



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:38 PM UTC

PDB ID : 2I9U / pdb_00002i9u
Title : Crystal Structure of Guanine Deaminase from *C. acetobutylicum* with bound guanine in the active site
Authors : Kumaran, D.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2006-09-06
Resolution : 2.05 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

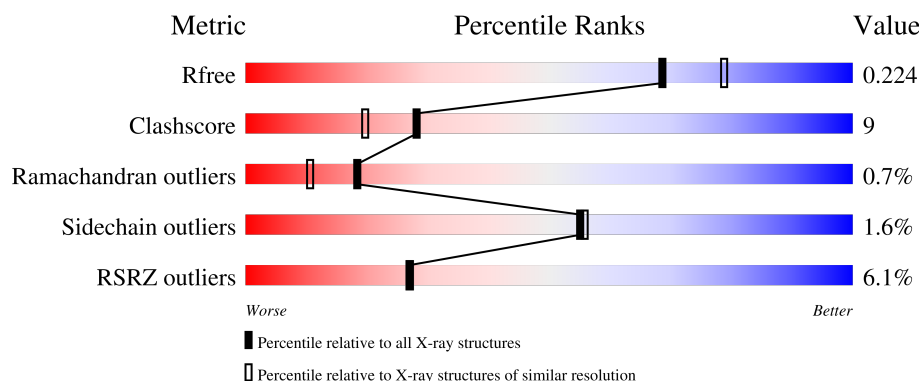
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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}	180053	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	439	10% 71% 23% • 5%
1	B	439	2% 77% 17% • 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	505	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7136 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 Cytosine/guanine deaminase related protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	0	0
			3343	2149	550	626	18			
1	B	419	Total	C	N	O	S	0	0	0
			3343	2149	550	626	18			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q97MB6
A	2	SER	-	cloning artifact	UNP Q97MB6
A	3	LEU	-	cloning artifact	UNP Q97MB6
A	4	LEU	-	cloning artifact	UNP Q97MB6
A	432	GLU	-	cloning artifact	UNP Q97MB6
A	433	GLY	-	cloning artifact	UNP Q97MB6
A	434	HIS	-	expression tag	UNP Q97MB6
A	435	HIS	-	expression tag	UNP Q97MB6
A	436	HIS	-	expression tag	UNP Q97MB6
A	437	HIS	-	expression tag	UNP Q97MB6
A	438	HIS	-	expression tag	UNP Q97MB6
A	439	HIS	-	expression tag	UNP Q97MB6
B	1	MET	-	initiating methionine	UNP Q97MB6
B	2	SER	-	cloning artifact	UNP Q97MB6
B	3	LEU	-	cloning artifact	UNP Q97MB6
B	4	LEU	-	cloning artifact	UNP Q97MB6
B	432	GLU	-	cloning artifact	UNP Q97MB6
B	433	GLY	-	cloning artifact	UNP Q97MB6
B	434	HIS	-	expression tag	UNP Q97MB6
B	435	HIS	-	expression tag	UNP Q97MB6
B	436	HIS	-	expression tag	UNP Q97MB6
B	437	HIS	-	expression tag	UNP Q97MB6
B	438	HIS	-	expression tag	UNP Q97MB6
B	439	HIS	-	expression tag	UNP Q97MB6

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 2 | A | 1 | Total Fe
1 1 | 0 | 0 |
| 2 | B | 1 | Total Fe
1 1 | 0 | 0 |

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- Chemical structure of Guanine (GUN) is shown. The structure is a purine base, consisting of a fused pyrimidine and imidazole ring system. The atoms are labeled as follows: N1, N2, N3, N7, N9 (Nitrogen atoms); C2, C4, C5, C6, C8 (Carbon atoms); and O6 (Oxygen atom). The structure is colored with blue for nitrogen atoms, green for carbon atoms, and red for the oxygen atom.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 11	C 5	N 5	O 1	0	0
3	B	1	Total 11	C 5	N 5	O 1	0	0

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

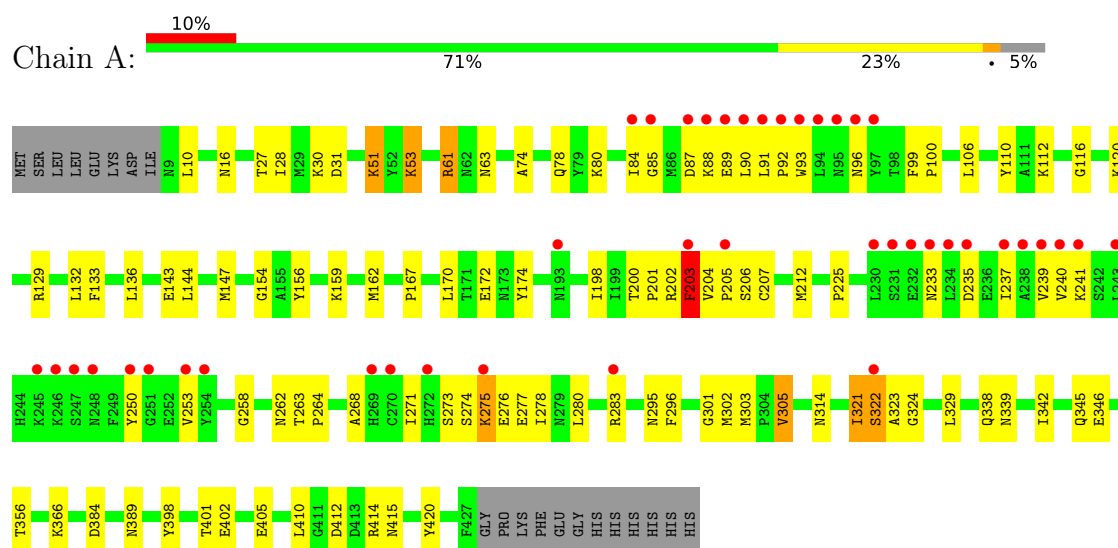
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	205	Total	O	0	0
			205	205		
5	B	215	Total	O	0	0
			215	215		

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: Cytosine/guanine deaminase related protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.39Å 88.99Å 139.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.50 – 2.05 46.50 – 2.05	Depositor EDS
% Data completeness (in resolution range)	89.8 (46.50-2.05) 89.9 (46.50-2.05)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.05Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.194 , 0.224 0.194 , 0.224	Depositor DCC
R_{free} test set	2499 reflections (3.85%)	wwPDB-VP
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.342	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7136	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GUN, FE, 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	0.38	0/3414	0.93	15/4605 (0.3%)
1	B	0.37	0/3414	0.93	15/4605 (0.3%)
All	All	0.37	0/6828	0.93	30/9210 (0.3%)

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	321	ILE	N-CA-C	9.20	122.67	109.51
1	A	323	ALA	N-CA-C	-8.88	101.56	111.07
1	B	323	ALA	N-CA-C	-8.59	101.88	111.07
1	A	106	LEU	N-CA-C	-7.92	102.64	111.82
1	B	106	LEU	N-CA-C	-7.72	102.87	111.82
1	B	321	ILE	N-CA-C	7.53	120.28	109.51
1	B	200	THR	N-CA-C	7.25	121.70	108.94
1	A	200	THR	N-CA-C	7.19	121.59	108.94
1	A	159	LYS	N-CA-C	-6.78	100.00	110.10
1	A	61	ARG	CB-CA-C	-6.33	109.26	116.54
1	A	132	LEU	N-CA-C	6.23	119.62	109.59
1	B	98	THR	N-CA-C	6.11	117.74	111.14
1	B	201	PRO	N-CA-C	-5.93	101.88	111.19
1	B	324	GLY	N-CA-C	-5.91	102.37	111.64
1	B	305	VAL	N-CA-C	5.90	116.64	110.62
1	A	324	GLY	N-CA-C	-5.89	102.40	111.64
1	A	201	PRO	N-CA-C	-5.86	101.99	111.19
1	A	305	VAL	N-CA-C	5.62	116.36	110.62
1	B	159	LYS	N-CA-C	-5.52	102.23	110.23
1	A	156	TYR	N-CA-C	-5.31	99.86	108.52
1	A	27	THR	N-CA-C	-5.31	99.86	108.52
1	B	400	LEU	N-CA-C	5.26	117.01	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	PHE	N-CA-C	-5.22	100.73	109.24
1	B	133	PHE	N-CA-C	-5.18	100.72	109.07
1	B	132	LEU	N-CA-C	5.17	118.17	109.95
1	B	72	LEU	N-CA-C	5.15	119.20	113.02
1	A	268	ALA	N-CA-C	5.14	118.32	110.20
1	B	365	LYS	N-CA-C	5.07	116.80	111.28
1	A	61	ARG	N-CA-C	5.06	116.00	108.31
1	B	27	THR	N-CA-C	-5.01	100.36	108.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	3343	0	3355	79	0
1	B	3343	0	3355	44	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	11	0	5	0	0
3	B	11	0	5	0	0
4	A	6	0	4	0	0
5	A	205	0	0	4	0
5	B	215	0	0	2	0
All	All	7136	0	6724	120	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 9.

All (120) 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:143:GLU:HG3	1:A:147:MET:HE2	1.49	0.93
1:A:303:MET:HE2	1:A:305:VAL:HG22	1.51	0.90
1:A:93:TRP:HA	5:A:584:HOH:O	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:ASN:HD21	1:B:11:LYS:HE3	1.48	0.78
1:A:78:GLN:HB3	1:A:322:SER:HB2	1.67	0.76
1:A:250:TYR:O	1:A:253:VAL:HG22	1.89	0.72
1:A:314:ASN:HD22	1:A:366:LYS:HZ3	1.37	0.72
1:B:78:GLN:HB3	1:B:322:SER:HB2	1.72	0.71
1:A:203:PHE:HE2	1:A:206:SER:HG	1.39	0.69
1:A:96:ASN:HB2	5:A:584:HOH:O	1.91	0.69
1:A:303:MET:CE	1:A:305:VAL:HG22	2.23	0.68
1:B:16:ASN:HD22	1:B:30:LYS:HA	1.61	0.66
1:B:16:ASN:ND2	1:B:30:LYS:HG3	2.11	0.66
1:B:146:ASN:O	1:B:150:LYS:HG3	1.98	0.64
1:B:181:THR:O	1:B:185:ILE:HG13	1.98	0.63
1:A:91:LEU:HB2	1:A:92:PRO:HD3	1.80	0.63
1:A:274:SER:O	1:A:278:ILE:HG12	1.99	0.63
1:A:314:ASN:HD22	1:A:366:LYS:NZ	1.97	0.62
1:B:389:ASN:HD22	1:B:417:MET:CE	2.13	0.62
1:A:273:SER:HB2	1:A:278:ILE:HD11	1.83	0.60
1:A:302:MET:HB3	1:A:339:ASN:HD21	1.67	0.59
1:B:112:LYS:HG2	1:B:143:GLU:HG2	1.84	0.59
1:A:80:LYS:HD2	1:A:110:TYR:OH	2.03	0.58
1:A:275:LYS:HA	1:A:275:LYS:HE2	1.86	0.57
1:B:238:ALA:O	1:B:241:LYS:HG3	2.06	0.56
1:A:162:MET:O	1:A:172:GLU:HG2	2.05	0.56
1:A:80:LYS:HG2	5:A:604:HOH:O	2.04	0.56
1:A:233:ASN:O	1:A:237:ILE:HG13	2.04	0.56
1:B:16:ASN:HD21	1:B:30:LYS:HG3	1.70	0.55
1:A:342:ILE:O	1:A:346:GLU:HG3	2.07	0.55
1:B:302:MET:HB3	1:B:339:ASN:HD21	1.71	0.54
1:A:78:GLN:HB3	1:A:322:SER:CB	2.38	0.54
1:A:80:LYS:HE2	5:B:718:HOH:O	2.08	0.54
1:A:338:GLN:HB3	1:B:296:PHE:HB3	1.90	0.53
1:A:53:LYS:HB2	1:A:53:LYS:NZ	2.23	0.52
1:A:202:ARG:O	1:A:203:PHE:HB3	2.09	0.52
1:A:16:ASN:HD22	1:A:30:LYS:HA	1.75	0.52
1:A:204:VAL:HG21	1:A:253:VAL:HG21	1.91	0.52
1:B:108:VAL:O	1:B:112:LYS:HG3	2.09	0.51
1:B:209:ASN:HD22	1:B:257:PHE:HZ	1.59	0.51
1:A:276:GLU:H	1:A:276:GLU:CD	2.18	0.51
1:A:87:ASP:O	1:A:88:LYS:HD3	2.10	0.51
1:B:389:ASN:HD22	1:B:417:MET:HE3	1.76	0.51
1:A:207:CYS:O	1:A:212:MET:HE2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:PHE:HE2	1:A:206:SER:OG	1.96	0.49
1:B:41:ILE:HD11	1:B:383:PHE:HD1	1.77	0.49
1:A:78:GLN:CB	1:A:322:SER:HB2	2.41	0.49
1:B:9:ASN:ND2	1:B:11:LYS:HE3	2.21	0.49
1:A:10:LEU:HD23	1:A:10:LEU:C	2.36	0.49
1:A:16:ASN:ND2	1:A:31:ASP:H	2.10	0.49
1:A:205:PRO:HD3	1:A:240:VAL:HG22	1.95	0.49
1:A:74:ALA:HB1	1:A:321:ILE:HG12	1.95	0.48
1:B:136:LEU:C	1:B:136:LEU:HD12	2.38	0.48
1:A:204:VAL:HG11	1:A:240:VAL:HG13	1.96	0.48
1:B:276:GLU:HG2	5:B:579:HOH:O	2.13	0.48
1:B:204:VAL:HB	1:B:205:PRO:HD3	1.95	0.48
1:A:89:GLU:O	1:A:92:PRO:HD2	2.14	0.47
1:A:314:ASN:ND2	1:A:366:LYS:NZ	2.61	0.47
1:A:144:LEU:HA	1:A:147:MET:HE3	1.95	0.47
1:B:271:ILE:HD11	1:B:295:ASN:CG	2.38	0.47
1:A:356:THR:HG21	1:A:405:GLU:HG2	1.95	0.47
1:B:342:ILE:O	1:B:346:GLU:HG3	2.14	0.47
1:A:89:GLU:HG3	1:A:233:ASN:HD21	1.80	0.47
1:B:60:PHE:HD2	1:B:65:ILE:HD11	1.80	0.47
1:A:84:ILE:HG22	1:A:85:GLY:N	2.29	0.47
1:B:263:THR:O	1:B:264:PRO:C	2.57	0.47
1:B:389:ASN:HD22	1:B:417:MET:HE1	1.79	0.47
1:A:167:PRO:HG2	1:A:170:LEU:HB3	1.96	0.46
1:A:296:PHE:HB3	1:B:338:GLN:HB3	1.97	0.46
1:A:204:VAL:HG21	1:A:253:VAL:CG2	2.46	0.46
1:A:78:GLN:OE1	1:A:322:SER:HB3	2.16	0.46
1:A:250:TYR:HB3	1:A:277:GLU:OE1	2.15	0.46
1:A:99:PHE:HB2	1:A:100:PRO:HD3	1.98	0.46
1:A:89:GLU:CG	1:A:233:ASN:HD21	2.29	0.46
1:A:258:GLY:HA2	1:A:262:ASN:HD21	1.81	0.46
1:B:129:ARG:HD3	1:B:154:GLY:HA3	1.98	0.46
1:B:204:VAL:HG11	1:B:240:VAL:HG13	1.98	0.46
1:A:28:ILE:HD11	1:A:401:THR:OG1	2.16	0.45
1:A:280:LEU:HA	1:A:283:ARG:NH1	2.31	0.45
1:A:412:ASP:H	1:A:415:ASN:HD22	1.63	0.45
1:B:78:GLN:HB3	1:B:322:SER:CB	2.43	0.45
1:B:398:TYR:HB3	1:B:402:GLU:HB2	1.97	0.45
1:A:321:ILE:O	1:A:322:SER:CB	2.65	0.45
1:A:295:ASN:HB3	1:A:301:GLY:O	2.17	0.45
1:B:200:THR:O	1:B:200:THR:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:ARG:HD3	1:A:154:GLY:HA3	1.98	0.44
1:B:202:ARG:O	1:B:203:PHE:HB3	2.18	0.44
1:B:99:PHE:HB2	1:B:100:PRO:HD3	1.98	0.44
1:A:61:ARG:NH1	1:A:61:ARG:HG3	2.33	0.43
1:A:271:ILE:HD11	1:A:295:ASN:OD1	2.18	0.43
1:B:61:ARG:HG3	1:B:61:ARG:NH1	2.34	0.43
1:A:235:ASP:O	1:A:239:VAL:HG23	2.18	0.43
1:A:414:ARG:HG3	1:B:414:ARG:NH1	2.34	0.43
1:A:174:TYR:CD1	1:A:174:TYR:C	2.97	0.42
1:A:63:ASN:ND2	1:A:389:ASN:HA	2.34	0.42
1:A:89:GLU:HG3	1:A:233:ASN:ND2	2.33	0.42
1:A:384:ASP:HA	1:A:420:TYR:O	2.18	0.42
1:B:63:ASN:ND2	1:B:389:ASN:HA	2.34	0.42
1:A:84:ILE:CG2	1:A:85:GLY:N	2.83	0.42
1:B:358:GLU:O	1:B:362:MET:HG3	2.20	0.42
1:A:112:LYS:HG3	1:A:143:GLU:HG2	2.02	0.42
1:A:302:MET:CB	1:A:339:ASN:HD21	2.30	0.42
1:B:41:ILE:HG12	1:B:381:TYR:O	2.20	0.42
1:A:51:LYS:NZ	1:A:51:LYS:HB2	2.35	0.41
1:A:89:GLU:HG2	5:A:656:HOH:O	2.20	0.41
1:A:136:LEU:C	1:A:136:LEU:HD12	2.45	0.41
1:A:61:ARG:HG3	1:A:61:ARG:HH11	1.85	0.41
1:A:258:GLY:HA2	1:A:262:ASN:ND2	2.35	0.41
1:A:116:GLY:O	1:A:120:LYS:HG3	2.20	0.41
1:B:384:ASP:HA	1:B:420:TYR:O	2.21	0.41
1:A:203:PHE:CZ	1:A:205:PRO:HG2	2.56	0.41
1:B:356:THR:HG21	1:B:405:GLU:HG2	2.02	0.41
1:A:398:TYR:HB3	1:A:402:GLU:HB2	2.03	0.41
1:B:302:MET:CB	1:B:339:ASN:HD21	2.33	0.41
1:B:314:ASN:HB3	1:B:366:LYS:HZ1	1.87	0.40
1:B:78:GLN:OE1	1:B:322:SER:HB3	2.20	0.40
1:A:198:ILE:HG13	1:A:225:PRO:HG2	2.04	0.40
1:A:329:LEU:HD12	1:A:329:LEU:HA	1.96	0.40
1:A:263:THR:O	1:A:264:PRO:C	2.63	0.40
1:B:145:PHE:CZ	1:B:157:VAL:HB	2.56	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	417/439 (95%)	399 (96%)	15 (4%)	3 (1%)	18	10
1	B	417/439 (95%)	399 (96%)	15 (4%)	3 (1%)	18	10
All	All	834/878 (95%)	798 (96%)	30 (4%)	6 (1%)	18	10

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	322	SER
1	B	322	SER
1	B	190	ASP
1	A	203	PHE
1	B	90	LEU
1	A	90	LEU

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	374/392 (95%)	367 (98%)	7 (2%)	50	50
1	B	374/392 (95%)	369 (99%)	5 (1%)	61	63
All	All	748/784 (95%)	736 (98%)	12 (2%)	55	56

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LYS
1	A	53	LYS
1	A	203	PHE
1	A	241	LYS
1	A	275	LYS
1	A	345	GLN
1	A	410	LEU
1	B	51	LYS
1	B	203	PHE
1	B	241	LYS
1	B	410	LEU
1	B	419	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	62	ASN
1	A	63	ASN
1	A	262	ASN
1	A	279	ASN
1	A	314	ASN
1	A	339	ASN
1	A	415	ASN
1	A	424	ASN
1	B	9	ASN
1	B	16	ASN
1	B	55	ASN
1	B	63	ASN
1	B	95	ASN
1	B	209	ASN
1	B	248	ASN
1	B	262	ASN
1	B	285	ASN
1	B	339	ASN

5.3.3 RNA ⓘ

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](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	GUN	B	504	2	12,12,12	1.31	2 (16%)	15,17,17	1.54	2 (13%)
4	GOL	A	505	-	5,5,5	4.75	5 (100%)	5,5,5	6.19	3 (60%)
3	GUN	A	503	2	12,12,12	1.35	2 (16%)	15,17,17	1.80	2 (13%)

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	GUN	B	504	2	-	-	0/2/2/2
4	GOL	A	505	-	-	3/4/4/4	-
3	GUN	A	503	2	-	-	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	505	GOL	C3-C2	-8.07	1.21	1.51
4	A	505	GOL	O1-C1	4.54	1.61	1.42
4	A	505	GOL	O3-C3	3.27	1.56	1.42
4	A	505	GOL	C1-C2	-2.95	1.40	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	505	GOL	O2-C2	-2.76	1.35	1.43
3	A	503	GUN	C8-N9	2.59	1.39	1.35
3	B	504	GUN	C8-N9	2.29	1.38	1.35
3	B	504	GUN	C4-N3	2.21	1.39	1.36
3	A	503	GUN	C2-N1	2.07	1.42	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	505	GOL	O3-C3-C2	11.34	161.43	110.38
4	A	505	GOL	O2-C2-C3	7.00	138.16	109.18
3	A	503	GUN	O6-C6-N1	4.23	128.06	120.11
3	B	504	GUN	O6-C6-N1	3.62	126.91	120.11
4	A	505	GOL	O1-C1-C2	3.55	126.35	110.38
3	A	503	GUN	N9-C8-N7	2.91	116.36	112.98
3	B	504	GUN	N9-C8-N7	2.74	116.16	112.98

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	505	GOL	O1-C1-C2-C3
4	A	505	GOL	C1-C2-C3-O3
4	A	505	GOL	O1-C1-C2-O2

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	419/439 (95%)	0.30	42 (10%) 12 12	16, 29, 52, 66	0
1	B	419/439 (95%)	0.07	9 (2%) 63 65	17, 29, 46, 66	0
All	All	838/878 (95%)	0.18	51 (6%) 27 27	16, 29, 51, 66	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	91	LEU	6.4
1	A	90	LEU	5.5
1	A	233	ASN	4.0
1	A	239	VAL	3.7
1	A	95	ASN	3.6
1	A	87	ASP	3.6
1	A	250	TYR	3.4
1	A	240	VAL	3.3
1	A	89	GLU	3.3
1	A	237	ILE	3.2
1	A	88	LYS	3.2
1	A	269	HIS	3.2
1	A	97	TYR	3.2
1	A	243	LEU	3.1
1	A	322	SER	3.0
1	B	322	SER	3.0
1	A	272	HIS	2.9
1	A	235	ASP	2.8
1	A	245	LYS	2.8
1	A	96	ASN	2.8
1	B	10	LEU	2.8
1	A	246	LYS	2.8
1	A	205	PRO	2.7
1	A	93	TRP	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	253	VAL	2.6
1	A	270	CYS	2.6
1	B	193	ASN	2.6
1	B	52	TYR	2.6
1	A	247	SER	2.6
1	A	94	LEU	2.5
1	A	248	ASN	2.5
1	A	283	ARG	2.5
1	A	251	GLY	2.5
1	A	85	GLY	2.4
1	A	84	ILE	2.4
1	A	275	LYS	2.4
1	B	190	ASP	2.3
1	A	193	ASN	2.3
1	A	230	LEU	2.3
1	A	254	TYR	2.3
1	A	92	PRO	2.3
1	B	9	ASN	2.3
1	A	238	ALA	2.1
1	A	234	LEU	2.1
1	B	51	LYS	2.1
1	B	192	SER	2.1
1	A	232	GLU	2.1
1	A	241	LYS	2.1
1	B	241	LYS	2.1
1	A	203	PHE	2.1
1	A	231	SER	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 oligosaccharides 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	GUN	A	503	11/11	0.66	0.18	32,36,38,40	0
4	GOL	A	505	6/6	0.78	0.23	42,44,45,49	0
2	FE	B	502	1/1	0.90	0.11	45,45,45,45	1
3	GUN	B	504	11/11	0.91	0.10	27,32,34,38	0
2	FE	A	501	1/1	0.98	0.07	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.