



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:02 PM UTC

PDB ID : 1I69 / pdb_00001i69
Title : CRYSTAL STRUCTURE OF THE REDUCED FORM OF OXYR
Authors : Choi, H.; Kim, S.; Ryu, S.
Deposited on : 2001-03-02
Resolution : 2.70 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

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

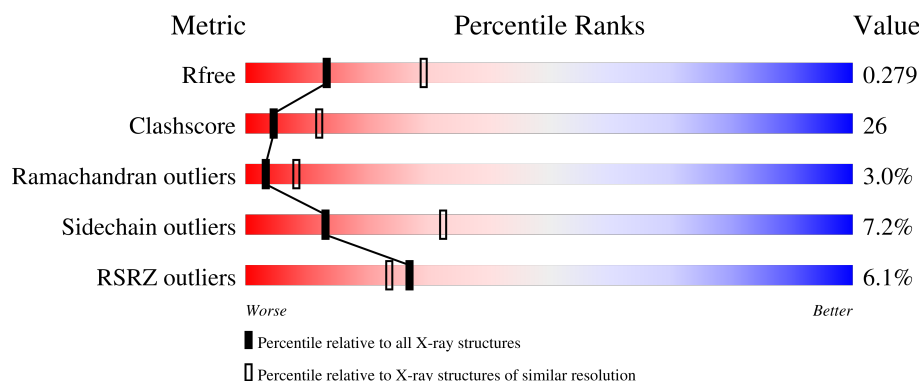
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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 ≥ 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	219	5% 53% 34% 6% 6%
1	B	219	6% 50% 37% 6% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3244 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 HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1617	1038	278	291	10			
1	B	206	Total	C	N	O	S	0	0	0
			1618	1039	278	291	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	ALA	CYS	engineered mutation	UNP P0ACQ4
A	180	ALA	CYS	engineered mutation	UNP P0ACQ4
A	199	SER	CYS	engineered mutation	UNP P0ACQ4
A	259	ALA	CYS	engineered mutation	UNP P0ACQ4
B	1143	ALA	CYS	engineered mutation	UNP P0ACQ4
B	1180	ALA	CYS	engineered mutation	UNP P0ACQ4
B	1199	SER	CYS	engineered mutation	UNP P0ACQ4
B	1259	ALA	CYS	engineered mutation	UNP P0ACQ4

- Molecule 2 is BENZOIC ACID (CCD ID: BEZ) (formula: C₇H₆O₂).

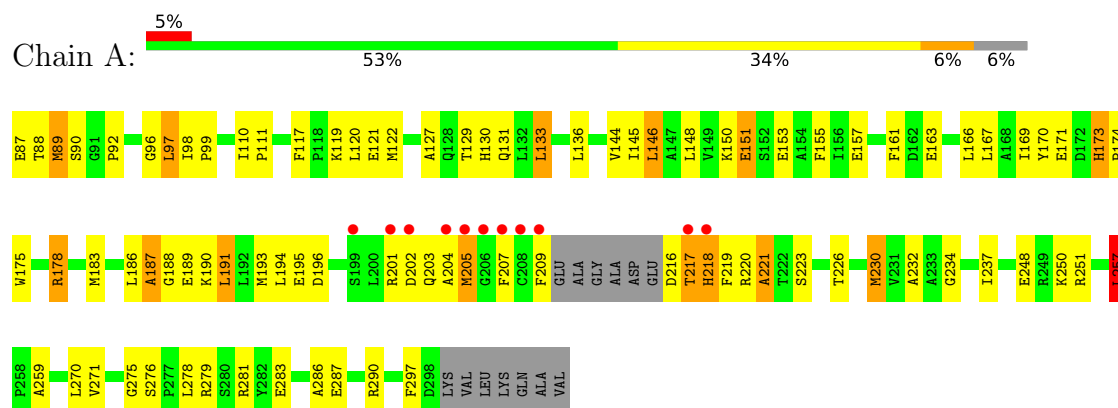


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			9	7	2		

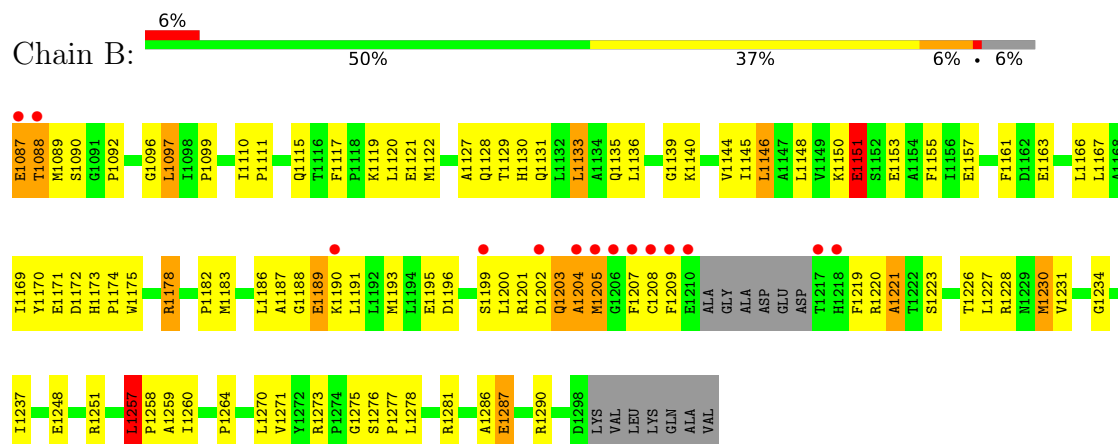
3 Residue-property plots

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: HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR



• Molecule 1: HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	79.49Å 79.49Å 210.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.70 74.36 – 2.70	Depositor EDS
% Data completeness (in resolution range)	93.3 (100.00-2.70) 93.5 (74.36-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	7.80	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.247 , 0.278 0.244 , 0.279	Depositor DCC
R_{free} test set	852 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 33.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3244	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.11% 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: BEZ

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	0.51	0/1657	1.02	8/2251 (0.4%)
1	B	0.52	0/1658	1.02	5/2252 (0.2%)
All	All	0.52	0/3315	1.02	13/4503 (0.3%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1230	MET	N-CA-C	-5.95	104.92	111.82
1	B	1151	GLU	N-CA-C	5.85	118.44	111.71
1	A	257	LEU	CA-C-N	5.61	125.62	119.90
1	A	257	LEU	C-N-CA	5.61	125.62	119.90
1	B	1221	ALA	N-CA-C	-5.36	103.31	110.55
1	A	230	MET	N-CA-C	-5.36	105.61	111.82
1	A	221	ALA	N-CA-C	-5.35	102.61	110.52
1	B	1257	LEU	CA-C-N	5.33	125.33	119.89
1	B	1257	LEU	C-N-CA	5.33	125.33	119.89
1	A	98	ILE	CA-C-N	5.29	126.45	119.84
1	A	98	ILE	C-N-CA	5.29	126.45	119.84
1	A	173	HIS	CA-C-N	5.26	124.71	119.24
1	A	173	HIS	C-N-CA	5.26	124.71	119.24

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	1617	0	1630	87	0
1	B	1618	0	1632	82	0
2	A	9	0	5	0	0
All	All	3244	0	3267	169	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 26.

All (169) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1205:MET:HE2	1:B:1264:PRO:HA	1.43	0.99
1:B:1183:MET:CE	1:B:1259:ALA:HB1	1.96	0.96
1:B:1097:LEU:HD13	1:B:1145:ILE:HB	1.48	0.94
1:A:97:LEU:HD13	1:A:145:ILE:HB	1.47	0.93
1:A:183:MET:CE	1:A:259:ALA:HB1	2.05	0.86
1:A:191:LEU:N	1:A:191:LEU:HD23	1.92	0.85
1:B:1089:MET:HE1	1:B:1281:ARG:HA	1.62	0.81
1:B:1135:GLN:HE21	1:B:1140:LYS:HD3	1.43	0.81
1:A:183:MET:HE3	1:A:259:ALA:HB1	1.67	0.77
1:A:202:ASP:HA	1:A:207:PHE:CZ	2.22	0.73
1:A:202:ASP:HA	1:A:207:PHE:HZ	1.52	0.73
1:B:1248:GLU:OE1	1:B:1251:ARG:HD2	1.88	0.73
1:A:193:MET:HE3	1:A:220:ARG:HH12	1.55	0.72
1:A:290:ARG:HB3	1:A:290:ARG:NH1	2.05	0.72
1:A:219:PHE:CE2	1:A:230:MET:HE2	2.26	0.70
1:A:223:SER:O	1:A:226:THR:HG22	1.91	0.70
1:B:1169:ILE:HG22	1:B:1237:ILE:CG2	2.21	0.70
1:B:1223:SER:O	1:B:1226:THR:HG22	1.91	0.70
1:A:87:GLU:HG2	1:A:88:THR:H	1.57	0.69
1:A:130:HIS:CD2	1:A:131:GLN:HE21	2.10	0.69
1:B:1135:GLN:NE2	1:B:1140:LYS:HD3	2.06	0.69
1:B:1290:ARG:NH1	1:B:1290:ARG:HB3	2.08	0.68
1:A:169:ILE:HG22	1:A:237:ILE:CG2	2.24	0.67
1:A:248:GLU:OE1	1:A:251:ARG:HD2	1.96	0.66
1:A:270:LEU:HD23	1:A:271:VAL:N	2.11	0.66
1:A:193:MET:HE3	1:A:220:ARG:NH1	2.11	0.65
1:A:195:GLU:HG2	1:A:196:ASP:N	2.12	0.64
1:A:129:THR:HG23	1:A:146:LEU:HD12	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1270:LEU:HD23	1:B:1271:VAL:N	2.13	0.64
1:A:190:LYS:HZ3	1:A:216:ASP:N	1.96	0.64
1:B:1167:LEU:HB3	1:B:1257:LEU:HD12	1.80	0.63
1:A:257:LEU:HD12	1:A:257:LEU:O	1.99	0.62
1:A:89:MET:HA	1:A:89:MET:HE2	1.79	0.62
1:B:1196:ASP:N	1:B:1201:ARG:HH11	1.97	0.62
1:B:1183:MET:HE3	1:B:1259:ALA:HB1	1.78	0.61
1:A:150:LYS:O	1:A:153:GLU:HB2	2.01	0.61
1:B:1150:LYS:O	1:B:1153:GLU:HB2	2.00	0.61
1:B:1219:PHE:CE2	1:B:1230:MET:HE2	2.35	0.61
1:A:167:LEU:HB3	1:A:257:LEU:HD12	1.82	0.60
1:A:151:GLU:H	1:A:151:GLU:CD	2.07	0.60
1:B:1196:ASP:N	1:B:1201:ARG:NH1	2.50	0.60
1:A:89:MET:HE1	1:A:281:ARG:HG3	1.84	0.60
1:B:1099:PRO:HD3	1:B:1127:ALA:O	2.03	0.59
1:A:97:LEU:CD1	1:A:145:ILE:HB	2.28	0.58
1:B:1205:MET:CE	1:B:1264:PRO:HA	2.28	0.58
1:A:89:MET:HG3	1:A:117:PHE:CD2	2.39	0.58
1:A:201:ARG:HH22	1:A:220:ARG:HD2	1.68	0.57
1:A:221:ALA:HB1	1:A:226:THR:HG23	1.86	0.57
1:B:1129:THR:HG23	1:B:1146:LEU:HD12	1.85	0.57
1:B:1151:GLU:H	1:B:1151:GLU:CD	2.12	0.57
1:B:1257:LEU:HD12	1:B:1257:LEU:O	2.04	0.56
1:B:1183:MET:HE1	1:B:1259:ALA:HB1	1.85	0.56
1:A:167:LEU:HB3	1:A:257:LEU:CD1	2.36	0.56
1:A:275:GLY:O	1:A:276:SER:C	2.49	0.56
1:B:1167:LEU:HB3	1:B:1257:LEU:CD1	2.37	0.55
1:B:1166:LEU:N	1:B:1166:LEU:HD12	2.23	0.54
1:B:1167:LEU:HD23	1:B:1257:LEU:HD11	1.90	0.54
1:B:1169:ILE:HG22	1:B:1237:ILE:HG22	1.88	0.54
1:A:171:GLU:OE2	1:A:250:LYS:HD2	2.09	0.53
1:A:99:PRO:HD3	1:A:127:ALA:O	2.09	0.52
1:A:186:LEU:O	1:A:188:GLY:N	2.42	0.52
1:A:196:ASP:N	1:A:201:ARG:HH21	2.08	0.52
1:B:1199:SER:O	1:B:1203:GLN:NE2	2.43	0.52
1:A:204:ALA:O	1:A:205:MET:C	2.52	0.51
1:B:1087:GLU:O	1:B:1089:MET:N	2.44	0.51
1:B:1195:GLU:HG2	1:B:1196:ASP:N	2.26	0.51
1:B:1270:LEU:HD13	1:B:1286:ALA:HB2	1.93	0.51
1:A:129:THR:HG23	1:A:146:LEU:CD1	2.41	0.51
1:A:169:ILE:HG22	1:A:237:ILE:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1170:TYR:CD1	1:B:1234:GLY:HA2	2.46	0.50
1:B:1090:SER:HA	1:B:1119:LYS:O	2.12	0.50
1:B:1186:LEU:O	1:B:1188:GLY:N	2.45	0.50
1:A:144:VAL:HG12	1:A:146:LEU:HD22	1.92	0.50
1:A:190:LYS:C	1:A:191:LEU:HD23	2.37	0.50
1:B:1278:LEU:O	1:B:1281:ARG:HB3	2.12	0.50
1:B:1088:THR:C	1:B:1089:MET:HE2	2.37	0.50
1:B:1089:MET:HG3	1:B:1117:PHE:CE2	2.47	0.50
1:A:117:PHE:O	1:A:120:LEU:HB2	2.12	0.49
1:A:196:ASP:HA	1:A:201:ARG:HE	1.76	0.49
1:B:1189:GLU:HG3	1:B:1190:LYS:H	1.76	0.49
1:B:1092:PRO:HA	1:B:1121:GLU:HB2	1.94	0.49
1:A:90:SER:HA	1:A:119:LYS:O	2.13	0.49
1:B:1275:GLY:O	1:B:1276:SER:C	2.55	0.49
1:A:191:LEU:HD23	1:A:191:LEU:H	1.75	0.49
1:A:166:LEU:HD12	1:A:166:LEU:N	2.27	0.48
1:A:136:LEU:HD23	1:A:155:PHE:CD2	2.47	0.48
1:A:290:ARG:HB3	1:A:290:ARG:CZ	2.43	0.48
1:A:130:HIS:HD2	1:A:131:GLN:HE21	1.57	0.48
1:A:167:LEU:HD23	1:A:257:LEU:HD11	1.94	0.48
1:A:270:LEU:HD13	1:A:286:ALA:HB2	1.95	0.48
1:B:1089:MET:HG3	1:B:1117:PHE:CD2	2.49	0.48
1:B:1128:GLN:HB2	1:B:1130:HIS:CE1	2.49	0.48
1:A:188:GLY:O	1:A:189:GLU:HB2	2.13	0.47
1:B:1096:GLY:C	1:B:1097:LEU:HD22	2.38	0.47
1:A:290:ARG:HB3	1:A:290:ARG:HH11	1.79	0.47
1:A:89:MET:HG3	1:A:117:PHE:CE2	2.49	0.47
1:A:161:PHE:HE1	1:A:163:GLU:HB2	1.79	0.47
1:A:92:PRO:HA	1:A:121:GLU:HB2	1.97	0.47
1:B:1169:ILE:HG22	1:B:1237:ILE:HG21	1.96	0.47
1:B:1290:ARG:HB3	1:B:1290:ARG:CZ	2.44	0.47
1:B:1087:GLU:C	1:B:1089:MET:N	2.72	0.47
1:B:1221:ALA:HB1	1:B:1226:THR:HG23	1.97	0.47
1:A:270:LEU:HD23	1:A:270:LEU:C	2.40	0.47
1:B:1146:LEU:HD23	1:B:1146:LEU:N	2.29	0.46
1:B:1173:HIS:CG	1:B:1174:PRO:HD2	2.51	0.46
1:A:279:ARG:O	1:A:283:GLU:HG2	2.15	0.46
1:A:88:THR:O	1:A:90:SER:N	2.47	0.46
1:B:1151:GLU:C	1:B:1153:GLU:H	2.24	0.46
1:B:1193:MET:HB2	1:B:1220:ARG:HH11	1.81	0.45
1:B:1195:GLU:HG2	1:B:1196:ASP:H	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:MET:HE2	1:A:89:MET:CA	2.46	0.45
1:B:1204:ALA:O	1:B:1205:MET:C	2.59	0.45
1:A:209:PHE:N	1:A:209:PHE:CD2	2.81	0.45
1:A:87:GLU:HG2	1:A:88:THR:N	2.30	0.45
1:A:186:LEU:O	1:A:187:ALA:C	2.60	0.45
1:A:191:LEU:N	1:A:191:LEU:CD2	2.64	0.44
1:B:1208:CYS:SG	1:B:1209:PHE:N	2.90	0.44
1:B:1270:LEU:HD23	1:B:1270:LEU:C	2.42	0.44
1:A:89:MET:HE1	1:A:281:ARG:HA	2.00	0.44
1:A:278:LEU:O	1:A:281:ARG:HB3	2.17	0.44
1:A:110:ILE:N	1:A:111:PRO:HD2	2.32	0.44
1:B:1175:TRP:HA	1:B:1178:ARG:HG3	1.98	0.44
1:A:175:TRP:HA	1:A:178:ARG:HG3	1.99	0.44
1:B:1111:PRO:O	1:B:1115:GLN:HG2	2.17	0.44
1:B:1110:ILE:N	1:B:1111:PRO:HD2	2.33	0.44
1:A:130:HIS:CD2	1:A:131:GLN:HG2	2.52	0.43
1:A:190:LYS:HA	1:A:191:LEU:HD23	2.00	0.43
1:A:232:ALA:C	1:A:234:GLY:H	2.26	0.43
1:B:1146:LEU:N	1:B:1146:LEU:CD2	2.81	0.43
1:A:194:LEU:HD23	1:A:221:ALA:HB3	2.00	0.43
1:A:148:LEU:HD22	1:A:157:GLU:OE1	2.18	0.43
1:A:151:GLU:CD	1:A:151:GLU:N	2.76	0.43
1:A:151:GLU:C	1:A:153:GLU:H	2.26	0.43
1:A:173:HIS:CG	1:A:174:PRO:HD2	2.53	0.43
1:A:129:THR:O	1:A:133:LEU:HB2	2.18	0.43
1:A:297:PHE:CD1	1:A:297:PHE:N	2.86	0.43
1:B:1228:ARG:O	1:B:1231:VAL:HB	2.19	0.43
1:B:1130:HIS:CD2	1:B:1131:GLN:HE21	2.36	0.43
1:B:1161:PHE:HE1	1:B:1163:GLU:HB2	1.84	0.43
1:A:120:LEU:HD12	1:A:120:LEU:HA	1.77	0.43
1:B:1097:LEU:CD1	1:B:1145:ILE:HB	2.34	0.43
1:B:1146:LEU:HD23	1:B:1146:LEU:H	1.84	0.42
1:A:169:ILE:HG22	1:A:237:ILE:HG22	2.01	0.42
1:B:1148:LEU:HD22	1:B:1157:GLU:OE1	2.19	0.42
1:B:1196:ASP:CA	1:B:1201:ARG:HH11	2.33	0.42
1:A:146:LEU:HD23	1:A:146:LEU:N	2.35	0.42
1:B:1136:LEU:HD23	1:B:1155:PHE:CD2	2.55	0.42
1:B:1196:ASP:CG	1:B:1201:ARG:NH1	2.78	0.42
1:B:1276:SER:HA	1:B:1277:PRO:HD3	1.92	0.42
1:B:1287:GLU:OE2	1:B:1290:ARG:NH1	2.53	0.42
1:B:1133:LEU:HD12	1:B:1133:LEU:HA	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1155:PHE:HB2	1:B:1271:VAL:CG1	2.50	0.42
1:B:1201:ARG:NH2	1:B:1220:ARG:NE	2.68	0.42
1:A:87:GLU:CG	1:A:88:THR:H	2.24	0.41
1:A:221:ALA:HB1	1:A:226:THR:CG2	2.49	0.41
1:B:1221:ALA:CB	1:B:1227:LEU:HD13	2.49	0.41
1:B:1248:GLU:H	1:B:1248:GLU:CD	2.28	0.41
1:A:170:TYR:CD1	1:A:234:GLY:HA2	2.55	0.41
1:A:201:ARG:HH22	1:A:220:ARG:CD	2.32	0.41
1:B:1290:ARG:HB3	1:B:1290:ARG:HH11	1.83	0.41
1:B:1117:PHE:O	1:B:1120:LEU:HB2	2.19	0.41
1:A:96:GLY:C	1:A:97:LEU:HD22	2.44	0.41
1:B:1182:PRO:HA	1:B:1260:ILE:O	2.21	0.41
1:B:1144:VAL:HG12	1:B:1146:LEU:HD22	2.01	0.41
1:A:97:LEU:HD22	1:A:97:LEU:N	2.36	0.40
1:B:1139:GLY:HA2	1:B:1273:ARG:NH1	2.36	0.40
1:A:89:MET:HA	1:A:89:MET:CE	2.51	0.40
1:B:1171:GLU:C	1:B:1173:HIS:H	2.29	0.40
1:B:1257:LEU:HA	1:B:1258:PRO:HD3	1.93	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	202/219 (92%)	175 (87%)	21 (10%)	6 (3%)	3	8
1	B	202/219 (92%)	179 (89%)	17 (8%)	6 (3%)	3	8
All	All	404/438 (92%)	354 (88%)	38 (9%)	12 (3%)	3	8

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	ALA
1	B	1088	THR
1	B	1187	ALA
1	B	1204	ALA
1	A	205	MET
1	B	1205	MET
1	A	89	MET
1	A	203	GLN
1	B	1202	ASP
1	A	217	THR
1	A	218	HIS
1	B	1172	ASP

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	173/182 (95%)	162 (94%)	11 (6%)	16	38
1	B	173/182 (95%)	159 (92%)	14 (8%)	11	27
All	All	346/364 (95%)	321 (93%)	25 (7%)	13	32

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	LEU
1	A	122	MET
1	A	133	LEU
1	A	146	LEU
1	A	151	GLU
1	A	178	ARG
1	A	191	LEU
1	A	217	THR
1	A	218	HIS
1	A	257	LEU
1	A	287	GLU
1	B	1087	GLU

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Mol	Chain	Res	Type
1	B	1097	LEU
1	B	1122	MET
1	B	1133	LEU
1	B	1146	LEU
1	B	1151	GLU
1	B	1178	ARG
1	B	1189	GLU
1	B	1191	LEU
1	B	1200	LEU
1	B	1203	GLN
1	B	1207	PHE
1	B	1257	LEU
1	B	1287	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	HIS
1	A	130	HIS
1	A	131	GLN
1	A	177	ASN
1	A	198	HIS
1	A	218	HIS
1	B	1125	HIS
1	B	1131	GLN
1	B	1135	GLN
1	B	1177	ASN
1	B	1203	GLN
1	B	1218	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BEZ	A	2000	-	9,9,9	2.75	5 (55%)	11,11,11	1.94	3 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BEZ	A	2000	-	-	0/4/4/4	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2000	BEZ	O1-C	-4.04	1.11	1.22
2	A	2000	BEZ	C1-C	3.84	1.57	1.49
2	A	2000	BEZ	C6-C1	3.68	1.45	1.39
2	A	2000	BEZ	C2-C1	3.23	1.44	1.39
2	A	2000	BEZ	C4-C3	2.34	1.43	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2000	BEZ	O2-C-O1	4.62	133.29	123.35
2	A	2000	BEZ	C6-C1-C	2.34	125.00	120.37
2	A	2000	BEZ	O2-C-C1	-2.18	109.25	114.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	206/219 (94%)	0.08	11 (5%) 32 28	26, 43, 67, 78	0
1	B	206/219 (94%)	0.11	14 (6%) 23 20	23, 42, 65, 72	0
All	All	412/438 (94%)	0.10	25 (6%) 27 24	23, 42, 67, 78	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1208	CYS	5.8
1	B	1204	ALA	4.8
1	A	204	ALA	4.5
1	A	207	PHE	4.3
1	B	1209	PHE	4.3
1	B	1207	PHE	3.5
1	A	217	THR	3.3
1	B	1205	MET	3.2
1	B	1210	GLU	3.0
1	A	199	SER	3.0
1	A	206	GLY	3.0
1	A	209	PHE	2.9
1	B	1199	SER	2.7
1	A	208	CYS	2.7
1	B	1202	ASP	2.6
1	B	1217	THR	2.5
1	A	201	ARG	2.5
1	B	1206	GLY	2.3
1	A	205	MET	2.2
1	B	1190	LYS	2.2
1	B	1218	HIS	2.2
1	A	218	HIS	2.2
1	B	1087	GLU	2.1
1	B	1088	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	202	ASP	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 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($\text{\AA}^2$)	Q<0.9
2	BEZ	A	2000	9/9	0.92	0.11	42,46,54,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.