



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 2, 2023 – 07:48 PM EDT

PDB ID : 3QZ9  
Title : Crystal structure of Co-type nitrile hydratase beta-Y215F from *Pseudomonas putida*.  
Authors : Brodtkin, H.R.; Novak, W.R.P.; Ringe, D.; Petsko, G.A.  
Deposited on : 2011-03-04  
Resolution : 2.40 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

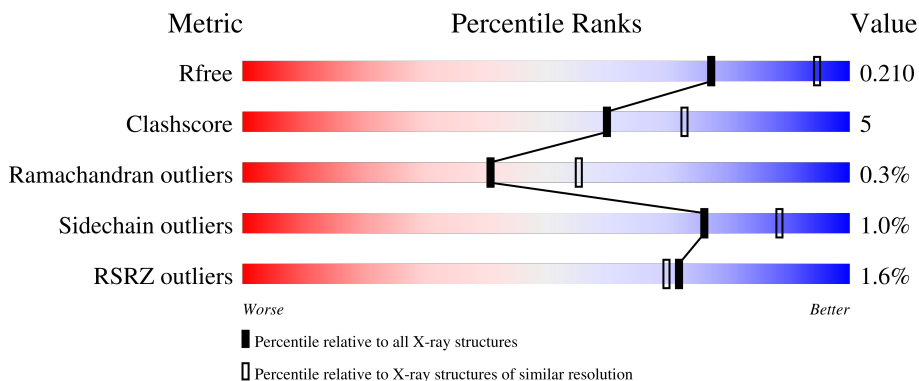
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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.



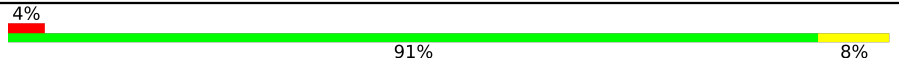
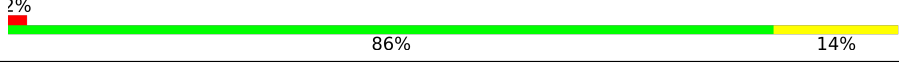
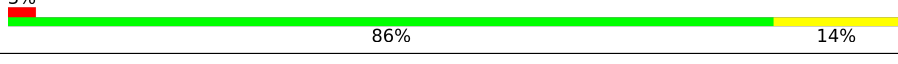
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 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	226	78% 11% 11%
1	C	226	78% 11% 11%
1	E	226	78% 10% 12%
1	G	226	2% 76% 12% 12%
2	B	219	2% 90% 9%

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Mol	Chain	Length	Quality of chain
2	D	219	 4% 91% 8%
2	F	219	 2% 86% 14%
2	H	219	 3% 86% 14%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13588 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 Co-type Nitrile Hydratase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	201	1547	985	264	290	8	0	0	0
1	C	201	1543	983	264	288	8	0	0	0
1	E	200	1526	974	257	287	8	0	0	0
1	G	200	1526	973	260	285	8	0	0	0

- Molecule 2 is a protein called Co-type Nitrile Hydratase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	219	1730	1093	311	322	4	0	3	0
2	D	219	1737	1098	312	323	4	0	4	0
2	F	219	1729	1093	311	321	4	0	3	0
2	H	219	1721	1089	307	321	4	0	3	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	G	1	Total C O 6 3 3	0	0

- Molecule 4 is COBALT (III) ION (three-letter code: 3CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Co 1 1	0	0
4	C	1	Total Co 1 1	0	0
4	E	1	Total Co 1 1	0	0
4	G	1	Total Co 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	78	Total O 78 78	0	0

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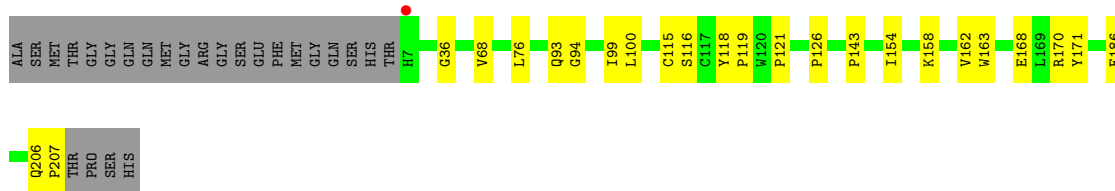
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
5	B	80	Total O 80 80	0	0
5	C	49	Total O 49 49	0	0
5	D	59	Total O 59 59	0	0
5	E	62	Total O 62 62	0	0
5	F	80	Total O 80 80	0	0
5	G	46	Total O 46 46	0	0
5	H	47	Total O 47 47	0	0

### 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.

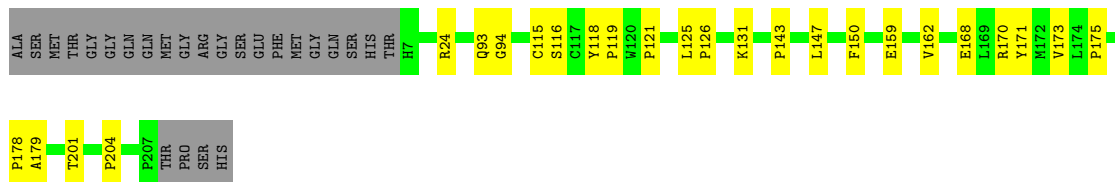
- Molecule 1: Co-type Nitrile Hydratase alpha subunit

Chain A: 




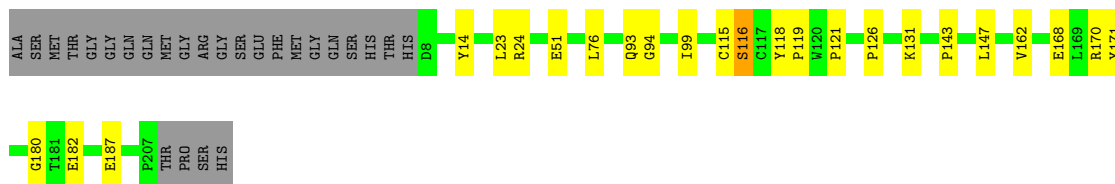
- Molecule 1: Co-type Nitrile Hydratase alpha subunit

Chain C: 




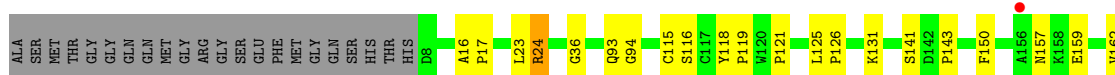
- Molecule 1: Co-type Nitrile Hydratase alpha subunit

Chain E: 



- Molecule 1: Co-type Nitrile Hydratase alpha subunit

Chain G: 

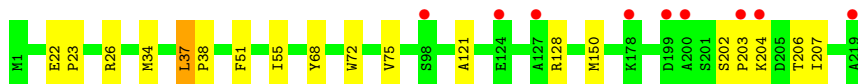
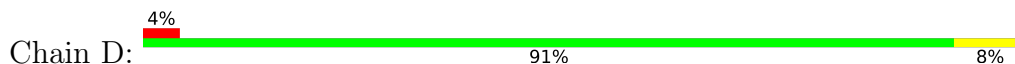




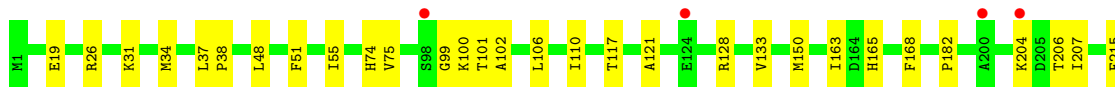
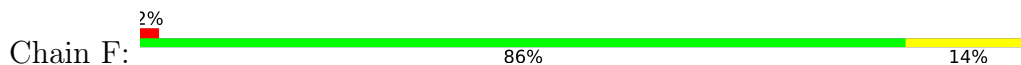
- Molecule 2: Co-type Nitrile Hydratase beta subunit



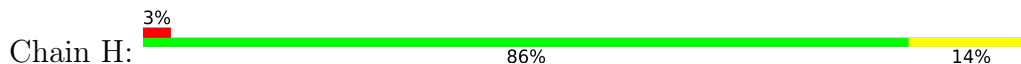
- Molecule 2: Co-type Nitrile Hydratase beta subunit



- Molecule 2: Co-type Nitrile Hydratase beta subunit



- Molecule 2: Co-type Nitrile Hydratase beta subunit





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.89Å 137.20Å 86.09Å 90.00° 91.77° 90.00°	Depositor
Resolution (Å)	29.80 – 2.40 29.81 – 2.38	Depositor EDS
% Data completeness (in resolution range)	96.9 (29.80-2.40) 96.9 (29.81-2.38)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.57 (at 2.39Å)	Xtrriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.185 , 0.215 0.178 , 0.210	Depositor DCC
$R_{free}$ test set	3723 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtrriage
Anisotropy	0.602	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 35.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.008 for l,k,-h 0.031 for h,-k,-l 0.083 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	13588	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CSD, 3CO

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	0/1572	0.54	0/2150
1	C	0.38	0/1568	0.74	3/2145 (0.1%)
1	E	0.40	0/1550	0.55	1/2122 (0.0%)
1	G	0.37	0/1550	0.55	2/2122 (0.1%)
2	B	0.41	0/1778	0.80	5/2420 (0.2%)
2	D	0.40	0/1785	0.74	5/2430 (0.2%)
2	F	0.43	0/1777	0.62	4/2420 (0.2%)
2	H	0.39	0/1769	0.55	2/2409 (0.1%)
All	All	0.40	0/13349	0.65	22/18218 (0.1%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	128	ARG	NE-CZ-NH1	-18.80	110.90	120.30
2	B	128	ARG	NE-CZ-NH2	18.04	129.32	120.30
1	C	24	ARG	NE-CZ-NH2	-17.13	111.74	120.30
2	D	26	ARG	NE-CZ-NH1	-16.34	112.13	120.30
1	C	24	ARG	NE-CZ-NH1	15.87	128.24	120.30
2	D	26	ARG	NE-CZ-NH2	15.25	127.92	120.30
2	B	128	ARG	CD-NE-CZ	9.07	136.30	123.60
2	D	26	ARG	CD-NE-CZ	7.67	134.34	123.60
1	C	24	ARG	CD-NE-CZ	7.54	134.15	123.60
2	F	26	ARG	NE-CZ-NH2	-7.48	116.56	120.30
2	F	26	ARG	NE-CZ-NH1	7.15	123.87	120.30
2	B	26	ARG	NE-CZ-NH2	-7.14	116.73	120.30
2	F	128	ARG	NE-CZ-NH2	-6.81	116.89	120.30
2	B	26	ARG	NE-CZ-NH1	6.62	123.61	120.30
2	H	128	ARG	NE-CZ-NH2	-6.35	117.12	120.30
2	D	128	ARG	NE-CZ-NH2	-6.21	117.20	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	128	ARG	NE-CZ-NH1	6.04	123.32	120.30
2	H	128	ARG	NE-CZ-NH1	5.75	123.18	120.30
2	D	128	ARG	NE-CZ-NH1	5.69	123.15	120.30
1	G	24	ARG	NE-CZ-NH1	-5.31	117.64	120.30
1	G	24	ARG	NE-CZ-NH2	5.26	122.93	120.30
1	E	24	ARG	NE-CZ-NH2	5.03	122.81	120.30

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	1547	0	1523	14	0
1	C	1543	0	1519	16	0
1	E	1526	0	1496	14	0
1	G	1526	0	1499	22	0
2	B	1730	0	1672	16	0
2	D	1737	0	1680	14	0
2	F	1729	0	1672	23	0
2	H	1721	0	1657	25	0
3	A	6	0	8	0	0
3	C	6	0	8	0	0
3	E	6	0	8	0	0
3	G	6	0	8	1	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
5	A	78	0	0	0	0
5	B	80	0	0	2	0
5	C	49	0	0	0	0
5	D	59	0	0	0	0
5	E	62	0	0	0	0
5	F	80	0	0	3	0
5	G	46	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	47	0	0	0	0
All	All	13588	0	12750	118	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 5.

All (118) 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)
2:B:204:LYS:HB2	5:B:469:HOH:O	1.66	0.96
2:F:74:HIS:HD2	5:F:475:HOH:O	1.66	0.76
1:E:119:PRO:HG3	1:E:171:TYR:O	1.90	0.70
1:A:119:PRO:HG3	1:A:171:TYR:O	1.95	0.67
1:C:119:PRO:HG3	1:C:171:TYR:O	1.94	0.67
2:B:113:GLY:HA3	2:F:110:ILE:HG22	1.78	0.65
1:G:119:PRO:HG3	1:G:171:TYR:O	1.98	0.63
2:B:37:LEU:HB3	2:B:38:PRO:HD3	1.82	0.61
1:G:150:PHE:CE2	2:H:18:ARG:HD3	2.36	0.61
2:D:37:LEU:HB3	2:D:38:PRO:HD3	1.82	0.60
1:G:24:ARG:HD3	5:G:452:HOH:O	2.01	0.59
3:G:212:GOL:H11	2:H:66:GLY:O	2.03	0.59
2:F:37:LEU:HB3	2:F:38:PRO:HD3	1.85	0.58
2:H:37:LEU:HB3	2:H:38:PRO:HD3	1.85	0.58
2:F:51:PHE:CD2	2:F:75:VAL:HG11	2.38	0.58
2:B:51:PHE:CD2	2:B:75:VAL:HG11	2.38	0.57
1:C:150:PHE:CD2	1:C:201:THR:HB	2.39	0.57
2:H:51:PHE:CD2	2:H:75:VAL:HG11	2.40	0.56
2:D:51:PHE:CD2	2:D:75:VAL:HG11	2.40	0.56
2:H:87:THR:OG1	2:H:90:GLU:HG3	2.05	0.56
2:B:202:SER:OG	5:B:469:HOH:O	2.17	0.56
1:E:94:GLY:HA3	1:E:121:PRO:HG2	1.87	0.56
2:F:106:LEU:HB3	5:F:248:HOH:O	2.06	0.55
1:E:168:GLU:HG3	2:F:121:ALA:HB3	1.88	0.55
1:G:163:TRP:CE2	2:H:208[B]:ARG:HD3	2.42	0.55
1:C:179:ALA:HB2	1:G:191:GLU:OE2	2.08	0.53
1:C:94:GLY:HA3	1:C:121:PRO:HG2	1.90	0.53
1:G:36:GLY:HA3	2:H:100:LYS:HE2	1.90	0.53
1:E:116:SER:HB2	1:E:131:LYS:HG2	1.90	0.53
1:A:94:GLY:HA3	1:A:121:PRO:HG2	1.90	0.53
1:G:150:PHE:CZ	2:H:18:ARG:HD3	2.44	0.52
1:G:181:THR:HA	1:G:184:TYR:CD1	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:37:LEU:HD12	2:D:72:TRP:CH2	2.46	0.51
2:D:150:MET:O	2:D:150:MET:HG3	2.12	0.50
2:B:37:LEU:HD12	2:B:72:TRP:CH2	2.47	0.50
1:E:14:TYR:CE2	2:F:19:GLU:HB2	2.47	0.50
1:A:168:GLU:HG3	2:B:121:ALA:HB3	1.94	0.49
1:E:168:GLU:HG3	2:F:121:ALA:CB	2.42	0.49
1:G:94:GLY:HA3	1:G:121:PRO:HG2	1.93	0.49
2:B:109:ALA:HB2	2:F:117:THR:HG21	1.93	0.49
2:H:207:ILE:N	2:H:207:ILE:HD12	2.29	0.48
2:F:99:GLY:O	2:F:101:THR:HG23	2.13	0.48
2:H:55:ILE:HG13	2:H:75:VAL:CG2	2.42	0.48
1:C:93:GLN:O	1:C:170:ARG:HG3	2.14	0.47
2:F:206:THR:C	2:F:207:ILE:HD12	2.35	0.47
1:A:36:GLY:HA3	2:B:100:LYS:HG3	1.96	0.47
1:C:168:GLU:HG3	2:D:121:ALA:CB	2.44	0.47
1:C:168:GLU:HG3	2:D:121:ALA:HB3	1.97	0.47
1:A:93:GLN:O	1:A:170:ARG:HG3	2.16	0.46
2:F:207:ILE:HD12	2:F:207:ILE:N	2.31	0.46
1:A:143:PRO:HG3	1:A:162:VAL:HG21	1.98	0.46
2:B:150:MET:HG3	2:B:150:MET:O	2.16	0.46
2:F:150:MET:HG3	2:F:150:MET:O	2.16	0.46
2:H:150:MET:O	2:H:150:MET:HG3	2.16	0.45
2:D:55:ILE:HG13	2:D:75:VAL:CG2	2.46	0.45
2:F:74:HIS:CD2	5:F:475:HOH:O	2.52	0.45
1:G:159:GLU:HA	2:H:204:LYS:HB3	1.98	0.45
2:H:19:GLU:HA	2:H:20:PRO:HD3	1.86	0.45
2:B:55:ILE:HG13	2:B:75:VAL:CG2	2.46	0.45
1:G:141:SER:HA	2:H:196:TRP:NE1	2.30	0.45
1:G:168:GLU:HG3	2:H:121:ALA:CB	2.47	0.45
2:H:206:THR:C	2:H:207:ILE:HD12	2.37	0.45
1:A:168:GLU:HG3	2:B:121:ALA:CB	2.48	0.44
2:F:55:ILE:HG13	2:F:75:VAL:CG2	2.47	0.44
2:F:100:LYS:HE3	2:F:102:ALA:O	2.16	0.44
1:C:131:LYS:HD2	2:D:68:TYR:CD1	2.52	0.44
1:G:157:ASN:O	2:H:204:LYS:NZ	2.49	0.44
2:H:55:ILE:HG13	2:H:75:VAL:HG21	1.99	0.44
2:D:206:THR:C	2:D:207:ILE:HD12	2.37	0.44
2:D:207:ILE:HD12	2:D:207:ILE:N	2.33	0.44
1:A:118:TYR:CG	1:A:126:PRO:HG3	2.53	0.44
2:D:22:GLU:HA	2:D:23:PRO:HD3	1.92	0.43
1:A:100:LEU:HD13	1:A:163:TRP:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:168:PHE:O	2:F:182:PRO:HA	2.19	0.43
1:E:93:GLN:O	1:E:170:ARG:HG3	2.19	0.43
1:G:163:TRP:CZ2	2:H:208[B]:ARG:HD3	2.53	0.43
1:C:147:LEU:HD23	1:C:147:LEU:HA	1.84	0.43
2:F:48:LEU:HD12	2:F:48:LEU:HA	1.85	0.43
1:G:93:GLN:O	1:G:170:ARG:HG3	2.18	0.43
2:B:207:ILE:HD12	2:B:207:ILE:N	2.33	0.43
1:A:68:VAL:HG21	1:A:186:GLU:HG2	2.02	0.42
2:B:55:ILE:HG13	2:B:75:VAL:HG21	2.01	0.42
1:E:143:PRO:HG3	1:E:162:VAL:HG21	2.01	0.42
1:C:143:PRO:HG3	1:C:162:VAL:HG21	2.01	0.42
1:C:118:TYR:CG	1:C:126:PRO:HG3	2.54	0.42
2:D:202:SER:HA	2:D:203:PRO:HD3	1.88	0.42
1:G:131:LYS:HD2	2:H:68:TYR:CD1	2.54	0.42
2:D:55:ILE:HG13	2:D:75:VAL:HG21	2.01	0.42
2:B:206:THR:C	2:B:207:ILE:HD12	2.40	0.42
1:E:118:TYR:CG	1:E:126:PRO:HG3	2.54	0.42
1:G:16:ALA:HA	1:G:17:PRO:HD3	1.91	0.42
1:G:167:ALA:HA	2:H:212:TRP:HH2	1.83	0.42
2:F:55:ILE:HG13	2:F:75:VAL:HG21	2.01	0.41
1:E:147:LEU:HD23	1:E:147:LEU:HA	1.83	0.41
1:A:206:GLN:HA	1:A:207:PRO:HD3	1.92	0.41
2:H:138[B]:ARG:HD2	2:H:217:GLU:OE2	2.20	0.41
2:B:138[B]:ARG:HD2	2:B:217:GLU:OE2	2.20	0.41
1:C:173:VAL:O	1:C:175:PRO:HD3	2.21	0.41
1:C:159:GLU:HA	2:D:204:LYS:HB3	2.02	0.41
1:A:76:LEU:HG	1:A:99:ILE:HG13	2.02	0.41
1:A:154:ILE:HG22	1:A:158:LYS:HB3	2.03	0.41
1:E:118:TYR:CB	1:E:126:PRO:HG3	2.51	0.41
1:G:143:PRO:HG3	1:G:162:VAL:HG21	2.02	0.41
1:A:118:TYR:CB	1:A:126:PRO:HG3	2.51	0.41
1:C:118:TYR:CB	1:C:126:PRO:HG3	2.51	0.41
2:F:150:MET:HB3	2:F:215:PHE:CD2	2.56	0.41
1:G:118:TYR:CG	1:G:126:PRO:HG3	2.56	0.41
1:G:168:GLU:HG3	2:H:121:ALA:HB3	2.03	0.41
2:H:163:ILE:HG21	2:H:165:HIS:CE1	2.56	0.41
2:F:204:LYS:HD3	2:F:204:LYS:HA	1.95	0.40
1:C:125:LEU:HA	1:C:126:PRO:HD3	1.95	0.40
1:C:178:PRO:HG3	1:C:204:PRO:HB2	2.03	0.40
1:E:51:GLU:OE2	2:F:31:LYS:HE2	2.22	0.40
1:E:76:LEU:HG	1:E:99:ILE:HG13	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:150:MET:HB3	2:H:215:PHE:CD2	2.56	0.40
1:E:180:GLY:HA2	1:E:182:GLU:OE2	2.21	0.40
2:F:163:ILE:HG21	2:F:165:HIS:CE1	2.56	0.40
1:G:125:LEU:HA	1:G:126:PRO:HD3	1.96	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	197/226 (87%)	189 (96%)	7 (4%)	1 (0%)	29	41
1	C	197/226 (87%)	188 (95%)	8 (4%)	1 (0%)	29	41
1	E	196/226 (87%)	190 (97%)	5 (3%)	1 (0%)	29	41
1	G	196/226 (87%)	188 (96%)	7 (4%)	1 (0%)	29	41
2	B	220/219 (100%)	216 (98%)	4 (2%)	0	100	100
2	D	221/219 (101%)	214 (97%)	7 (3%)	0	100	100
2	F	220/219 (100%)	216 (98%)	4 (2%)	0	100	100
2	H	220/219 (100%)	215 (98%)	4 (2%)	1 (0%)	29	41
All	All	1667/1780 (94%)	1616 (97%)	46 (3%)	5 (0%)	41	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	98	SER
1	E	116	SER
1	C	116	SER
1	G	116	SER
1	A	116	SER

### 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	160/180 (89%)	160 (100%)	0	100	100
1	C	159/180 (88%)	159 (100%)	0	100	100
1	E	156/180 (87%)	154 (99%)	2 (1%)	69	84
1	G	156/180 (87%)	155 (99%)	1 (1%)	86	94
2	B	180/177 (102%)	177 (98%)	3 (2%)	60	78
2	D	181/177 (102%)	179 (99%)	2 (1%)	73	87
2	F	180/177 (102%)	178 (99%)	2 (1%)	73	87
2	H	178/177 (101%)	175 (98%)	3 (2%)	60	78
All	All	1350/1428 (94%)	1337 (99%)	13 (1%)	76	88

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	34	MET
2	B	37	LEU
2	B	133	VAL
2	D	34	MET
2	D	37	LEU
1	E	23	LEU
1	E	187	GLU
2	F	34	MET
2	F	133	VAL
1	G	23	LEU
2	H	34	MET
2	H	95	LYS
2	H	133	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.



### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

8 non-standard protein/DNA/RNA residues 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
1	CSD	E	117	4,1	3,7,8	0.99	0	1,8,10	1.25	0
1	CSD	E	115	4,1	3,7,8	1.08	0	1,8,10	3.11	1 (100%)
1	CSD	A	115	4,1	3,7,8	1.01	0	1,8,10	2.15	1 (100%)
1	CSD	G	117	4,1	3,7,8	0.99	0	1,8,10	1.01	0
1	CSD	C	115	4,1	3,7,8	1.02	0	1,8,10	2.13	1 (100%)
1	CSD	A	117	4,1	3,7,8	0.97	0	1,8,10	0.71	0
1	CSD	C	117	4,1	3,7,8	1.13	0	1,8,10	1.14	0
1	CSD	G	115	4,1	3,7,8	1.04	0	1,8,10	3.75	1 (100%)

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
1	CSD	E	117	4,1	-	1/2/6/8	-
1	CSD	E	115	4,1	-	1/2/6/8	-
1	CSD	A	115	4,1	-	1/2/6/8	-
1	CSD	G	117	4,1	-	2/2/6/8	-
1	CSD	C	115	4,1	-	1/2/6/8	-
1	CSD	A	117	4,1	-	1/2/6/8	-
1	CSD	C	117	4,1	-	1/2/6/8	-
1	CSD	G	115	4,1	-	1/2/6/8	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	115	CSD	OD1-SG-CB	-3.75	98.39	105.54
1	E	115	CSD	OD1-SG-CB	-3.11	99.61	105.54
1	A	115	CSD	OD1-SG-CB	-2.15	101.44	105.54
1	C	115	CSD	OD1-SG-CB	-2.13	101.49	105.54

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	115	CSD	CA-CB-SG-OD1
1	A	117	CSD	CA-CB-SG-OD1
1	C	115	CSD	CA-CB-SG-OD1
1	C	117	CSD	CA-CB-SG-OD1
1	E	115	CSD	CA-CB-SG-OD1
1	E	117	CSD	CA-CB-SG-OD1
1	G	115	CSD	CA-CB-SG-OD1
1	G	117	CSD	CA-CB-SG-OD1
1	G	117	CSD	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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
3	GOL	C	212	-	5,5,5	0.41	0	5,5,5	0.27	0
3	GOL	E	212	-	5,5,5	0.45	0	5,5,5	0.25	0
3	GOL	A	212	-	5,5,5	0.39	0	5,5,5	0.18	0
3	GOL	G	212	-	5,5,5	0.38	0	5,5,5	0.63	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
3	GOL	C	212	-	-	4/4/4/4	-
3	GOL	E	212	-	-	0/4/4/4	-
3	GOL	A	212	-	-	0/4/4/4	-
3	GOL	G	212	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	212	GOL	C1-C2-C3-O3
3	C	212	GOL	O1-C1-C2-C3
3	C	212	GOL	C1-C2-C3-O3
3	G	212	GOL	O1-C1-C2-C3
3	G	212	GOL	O2-C2-C3-O3
3	C	212	GOL	O1-C1-C2-O2
3	C	212	GOL	O2-C2-C3-O3
3	G	212	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	212	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

### 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	199/226 (88%)	-0.21	1 (0%) 91 89	10, 25, 43, 60	0
1	C	199/226 (88%)	-0.20	0 100 100	11, 27, 48, 62	0
1	E	198/226 (87%)	-0.21	0 100 100	11, 25, 41, 54	1 (0%)
1	G	198/226 (87%)	-0.17	2 (1%) 82 80	12, 27, 44, 63	0
2	B	219/219 (100%)	-0.28	5 (2%) 60 58	15, 25, 54, 73	1 (0%)
2	D	219/219 (100%)	-0.28	9 (4%) 37 36	15, 27, 56, 73	0
2	F	219/219 (100%)	-0.27	4 (1%) 68 66	16, 26, 54, 72	0
2	H	219/219 (100%)	-0.19	6 (2%) 54 52	16, 27, 56, 73	0
All	All	1670/1780 (93%)	-0.23	27 (1%) 72 70	10, 26, 50, 73	2 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	219	ALA	4.0
2	B	203	PRO	3.8
2	H	219	ALA	3.5
2	H	199	ASP	3.5
2	H	200	ALA	3.5
2	B	219	ALA	3.4
2	D	204	LYS	3.2
2	H	124	GLU	3.2
2	D	124	GLU	3.1
2	D	203	PRO	3.1
1	G	156	ALA	3.0
2	B	124	GLU	3.0
2	F	200	ALA	3.0
2	D	200	ALA	2.9
2	B	125	GLU	2.8
2	H	126	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	98	SER	2.6
1	A	7	HIS	2.5
2	F	124	GLU	2.5
2	D	98	SER	2.5
1	G	180	GLY	2.5
2	F	204	LYS	2.3
2	D	199	ASP	2.3
2	D	127	ALA	2.1
2	F	98	SER	2.1
2	D	178	LYS	2.0
2	H	134	GLY	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CSD	A	115	8/9	0.99	0.16	5,11,13,14	0
1	CSD	A	117	8/9	0.99	0.19	9,11,17,21	0
1	CSD	C	115	8/9	0.99	0.17	11,13,19,25	0
1	CSD	C	117	8/9	0.99	0.17	9,18,22,25	0
1	CSD	E	115	8/9	0.99	0.16	10,14,18,19	0
1	CSD	E	117	8/9	0.99	0.20	9,15,20,24	0
1	CSD	G	115	8/9	0.99	0.15	12,15,21,22	0
1	CSD	G	117	8/9	0.99	0.19	14,17,20,23	0

## 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	GOL	E	212	6/6	0.95	0.15	17,19,27,30	0
3	GOL	G	212	6/6	0.95	0.12	20,28,30,39	0
3	GOL	A	212	6/6	0.96	0.13	18,26,26,41	0
3	GOL	C	212	6/6	0.96	0.11	15,20,31,36	0
4	3CO	E	213	1/1	0.99	0.14	14,14,14,14	0
4	3CO	G	213	1/1	0.99	0.14	16,16,16,16	0
4	3CO	A	213	1/1	1.00	0.14	14,14,14,14	0
4	3CO	C	213	1/1	1.00	0.12	14,14,14,14	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.