



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 21, 2024 – 08:21 AM EST

PDB ID : 4XBZ
Title : Crystal Structure of EvdO1 from *Micromonospora carbonacea* var. *aurantiaca*
Authors : McCulloch, K.M.; McCranie, E.K.; Sarwar, M.; Mathieu, J.L.; Gitschlag, B.L.;
Du, Y.; Bachmann, B.O.; Iverson, T.M.
Deposited on : 2014-12-17
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 ⓘ 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 ⓘ](#)) 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 : 2.36
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) : 2.36

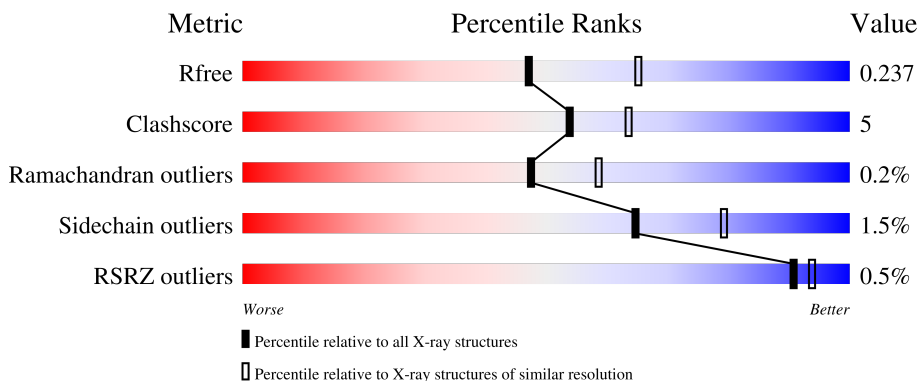
1 Overall quality at a glance i

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 $\leq 5\%$. 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	334	 78% 14% • 7%
1	B	334	 75% 10% 14%
1	C	334	 81% 13% 5%
1	D	334	 78% 9% 13%
1	E	334	 70% 13% • 15%

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Mol	Chain	Length	Quality of chain
1	F	334	 <p>% 84% 8% 7%</p>
1	G	334	 <p>76% 11% 13%</p>
1	H	334	 <p>% 83% 10% 7%</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 20394 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 EvdO1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	312	Total 2467	C 1560	N 442	O 454	S 11	0	0	0
1	B	286	Total 2270	C 1436	N 406	O 418	S 10	0	0	0
1	C	317	Total 2495	C 1573	N 451	O 460	S 11	8	0	0
1	D	290	Total 2320	C 1470	N 414	O 426	S 10	0	0	0
1	E	283	Total 2254	C 1428	N 405	O 411	S 10	1	0	0
1	F	309	Total 2449	C 1549	N 439	O 450	S 11	2	0	0
1	G	292	Total 2313	C 1462	N 414	O 427	S 10	1	0	0
1	H	312	Total 2449	C 1549	N 438	O 451	S 11	0	0	0

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

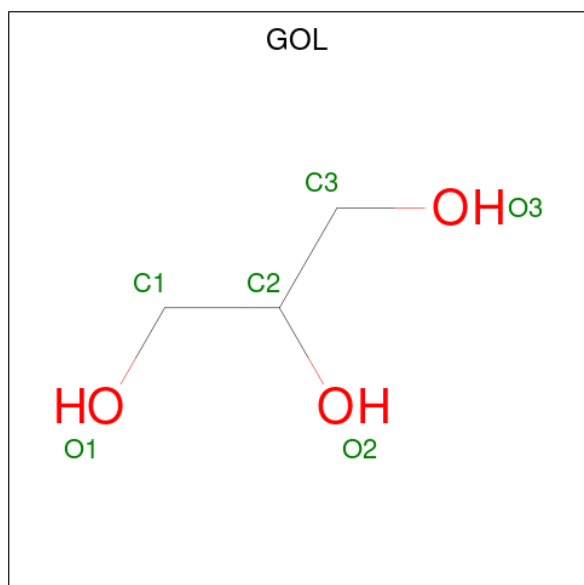
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Ni 1	0	0
2	B	1	Total 1	Ni 1	0	0
2	C	1	Total 1	Ni 1	0	0
2	D	1	Total 1	Ni 1	0	0
2	E	1	Total 1	Ni 1	0	0
2	F	1	Total 1	Ni 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Ni 1 1	0	0
2	H	1	Total Ni 1 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	163	Total O 163 163	0	0

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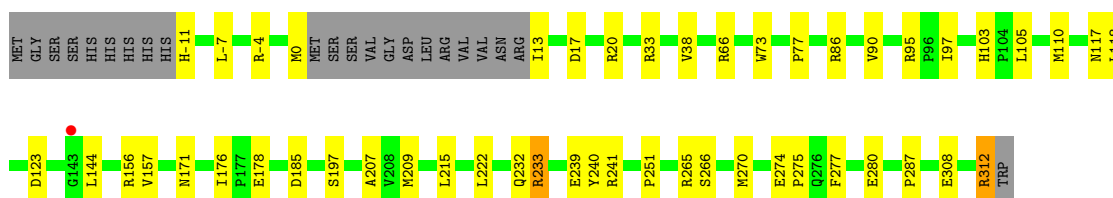
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	134	Total 134	O 134	0	0
4	C	209	Total 209	O 209	0	0
4	D	165	Total 165	O 165	0	0
4	E	168	Total 168	O 168	0	0
4	F	178	Total 178	O 178	0	0
4	G	168	Total 168	O 168	0	0
4	H	148	Total 148	O 148	0	0

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.

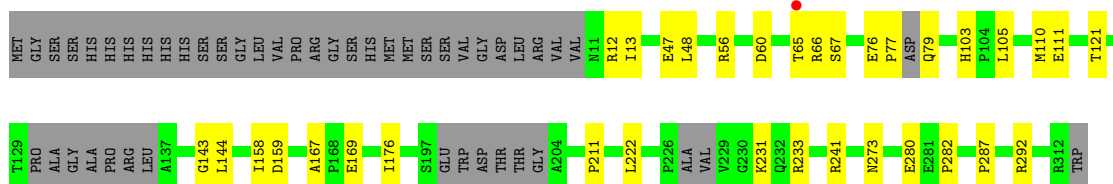
- Molecule 1: EvdO1

Chain A: 




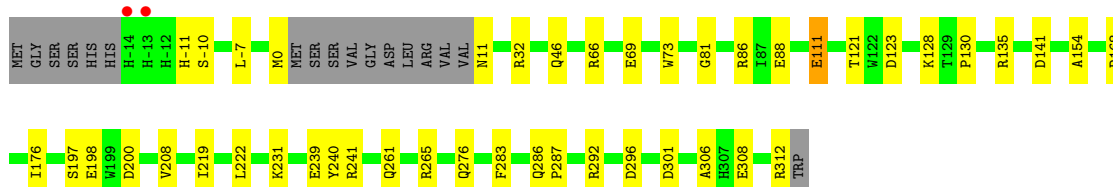
- Molecule 1: EvdO1

Chain B: 




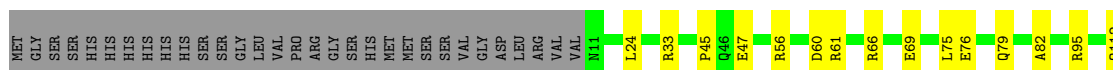
- Molecule 1: EvdO1

Chain C: 



- Molecule 1: EvdO1

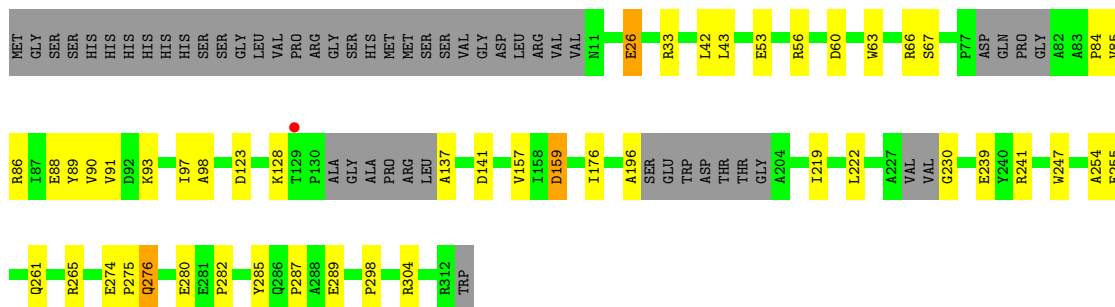
Chain D: 





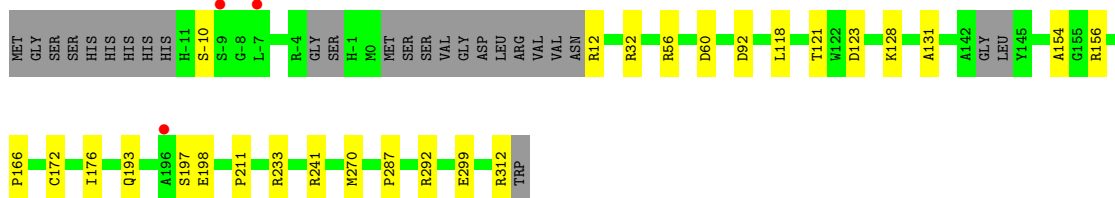
- Molecule 1: EvdO1

Chain E: 70% 13% 15%



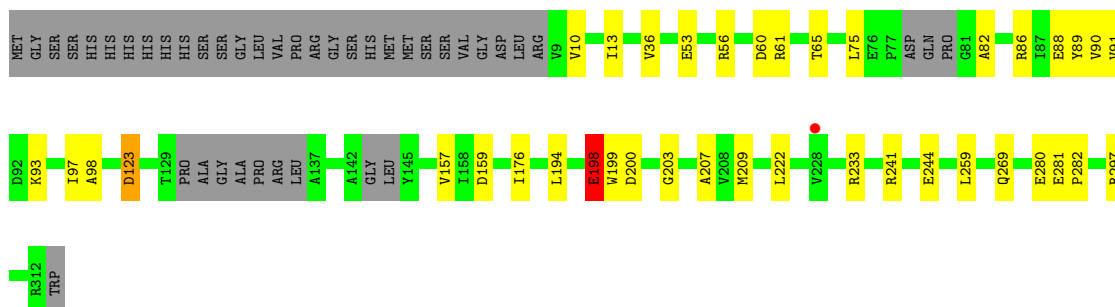
- Molecule 1: EvdO1

Chain F: 84% 8% 7%



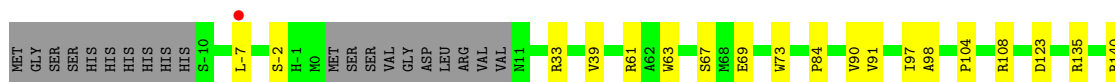
- Molecule 1: EvdO1

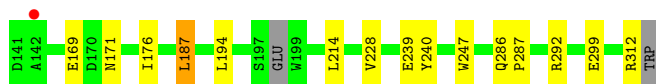
Chain G: 76% 11% 13%



- Molecule 1: EvdO1

Chain H: 83% 10% 7%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.61Å 109.43Å 146.05Å 90.00° 108.27° 90.00°	Depositor
Resolution (Å)	46.32 – 2.30 46.32 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.32-2.30) 99.4 (46.32-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.29Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.183 , 0.237 0.183 , 0.237	Depositor DCC
R_{free} test set	6081 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtrriage
Anisotropy	0.608	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20394	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.22% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NI, 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	0.42	0/2534	0.55	0/3461
1	B	0.37	0/2327	0.51	0/3171
1	C	0.43	0/2564	0.55	0/3500
1	D	0.40	0/2379	0.54	0/3244
1	E	0.40	0/2311	0.54	0/3149
1	F	0.41	0/2514	0.53	0/3431
1	G	0.42	0/2370	0.54	0/3232
1	H	0.40	0/2514	0.54	0/3432
All	All	0.41	0/19513	0.54	0/26620

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	2467	0	2399	36	0
1	B	2270	0	2193	20	0
1	C	2495	0	2395	30	0
1	D	2320	0	2250	25	0
1	E	2254	0	2189	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2449	0	2379	17	0
1	G	2313	0	2242	24	0
1	H	2449	0	2374	21	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	6	0	7	0	0
3	E	6	0	8	0	0
3	G	6	0	8	0	0
3	H	6	0	8	0	0
4	A	163	0	0	12	0
4	B	134	0	0	6	0
4	C	209	0	0	7	0
4	D	165	0	0	14	1
4	E	168	0	0	12	1
4	F	178	0	0	8	1
4	G	168	0	0	7	1
4	H	148	0	0	5	0
All	All	20394	0	18468	200	2

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 (200) 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:280:GLU:O	4:A:501:HOH:O	1.84	0.96
1:B:169:GLU:OE2	4:B:501:HOH:O	1.85	0.94
1:E:255:GLU:OE1	4:E:501:HOH:O	1.86	0.92
1:F:312:ARG:O	4:F:501:HOH:O	1.87	0.91
1:A:86:ARG:NH1	4:A:503:HOH:O	2.09	0.84
1:B:56:ARG:NH1	1:B:60:ASP:OD2	2.11	0.84
1:B:111:GLU:OE1	4:B:502:HOH:O	1.99	0.81
1:E:196:ALA:O	4:E:502:HOH:O	2.00	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:281:GLU:OE1	4:G:503:HOH:O	1.99	0.80
1:G:123:ASP:OD1	4:G:504:HOH:O	2.02	0.78
1:A:308:GLU:OE1	4:A:502:HOH:O	2.01	0.78
1:A:156:ARG:NH2	4:A:506:HOH:O	2.14	0.77
1:H:286:GLN:OE1	1:H:292:ARG:NH2	2.17	0.76
1:A:-11:HIS:N	4:A:504:HOH:O	2.11	0.76
1:D:45:PRO:O	4:D:502:HOH:O	2.03	0.76
1:G:244:GLU:OE2	4:G:505:HOH:O	2.05	0.74
1:H:169:GLU:OE2	4:H:501:HOH:O	2.06	0.73
1:A:207:ALA:HB1	1:A:209:MET:HE3	1.71	0.73
1:C:301:ASP:OD1	4:C:501:HOH:O	2.05	0.73
1:A:232:GLN:N	4:A:505:HOH:O	2.23	0.72
1:E:176:ILE:HD12	1:E:222:LEU:HD23	1.70	0.72
1:A:176:ILE:HD12	1:A:222:LEU:HD23	1.71	0.72
1:G:88:GLU:OE1	4:G:506:HOH:O	2.08	0.72
1:F:60:ASP:OD2	4:F:502:HOH:O	2.07	0.72
1:C:286:GLN:OE1	1:C:292:ARG:NH2	2.22	0.70
1:C:81:GLY:O	4:C:502:HOH:O	2.10	0.69
1:D:299:GLU:HB2	4:D:541:HOH:O	1.93	0.69
1:D:47:GLU:OE2	4:D:503:HOH:O	2.11	0.67
1:D:144:LEU:N	4:D:510:HOH:O	2.27	0.67
1:D:194:LEU:O	4:D:504:HOH:O	2.12	0.66
1:E:128:LYS:O	4:E:503:HOH:O	2.13	0.66
1:A:312:ARG:O	4:A:507:HOH:O	2.14	0.65
1:C:200:ASP:OD2	4:C:503:HOH:O	2.14	0.65
1:E:123:ASP:OD1	4:E:504:HOH:O	2.15	0.64
1:C:69:GLU:OE2	4:C:504:HOH:O	2.15	0.64
1:A:144:LEU:HD13	1:A:251:PRO:HB3	1.82	0.61
1:D:56:ARG:NH1	1:D:60:ASP:OD2	2.34	0.61
1:C:306:ALA:HB1	1:C:308:GLU:OE2	2.00	0.60
1:G:176:ILE:HD12	1:G:222:LEU:HD23	1.82	0.60
1:F:128:LYS:HD2	1:F:233:ARG:HG2	1.83	0.60
1:H:287:PRO:HG2	1:H:292:ARG:HG2	1.84	0.59
1:D:24:LEU:HD22	1:E:298:PRO:HD3	1.84	0.59
1:F:12:ARG:N	4:F:509:HOH:O	2.36	0.59
1:A:157:VAL:HG13	1:A:241:ARG:HG2	1.85	0.59
1:G:176:ILE:HD11	1:G:194:LEU:HD11	1.85	0.58
1:A:33:ARG:NH1	1:A:178:GLU:OE2	2.37	0.58
1:C:286:GLN:O	1:D:33:ARG:NH1	2.36	0.58
1:F:92:ASP:OD2	4:F:503:HOH:O	2.17	0.58
1:H:91:VAL:HG13	1:H:98:ALA:HA	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:261:GLN:O	1:E:265:ARG:HG3	2.04	0.57
1:E:304:ARG:NH1	4:E:505:HOH:O	2.23	0.57
1:B:47:GLU:OE2	4:B:503:HOH:O	2.18	0.56
1:A:265:ARG:HD3	4:A:514:HOH:O	2.04	0.56
1:F:287:PRO:HG2	1:F:292:ARG:HG2	1.88	0.56
1:B:77:PRO:O	1:B:79:GLN:N	2.39	0.55
1:D:156:ARG:NH2	4:D:522:HOH:O	2.40	0.55
1:D:174:TRP:CE2	1:D:206:PRO:HB3	2.42	0.55
1:D:112:GLN:HG3	4:D:644:HOH:O	2.07	0.55
1:E:88:GLU:HG3	4:E:646:HOH:O	2.08	0.54
1:A:207:ALA:HB1	1:A:209:MET:CE	2.38	0.53
1:E:276:GLN:NE2	4:E:515:HOH:O	2.42	0.53
1:D:75:LEU:HB2	1:D:82:ALA:HB2	1.89	0.53
1:C:86:ARG:NE	1:C:88:GLU:OE2	2.31	0.52
1:H:90:VAL:HG23	1:H:97:ILE:HG21	1.92	0.52
1:B:143:GLY:HA3	1:B:241:ARG:HH22	1.75	0.51
1:G:86:ARG:NH2	1:G:88:GLU:OE2	2.33	0.51
1:A:171:ASN:OD1	1:A:233:ARG:HD3	2.11	0.51
1:F:32:ARG:HD3	1:F:154:ALA:O	2.10	0.51
1:H:176:ILE:HD11	1:H:194:LEU:HD11	1.93	0.51
1:H:247:TRP:O	1:H:312:ARG:NH2	2.44	0.51
1:C:128:LYS:O	1:C:130:PRO:HD3	2.12	0.50
1:C:66:ARG:HA	1:C:73:TRP:CZ2	2.46	0.50
1:D:66:ARG:NE	4:D:525:HOH:O	2.44	0.50
1:F:156:ARG:NH2	4:F:516:HOH:O	2.44	0.50
1:B:79:GLN:N	4:B:509:HOH:O	2.45	0.49
1:H:312:ARG:NE	4:H:505:HOH:O	2.26	0.49
1:A:209:MET:HE1	1:A:215:LEU:HD13	1.93	0.49
1:D:304:ARG:NH2	4:D:512:HOH:O	2.29	0.49
1:E:42:LEU:HG	1:E:43:LEU:HD23	1.95	0.49
1:H:73:TRP:CZ3	1:H:84:PRO:HD3	2.48	0.49
1:B:65:THR:O	1:B:67:SER:N	2.40	0.49
1:C:141:ASP:HB2	1:C:219:ILE:HB	1.94	0.49
1:E:285:TYR:CZ	1:E:287:PRO:HG3	2.48	0.49
1:H:299:GLU:OE2	4:H:502:HOH:O	2.20	0.49
1:E:56:ARG:NH1	1:E:60:ASP:OD2	2.46	0.49
1:A:13:ILE:HG21	1:A:38:VAL:HG23	1.95	0.49
1:F:131:ALA:O	4:F:504:HOH:O	2.20	0.48
1:C:111:GLU:HG3	1:C:283:PHE:HZ	1.78	0.48
1:D:61:ARG:HH11	1:H:-7:LEU:HD13	1.78	0.48
1:A:233:ARG:NH2	4:A:517:HOH:O	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:176:ILE:HD12	1:B:222:LEU:HD23	1.95	0.48
1:D:144:LEU:HB2	4:D:510:HOH:O	2.12	0.48
1:E:157:VAL:HG13	1:E:241:ARG:HG2	1.95	0.48
1:C:135:ARG:NH1	1:C:198:GLU:O	2.46	0.48
1:B:103:HIS:CE1	1:B:105:LEU:HB2	2.49	0.47
1:C:287:PRO:HG2	1:C:292:ARG:HG2	1.95	0.47
1:F:299:GLU:HG2	4:F:543:HOH:O	2.13	0.47
1:A:233:ARG:N	4:A:505:HOH:O	2.12	0.47
1:E:141:ASP:HB2	1:E:219:ILE:HB	1.96	0.47
1:G:61:ARG:O	1:G:65:THR:HG23	2.14	0.47
1:B:280:GLU:O	1:B:282:PRO:HD3	2.14	0.47
1:C:111:GLU:HG3	1:C:283:PHE:CZ	2.50	0.47
1:D:76:GLU:HB2	1:D:79:GLN:HG2	1.95	0.47
1:G:56:ARG:NH1	1:G:60:ASP:OD2	2.47	0.47
1:A:95:ARG:HG3	1:A:270:MET:HE1	1.97	0.47
1:B:273:ASN:ND2	4:B:520:HOH:O	2.44	0.47
1:D:225:ALA:O	4:D:505:HOH:O	2.20	0.47
1:A:117:ASN:HA	1:A:287:PRO:HB3	1.97	0.47
1:A:266:SER:O	1:A:270:MET:HG2	2.15	0.46
1:B:110:MET:HE3	1:B:158:ILE:HD12	1.96	0.46
1:B:167:ALA:HB2	1:B:233:ARG:HD2	1.98	0.46
1:C:168:PRO:HA	1:C:208:VAL:HG13	1.96	0.46
1:C:308:GLU:H	1:C:308:GLU:CD	2.18	0.46
1:G:91:VAL:HG13	1:G:98:ALA:HA	1.98	0.46
1:D:69:GLU:O	1:D:69:GLU:HG3	2.15	0.46
1:A:277:PHE:O	1:A:280:GLU:HB2	2.16	0.46
1:G:89:TYR:O	1:G:93:LYS:HG3	2.16	0.46
1:H:63:TRP:CZ2	1:H:84:PRO:HD2	2.51	0.46
1:B:76:GLU:O	1:B:79:GLN:N	2.49	0.46
1:C:-11:HIS:O	1:G:53:GLU:HG2	2.14	0.46
1:E:230:GLY:N	4:E:510:HOH:O	2.48	0.46
1:A:110:MET:HA	1:A:110:MET:HE2	1.98	0.46
1:A:239:GLU:HG2	1:A:240:TYR:N	2.31	0.46
1:E:91:VAL:HG13	1:E:98:ALA:HA	1.98	0.46
1:G:157:VAL:HG13	1:G:241:ARG:HG2	1.97	0.46
1:G:198:GLU:O	1:G:200:ASP:N	2.42	0.45
1:H:171:ASN:ND2	1:H:228:VAL:HG11	2.30	0.45
1:C:46:GLN:HG2	1:C:276:GLN:OE1	2.16	0.45
1:F:270:MET:HB2	1:F:270:MET:HE3	1.83	0.45
1:C:231:LYS:HA	1:C:231:LYS:HD3	1.73	0.45
1:E:274:GLU:HA	1:E:275:PRO:HD3	1.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:THR:HG21	1:C:241:ARG:HG3	1.99	0.45
1:C:296:ASP:OD2	4:C:505:HOH:O	2.21	0.45
1:H:140:ARG:CZ	1:H:187:LEU:HD13	2.47	0.45
1:H:239:GLU:HG2	1:H:240:TYR:N	2.31	0.45
1:B:144:LEU:HB2	4:B:560:HOH:O	2.16	0.45
1:H:39:VAL:HB	1:H:214:LEU:HB3	1.99	0.45
1:C:261:GLN:O	1:C:265:ARG:HG3	2.16	0.45
1:F:121:THR:HG21	1:F:241:ARG:HG3	1.98	0.45
1:A:-11:HIS:O	1:E:53:GLU:HG2	2.17	0.44
1:E:90:VAL:HG23	1:E:97:ILE:HG21	1.98	0.44
1:A:90:VAL:HG23	1:A:97:ILE:HG21	2.00	0.44
1:F:233:ARG:NH1	1:F:233:ARG:HG3	2.31	0.44
1:A:233:ARG:NE	4:A:511:HOH:O	2.30	0.44
1:B:12:ARG:HG2	1:B:13:ILE:N	2.33	0.44
1:G:259:LEU:HD21	1:G:297:ARG:HG3	1.99	0.44
1:A:66:ARG:HB3	1:A:77:PRO:HB3	2.00	0.44
1:D:121:THR:HG21	1:D:241:ARG:HG3	1.99	0.44
1:F:166:PRO:HD3	1:F:211:PRO:HG3	2.00	0.44
1:G:75:LEU:HB2	1:G:82:ALA:HB2	1.98	0.44
1:C:176:ILE:HD12	1:C:222:LEU:HD23	2.00	0.44
1:G:207:ALA:C	1:G:209:MET:HE2	2.38	0.44
1:G:233:ARG:NH2	4:G:502:HOH:O	1.96	0.43
1:H:104:PRO:HB2	1:H:108:ARG:NH1	2.33	0.43
1:E:63:TRP:CZ2	1:E:84:PRO:HD2	2.52	0.43
1:G:280:GLU:O	1:G:282:PRO:HD3	2.18	0.43
1:C:312:ARG:NH2	4:C:524:HOH:O	2.45	0.43
1:E:89:TYR:HB2	1:E:93:LYS:HZ3	1.83	0.43
1:A:0:MET:HE2	1:A:0:MET:HB2	1.92	0.43
1:E:26:GLU:HB3	4:E:542:HOH:O	2.18	0.43
1:G:10:VAL:HG21	1:G:203:GLY:HA2	2.00	0.43
1:D:233:ARG:HB3	4:D:573:HOH:O	2.19	0.43
1:F:197:SER:OG	1:F:198:GLU:N	2.51	0.43
1:G:90:VAL:HG13	1:G:97:ILE:HG21	2.00	0.43
1:E:86:ARG:NH2	1:E:88:GLU:OE2	2.50	0.43
1:C:32:ARG:HD3	1:C:154:ALA:O	2.18	0.43
1:E:63:TRP:O	1:E:66:ARG:NH1	2.51	0.42
1:D:175:CYS:O	1:D:177:PRO:HD3	2.19	0.42
1:A:66:ARG:HA	1:A:73:TRP:CZ2	2.54	0.42
1:A:233:ARG:NH2	4:A:511:HOH:O	2.41	0.42
1:F:56:ARG:NH2	4:F:521:HOH:O	2.52	0.42
1:G:93:LYS:NZ	4:G:516:HOH:O	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:159:ASP:OD1	1:E:239:GLU:HG3	2.20	0.42
1:H:61:ARG:HG2	1:H:61:ARG:HH11	1.84	0.42
1:D:95:ARG:NH2	4:D:528:HOH:O	2.51	0.42
1:E:289:GLU:CG	4:E:512:HOH:O	2.67	0.42
1:D:192:ASP:OD1	4:D:506:HOH:O	2.20	0.42
1:A:103:HIS:CE1	1:A:105:LEU:HB2	2.55	0.41
1:C:0:MET:HE2	1:C:0:MET:HB2	1.89	0.41
1:C:197:SER:OG	1:C:198:GLU:N	2.52	0.41
1:E:85:VAL:HG22	1:E:128:LYS:HA	2.02	0.41
1:A:17:ASP:HB3	1:A:20:ARG:HB3	2.03	0.41
1:A:274:GLU:HA	1:A:275:PRO:HD2	1.82	0.41
1:G:269:GLN:NE2	4:G:523:HOH:O	2.49	0.41
1:H:33:ARG:NH1	4:H:513:HOH:O	2.43	0.41
1:B:121:THR:HG21	1:B:241:ARG:HG3	2.01	0.41
1:B:287:PRO:HG2	1:B:292:ARG:HG2	2.03	0.41
1:D:174:TRP:CZ2	1:D:206:PRO:HB3	2.55	0.41
1:H:312:ARG:NH2	4:H:505:HOH:O	2.51	0.41
1:F:172:CYS:HA	1:F:233:ARG:HH21	1.85	0.41
1:E:137:ALA:N	4:E:527:HOH:O	2.54	0.41
1:C:239:GLU:HG2	1:C:240:TYR:N	2.36	0.40
1:E:33:ARG:NH1	4:E:513:HOH:O	2.38	0.40
1:E:280:GLU:O	1:E:282:PRO:HD3	2.21	0.40
1:H:67:SER:OG	1:H:69:GLU:HB2	2.22	0.40
1:B:48:LEU:HD21	1:B:211:PRO:HB2	2.03	0.40
1:G:13:ILE:HG23	1:G:36:VAL:HG13	2.02	0.40
1:C:-10:SER:HA	4:C:526:HOH:O	2.21	0.40
1:A:-4:ARG:HH21	1:E:67:SER:HB2	1.87	0.40
1:E:247:TRP:CZ3	1:E:254:ALA:HB1	2.56	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:667:HOH:O	4:F:673:HOH:O[2_655]	1.92	0.28
4:D:655:HOH:O	4:G:668:HOH:O[1_545]	2.17	0.03

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	308/334 (92%)	298 (97%)	10 (3%)	0	100	100
1	B	276/334 (83%)	263 (95%)	12 (4%)	1 (0%)	34	42
1	C	313/334 (94%)	301 (96%)	12 (4%)	0	100	100
1	D	280/334 (84%)	270 (96%)	10 (4%)	0	100	100
1	E	273/334 (82%)	264 (97%)	9 (3%)	0	100	100
1	F	301/334 (90%)	290 (96%)	10 (3%)	1 (0%)	41	50
1	G	284/334 (85%)	271 (95%)	11 (4%)	2 (1%)	22	26
1	H	306/334 (92%)	292 (95%)	14 (5%)	0	100	100
All	All	2341/2672 (88%)	2249 (96%)	88 (4%)	4 (0%)	47	58

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	66	ARG
1	G	198	GLU
1	G	199	TRP
1	F	-10	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	258/278 (93%)	251 (97%)	7 (3%)	44	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	236/278 (85%)	234 (99%)	2 (1%)	81	91
1	C	259/278 (93%)	255 (98%)	4 (2%)	65	79
1	D	243/278 (87%)	241 (99%)	2 (1%)	81	91
1	E	234/278 (84%)	231 (99%)	3 (1%)	69	82
1	F	256/278 (92%)	252 (98%)	4 (2%)	62	78
1	G	241/278 (87%)	238 (99%)	3 (1%)	71	84
1	H	255/278 (92%)	251 (98%)	4 (2%)	62	78
All	All	1982/2224 (89%)	1953 (98%)	29 (2%)	65	79

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-7	LEU
1	A	118	LEU
1	A	123	ASP
1	A	185	ASP
1	A	197	SER
1	A	233	ARG
1	A	312	ARG
1	B	159	ASP
1	B	231	LYS
1	C	-7	LEU
1	C	11	ASN
1	C	111	GLU
1	C	123	ASP
1	D	144	LEU
1	D	205	VAL
1	E	26	GLU
1	E	159	ASP
1	E	276	GLN
1	F	118	LEU
1	F	123	ASP
1	F	176	ILE
1	F	193	GLN
1	G	123	ASP
1	G	159	ASP
1	G	198	GLU
1	H	-2	SER
1	H	123	ASP
1	H	135	ARG

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Mol	Chain	Res	Type
1	H	187	LEU

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](#)

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](#)

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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	E	402	2	5,5,5	0.22	0	5,5,5	0.38	0
3	GOL	A	402	2	5,5,5	0.29	0	5,5,5	0.54	0
3	GOL	G	402	2	5,5,5	0.30	0	5,5,5	0.48	0
3	GOL	H	402	-	5,5,5	0.31	0	5,5,5	0.34	0
3	GOL	C	402	2	5,5,5	0.21	0	5,5,5	0.44	0
3	GOL	B	402	2	5,5,5	0.33	0	5,5,5	0.19	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	E	402	2	-	2/4/4/4	-
3	GOL	A	402	2	-	1/4/4/4	-
3	GOL	G	402	2	-	0/4/4/4	-
3	GOL	H	402	-	-	0/4/4/4	-
3	GOL	C	402	2	-	2/4/4/4	-
3	GOL	B	402	2	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	GOL	O2-C2-C3-O3
3	E	402	GOL	O1-C1-C2-O2
3	C	402	GOL	O2-C2-C3-O3
3	C	402	GOL	O1-C1-C2-C3
3	E	402	GOL	O1-C1-C2-C3

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	312/334 (93%)	-0.12	1 (0%) 94 96	23, 33, 50, 60	0
1	B	286/334 (85%)	-0.00	1 (0%) 94 96	24, 37, 58, 74	0
1	C	315/334 (94%)	-0.07	2 (0%) 89 92	19, 30, 50, 67	0
1	D	290/334 (86%)	-0.10	1 (0%) 94 96	20, 33, 52, 62	0
1	E	283/334 (84%)	-0.16	1 (0%) 92 95	20, 32, 49, 69	1 (0%)
1	F	309/334 (92%)	-0.02	3 (0%) 82 86	21, 34, 53, 70	1 (0%)
1	G	292/334 (87%)	-0.12	1 (0%) 94 96	20, 32, 50, 64	0
1	H	312/334 (93%)	0.00	2 (0%) 89 92	23, 35, 52, 62	0
All	All	2399/2672 (89%)	-0.07	12 (0%) 91 94	19, 33, 52, 74	2 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	142	ALA	10.3
1	G	228	VAL	3.4
1	D	313	TRP	3.0
1	F	196	ALA	2.7
1	E	129	THR	2.5
1	C	-13	HIS	2.5
1	B	65	THR	2.4
1	F	-7	LEU	2.3
1	A	143	GLY	2.3
1	F	-9	SER	2.2
1	C	-14	HIS	2.2
1	H	-7	LEU	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
3	GOL	A	402	6/6	0.70	0.14	36,39,41,43	0
3	GOL	H	402	6/6	0.71	0.15	41,48,50,56	0
3	GOL	C	402	6/6	0.85	0.13	36,41,45,48	0
3	GOL	E	402	6/6	0.86	0.13	39,40,46,47	0
3	GOL	B	402	6/6	0.88	0.11	35,39,41,43	0
3	GOL	G	402	6/6	0.89	0.12	31,37,41,42	0
2	NI	B	401	1/1	0.97	0.06	53,53,53,53	0
2	NI	D	401	1/1	0.97	0.07	64,64,64,64	0
2	NI	F	401	1/1	0.98	0.04	56,56,56,56	0
2	NI	G	401	1/1	0.98	0.05	51,51,51,51	0
2	NI	H	401	1/1	0.98	0.07	55,55,55,55	0
2	NI	C	401	1/1	0.99	0.07	49,49,49,49	0
2	NI	A	401	1/1	0.99	0.04	49,49,49,49	0
2	NI	E	401	1/1	0.99	0.04	52,52,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.