0.54
1:A:196:ALA:HB3	2:A:548:HOH:O	2.08	0.53
1:A:275:TYR:N	1:A:276:PRO:HD2	2.22	0.52
1:A:369:GLN:HA	1:A:376:TYR:CE2	2.46	0.49
1:A:233:VAL:HA	1:A:236:LEU:HD12	1.94	0.48
1:A:218:LEU:O	1:A:223:LYS:HE3	2.14	0.48
1:A:283:GLU:HG3	1:A:322:TYR:O	2.14	0.48
1:A:138:LEU:HD13	1:A:362:ILE:HD11	1.97	0.47
1:A:140:TYR:N	1:A:141:PRO:HD3	2.30	0.47
1:A:311:ALA:HB1	1:A:429:GLN:HE21	1.80	0.46
1:A:201:ASN:HD21	1:A:232:ARG:NE	1.95	0.46
1:A:351:TYR:HB2	1:A:413:GLN:HG2	1.97	0.46
1:A:67:LEU:O	1:A:71:ILE:HG12	2.16	0.46
1:A:53:LYS:HG3	1:A:54:THR:HG22	1.98	0.45
1:A:175:LEU:HB2	1:A:209:THR:HB	1.97	0.45
1:A:57:PRO:HG2	1:A:94:PHE:CD2	2.51	0.45
1:A:130:GLY:C	1:A:131:ASN:HD22	2.20	0.45
1:A:140:TYR:N	1:A:141:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:PHE:CG	1:A:152:MSE:HE1	2.52	0.44
1:A:323:VAL:O	1:A:326:GLN:HG2	2.17	0.44
1:A:117:ASN:OD1	1:A:137:LYS:HE3	2.17	0.44
1:A:269:MSE:HA	1:A:281:LEU:HD13	2.01	0.43
1:A:350:LEU:HD22	1:A:351:TYR:N	2.34	0.43
1:A:180:PHE:O	1:A:184:ILE:HG12	2.19	0.42
1:A:138:LEU:CB	1:A:351:TYR:OH	2.68	0.42
1:A:92:MSE:HE3	1:A:92:MSE:O	2.20	0.42
1:A:71:ILE:HD11	1:A:339:ILE:HD11	2.01	0.42
1:A:96:LEU:HD12	1:A:96:LEU:HA	1.95	0.41
1:A:138:LEU:HB2	1:A:351:TYR:OH	2.20	0.41
1:A:231:GLU:O	1:A:235:ARG:HG2	2.20	0.41
1:A:204:GLU:HG3	2:A:675:HOH:O	2.19	0.41
1:A:93:LYS:O	1:A:97:VAL:HG23	2.21	0.41
1:A:224:GLU:OE2	1:A:271:LEU:HD11	2.20	0.41
1:A:65:LYS:N	1:A:66:PRO:CD	2.85	0.40
1:A:43:LYS:HE2	2:A:660:HOH:O	2.21	0.40
1:A:205:LEU:HD13	1:A:226:PHE:HB3	2.03	0.40
1:A:37:VAL:HB	1:A:38:GLN:H	1.48	0.40
1:A:41:ILE:HG22	1:A:396:GLN:HB3	2.04	0.40
1:A:275:TYR:O	1:A:279:ILE:HG12	2.20	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	384/445 (86%)	366 (95%)	12 (3%)	6 (2%)	<b>8</b> <b>1</b>

All (6) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	37	VAL
1	A	38	GLN
1	A	34	GLY
1	A	138	LEU
1	A	139	LEU
1	A	275	TYR

### 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	346/376 (92%)	341 (99%)	5 (1%)	62 49

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	VAL
1	A	94	PHE
1	A	96	LEU
1	A	171	ASP
1	A	350	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	82	ASN
1	A	84	HIS
1	A	108	ASN
1	A	117	ASN
1	A	126	GLN
1	A	131	ASN
1	A	156	ASN
1	A	201	ASN
1	A	326	GLN
1	A	334	ASN

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Mol	Chain	Res	Type
1	A	347	ASN
1	A	369	GLN
1	A	375	ASN
1	A	429	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 oligosaccharides 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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	381/445 (85%)	0.64	39 (10%) <b>13</b> <b>13</b>	10, 22, 38, 46	1 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	33	SER	6.4
1	A	34	GLY	6.2
1	A	36	SER	6.0
1	A	353	GLU	5.6
1	A	37	VAL	5.6
1	A	138	LEU	5.5
1	A	35	GLN	5.5
1	A	354	TYR	4.7
1	A	360	GLY	4.3
1	A	376	TYR	4.3
1	A	351	TYR	4.2
1	A	58	SER	4.2
1	A	272	PRO	3.9
1	A	41	ILE	3.7
1	A	240	GLU	3.5
1	A	274	ASP	3.4
1	A	193	ASP	3.3
1	A	352	SER	3.2
1	A	39	LYS	3.1
1	A	369	GLN	3.1
1	A	275	TYR	3.1
1	A	314	ILE	2.9
1	A	235	ARG	2.9
1	A	371	VAL	2.7
1	A	273	ASN	2.7
1	A	190	HIS	2.7
1	A	361	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	162	LYS	2.5
1	A	239	ASP	2.3
1	A	137	LYS	2.2
1	A	238	LYS	2.2
1	A	318	LYS	2.1
1	A	333	ASP	2.1
1	A	220	PRO	2.1
1	A	213	GLN	2.1
1	A	327	PHE	2.1
1	A	214	GLU	2.0
1	A	139	LEU	2.0
1	A	284	GLN	2.0

## 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.