



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:02 PM UTC

PDB ID : 1IQX / pdb_00001iqx
Title : CRYSTAL STRUCTURE OF COBALT-SUBSTITUTED AMINE OXIDASE
FROM ARTHROBACTER GLOBIFORMIS
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Deposited on : 2001-08-27
Resolution : 2.00 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

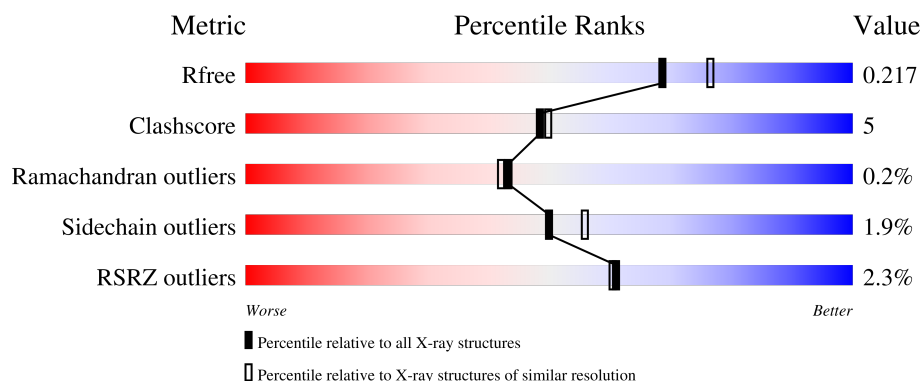
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	638	3% 78% 18% ..
1	B	638	% 83% 13% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10693 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(II)-SUBSTITUTED AMINE OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	620	Total 4868	C 3074	N 855	O 930	S 9	0	0	0
1	B	620	Total 4868	C 3074	N 855	O 930	S 9	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	382	TPQ	TYR	modified residue	UNP P46881
B	382	TPQ	TYR	modified residue	UNP P46881

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Co 1	0	0
2	B	1	Total 1	Co 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	425	Total 425	O 425	0	0
3	B	530	Total 530	O 530	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	157.99Å 62.77Å 184.19Å 90.00° 111.85° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00 10.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (10.00-2.00) 99.1 (10.00-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 1.80Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.211 , 0.260 0.178 , 0.217	Depositor DCC
R_{free} test set	7761 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	16.8	Xtriage
Anisotropy	0.716	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 82.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10693	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.20 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.5401e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CO, TPQ

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	0.57	1/4975 (0.0%)	1.02	25/6774 (0.4%)
1	B	0.59	0/4975	1.00	26/6774 (0.4%)
All	All	0.58	1/9950 (0.0%)	1.01	51/13548 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	MET	SD-CE	-5.26	1.66	1.79

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	562	SER	N-CA-C	7.75	120.62	111.71
1	B	34	GLY	CA-C-N	7.18	127.18	119.28
1	B	34	GLY	C-N-CA	7.18	127.18	119.28
1	A	107	VAL	N-CA-C	6.84	118.41	110.62
1	A	446	PHE	N-CA-C	6.82	121.43	113.18
1	B	446	PHE	N-CA-C	6.51	121.05	113.18
1	B	592	HIS	N-CA-C	6.30	119.22	109.07
1	A	602	MET	N-CA-C	6.30	117.58	109.65
1	B	95	THR	N-CA-C	6.27	120.92	113.28
1	B	199	ALA	N-CA-C	6.25	121.13	112.45
1	A	408	THR	N-CA-C	6.19	119.62	110.46
1	A	567	LEU	N-CA-C	6.17	121.27	113.25
1	B	224	GLN	CA-C-N	6.07	126.52	119.47
1	B	224	GLN	C-N-CA	6.07	126.52	119.47
1	A	592	HIS	N-CA-C	6.07	118.84	109.07
1	A	593	PHE	N-CA-C	-6.05	94.65	108.27
1	B	92	THR	N-CA-C	6.05	118.67	111.71
1	A	268	LEU	N-CA-C	-5.95	98.83	108.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	602	MET	N-CA-C	5.95	118.24	109.50
1	A	413	GLU	N-CA-C	-5.79	101.28	109.96
1	A	310	SER	N-CA-C	-5.75	99.83	108.96
1	A	603	PRO	N-CA-C	-5.63	102.28	111.68
1	B	604	VAL	N-CA-C	5.62	116.66	109.30
1	B	310	SER	N-CA-C	-5.60	100.05	108.96
1	B	408	THR	N-CA-C	5.54	118.65	110.46
1	A	604	VAL	N-CA-C	5.54	116.84	109.37
1	B	582	ILE	N-CA-C	5.41	116.64	108.96
1	B	294	GLN	N-CA-C	5.41	116.93	109.15
1	A	455	VAL	N-CA-C	-5.39	102.63	109.80
1	B	161	ASP	N-CA-C	5.33	117.84	111.71
1	B	324	LEU	N-CA-C	-5.26	100.82	109.40
1	A	211	GLY	N-CA-C	-5.24	101.66	112.34
1	B	52	GLY	N-CA-C	-5.23	108.17	114.66
1	A	304	VAL	N-CA-C	5.22	117.57	111.05
1	B	478	THR	N-CA-C	5.21	119.73	112.90
1	A	582	ILE	N-CA-C	5.19	116.33	108.96
1	A	410	ALA	N-CA-C	-5.19	102.07	110.32
1	B	593	PHE	N-CA-C	-5.15	96.68	108.27
1	B	162	PHE	N-CA-C	-5.13	103.60	108.22
1	B	135	ALA	CA-C-N	5.12	126.24	119.84
1	B	135	ALA	C-N-CA	5.12	126.24	119.84
1	B	603	PRO	N-CA-C	-5.11	103.14	111.68
1	B	374	SER	N-CA-C	5.10	116.95	109.24
1	A	84	VAL	N-CA-C	-5.10	100.54	107.99
1	B	455	VAL	N-CA-C	-5.10	103.00	109.58
1	A	324	LEU	N-CA-C	-5.09	101.10	109.40
1	A	288	SER	CA-C-N	5.07	124.73	119.56
1	A	288	SER	C-N-CA	5.07	124.73	119.56
1	A	374	SER	N-CA-C	5.05	116.86	109.24
1	A	34	GLY	CA-C-N	5.01	124.61	119.05
1	A	34	GLY	C-N-CA	5.01	124.61	119.05

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	4868	0	4686	56	0
1	B	4868	0	4686	50	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	425	0	0	4	0
3	B	530	0	0	6	0
All	All	10693	0	9372	104	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 (104) 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:263:ARG:NH1	1:B:268:LEU:HD13	1.92	0.85
1:A:78:SER:HB2	1:A:85:ILE:HD11	1.59	0.85
1:A:45:LEU:HD11	1:A:61:ARG:HB2	1.64	0.79
1:A:458:GLN:HE22	1:B:418:ASN:HD21	1.32	0.75
1:B:125:ARG:HG2	1:B:194:VAL:HG23	1.67	0.75
1:B:263:ARG:HH11	1:B:268:LEU:HD13	1.56	0.70
1:A:170:HIS:HD2	1:A:198:PRO:O	1.79	0.65
1:B:533:ARG:HD2	1:B:561:HIS:O	1.97	0.64
1:B:628:ASN:HB2	3:B:738:HOH:O	1.97	0.63
1:B:505:ARG:HD3	1:B:618:ASP:HB3	1.81	0.62
1:A:483:ALA:HB1	1:A:543:VAL:HB	1.81	0.61
1:B:499:ASN:HD22	1:B:501:GLU:H	1.48	0.61
1:A:162:PHE:HB2	1:A:163:PRO:HD2	1.82	0.61
1:A:401:LYS:HG2	1:A:606:THR:HG22	1.82	0.60
1:A:163:PRO:HG2	3:A:1029:HOH:O	2.02	0.60
1:A:294:GLN:HG3	1:A:296:TYR:CZ	2.36	0.60
1:B:236:ASN:HD22	1:B:236:ASN:H	1.49	0.60
1:A:111:LEU:HD12	1:A:179:VAL:HG11	1.84	0.59
1:B:443:ILE:H	1:B:448:ASN:HD21	1.51	0.59
1:A:137:LEU:HD13	1:A:296:TYR:OH	2.03	0.58
1:A:294:GLN:HG3	1:A:296:TYR:OH	2.04	0.58
1:A:59:ARG:CZ	1:A:85:ILE:HD13	2.33	0.58
1:B:170:HIS:HD2	1:B:198:PRO:O	1.86	0.58
1:B:137:LEU:HD13	1:B:296:TYR:OH	2.05	0.57
1:A:350:GLY:HA2	1:A:367:ARG:NH2	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:267:ARG:HG2	1:B:267:ARG:HH11	1.71	0.56
1:A:22:GLU:HG2	1:A:79:VAL:HG13	1.87	0.55
1:B:146:GLU:O	1:B:150:ARG:HD3	2.06	0.55
1:A:237:HIS:HD2	1:A:246:ASP:OD1	1.90	0.55
1:B:504:ASN:C	1:B:504:ASN:HD22	2.15	0.55
1:A:223:THR:HG23	1:B:221:SER:HB3	1.90	0.53
1:B:504:ASN:ND2	1:B:508:GLU:H	2.06	0.53
1:A:291:ARG:HG2	1:A:294:GLN:OE1	2.09	0.52
1:A:443:ILE:H	1:A:448:ASN:HD21	1.58	0.52
1:A:422:LEU:HD11	1:A:428:ALA:HB2	1.91	0.52
1:A:406:VAL:HG21	1:A:422:LEU:HD11	1.92	0.51
1:A:75:VAL:HG22	1:A:87:ALA:HA	1.92	0.51
1:B:236:ASN:HD22	1:B:236:ASN:N	2.06	0.51
1:A:146:GLU:O	1:A:150:ARG:HD3	2.10	0.50
1:A:251:VAL:CG2	1:A:306:GLN:HB3	2.42	0.50
1:B:499:ASN:HD22	1:B:499:ASN:C	2.19	0.50
1:B:350:GLY:HA2	1:B:367:ARG:NH2	2.27	0.49
1:A:137:LEU:HD22	1:A:296:TYR:CZ	2.47	0.49
1:B:401:LYS:HG2	1:B:606:THR:HG22	1.95	0.49
1:A:20:ILE:HD12	1:A:327:VAL:HG12	1.95	0.49
1:A:19:GLU:O	1:A:23:VAL:HG23	2.13	0.49
1:A:436:SER:HB2	1:A:536:PHE:CE2	2.47	0.48
1:B:533:ARG:CD	1:B:561:HIS:O	2.61	0.48
1:B:599:TRP:CD2	1:B:600:PRO:HA	2.48	0.48
1:A:505:ARG:HD3	1:A:618:ASP:HB3	1.95	0.48
1:A:347:GLU:OE1	1:A:370:ARG:HD2	2.13	0.48
1:B:291:ARG:HG2	1:B:294:GLN:OE1	2.13	0.48
1:A:139:ALA:O	1:A:154:ARG:NH1	2.47	0.48
1:A:324:LEU:HB2	1:A:342:ILE:HB	1.95	0.48
1:B:484:VAL:HG12	1:B:539:LYS:HG3	1.94	0.48
1:A:102:GLU:HG3	1:A:307:TYR:HE1	1.80	0.47
1:A:26:ILE:HD11	1:A:82:GLY:HA2	1.98	0.46
1:B:154:ARG:HD2	1:B:293:TRP:CE3	2.50	0.46
1:A:111:LEU:HD12	1:A:179:VAL:CG1	2.45	0.46
1:A:75:VAL:HG13	1:A:86:SER:O	2.16	0.46
1:B:602:MET:HE3	3:B:1014:HOH:O	2.15	0.45
1:B:19:GLU:O	1:B:23:VAL:HG23	2.15	0.45
1:A:151:ARG:HG2	1:A:181:VAL:CG2	2.47	0.45
1:A:72:PRO:HG2	1:A:90:LEU:HB2	1.99	0.45
1:A:345:HIS:HE1	3:A:968:HOH:O	1.99	0.45
1:A:310:SER:HB3	1:A:339:ARG:HH21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:LEU:HD12	1:B:179:VAL:CG1	2.46	0.45
1:B:263:ARG:NH1	3:B:1184:HOH:O	2.49	0.45
1:A:484:VAL:HG12	1:A:539:LYS:HG3	1.99	0.45
1:B:251:VAL:HG22	1:B:306:GLN:HB3	1.98	0.45
1:B:137:LEU:HB3	1:B:296:TYR:CE1	2.52	0.44
1:B:484:VAL:CG1	1:B:539:LYS:HG3	2.46	0.44
1:A:56:GLU:O	1:A:80:THR:HG21	2.18	0.44
1:B:263:ARG:HH11	1:B:263:ARG:HB2	1.82	0.44
1:A:194:VAL:HG13	3:A:724:HOH:O	2.17	0.43
1:A:147:GLU:HG2	1:A:152:ILE:HG13	1.99	0.43
1:B:230:PHE:HB3	1:B:240:TRP:HB2	2.00	0.43
1:B:233:THR:HB	3:B:826:HOH:O	2.17	0.43
1:B:483:ALA:HB1	1:B:543:VAL:HB	1.99	0.43
1:B:251:VAL:CG2	1:B:306:GLN:HB3	2.48	0.43
1:B:20:ILE:HD12	1:B:327:VAL:HG12	2.01	0.43
1:B:206:ASP:HA	1:B:207:PRO:HD2	1.92	0.42
1:B:252:ARG:O	1:B:299:THR:HG23	2.19	0.42
1:A:49:ARG:HE	1:A:49:ARG:HB3	1.69	0.42
1:B:468:ASN:HD22	1:B:468:ASN:H	1.67	0.42
1:B:551:ARG:HG2	3:B:884:HOH:O	2.19	0.42
1:A:510:VAL:HB	1:A:616:PHE:HA	2.01	0.41
1:A:303:LEU:O	1:A:306:GLN:HG2	2.21	0.41
1:A:561:HIS:CE1	1:A:565:ALA:HB2	2.56	0.41
1:A:599:TRP:CD2	1:A:600:PRO:HA	2.55	0.41
1:A:115:ASP:OD1	1:A:117:ARG:HB2	2.21	0.41
1:A:239:GLU:HG3	3:A:922:HOH:O	2.19	0.41
1:A:375:PHE:CE1	1:A:386:PHE:HB2	2.55	0.41
1:A:206:ASP:CG	1:A:208:GLU:HG2	2.45	0.41
1:A:242:LYS:HZ1	1:A:624:ASP:CG	2.28	0.41
1:A:116:GLU:O	1:A:120:LYS:HB2	2.21	0.41
1:B:137:LEU:HB3	1:B:296:TYR:HE1	1.85	0.41
1:B:324:LEU:HB2	1:B:342:ILE:HB	2.03	0.40
1:B:499:ASN:ND2	1:B:501:GLU:H	2.15	0.40
1:A:137:LEU:HB3	1:A:296:TYR:CE1	2.57	0.40
1:B:280:MET:HG3	1:B:298:ASP:HB2	2.02	0.40
1:B:406:VAL:HG23	3:B:743:HOH:O	2.22	0.40
1:B:519:GLN:HE21	1:B:519:GLN:HA	1.86	0.40
1:B:233:THR:O	1:B:237:HIS:HB3	2.21	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	617/638 (97%)	588 (95%)	27 (4%)	2 (0%)	36	35
1	B	617/638 (97%)	593 (96%)	23 (4%)	1 (0%)	43	42
All	All	1234/1276 (97%)	1181 (96%)	50 (4%)	3 (0%)	43	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	GLU
1	B	627	ALA
1	A	50	GLY

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	513/529 (97%)	504 (98%)	9 (2%)	51	58
1	B	513/529 (97%)	502 (98%)	11 (2%)	47	52
All	All	1026/1058 (97%)	1006 (98%)	20 (2%)	50	56

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	LEU
1	A	102	GLU
1	A	263	ARG

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Mol	Chain	Res	Type
1	A	267	ARG
1	A	280	MET
1	A	376	PHE
1	A	541	LEU
1	A	625	VAL
1	A	628	ASN
1	B	188	ARG
1	B	233	THR
1	B	236	ASN
1	B	263	ARG
1	B	312	GLU
1	B	444	ASP
1	B	468	ASN
1	B	499	ASN
1	B	504	ASN
1	B	519	GLN
1	B	541	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	81	ASN
1	A	170	HIS
1	A	237	HIS
1	A	309	ASN
1	A	345	HIS
1	A	418	ASN
1	A	421	GLN
1	A	468	ASN
1	A	515	HIS
1	A	573	GLN
1	A	628	ASN
1	B	24	GLN
1	B	170	HIS
1	B	236	ASN
1	B	273	ASN
1	B	306	GLN
1	B	334	ASN
1	B	345	HIS
1	B	418	ASN
1	B	458	GLN

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Mol	Chain	Res	Type
1	B	468	ASN
1	B	499	ASN
1	B	504	ASN
1	B	515	HIS
1	B	519	GLN
1	B	628	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	TPQ	B	382	1	13,14,15	2.28	5 (38%)	13,19,21	1.18	1 (7%)
1	TPQ	A	382	1	13,14,15	2.51	6 (46%)	13,19,21	1.14	1 (7%)

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	TPQ	B	382	1	-	2/5/22/24	0/1/1/1
1	TPQ	A	382	1	-	2/5/22/24	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	382	TPQ	O2-C2	3.97	1.35	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	382	TPQ	O2-C2	3.76	1.34	1.24
1	A	382	TPQ	O5-C5	3.68	1.34	1.24
1	A	382	TPQ	C1-C2	-3.62	1.44	1.49
1	B	382	TPQ	C1-C2	-3.58	1.44	1.49
1	B	382	TPQ	O5-C5	3.30	1.33	1.24
1	A	382	TPQ	C3-C4	3.25	1.42	1.36
1	B	382	TPQ	C3-C4	3.14	1.41	1.36
1	A	382	TPQ	C6-C1	2.94	1.41	1.34
1	A	382	TPQ	CB-CA	2.47	1.58	1.53
1	B	382	TPQ	C6-C1	2.43	1.40	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	382	TPQ	O2-C2-C3	-2.72	115.63	121.83
1	A	382	TPQ	O2-C2-C3	-2.61	115.88	121.83

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	382	TPQ	N-CA-CB-C1
1	B	382	TPQ	N-CA-CB-C1
1	A	382	TPQ	C-CA-CB-C1
1	B	382	TPQ	C-CA-CB-C1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	619/638 (97%)	-0.37	19 (3%) 51 50	4, 17, 41, 113	0
1	B	619/638 (97%)	-0.65	9 (1%) 72 71	3, 13, 30, 89	0
All	All	1238/1276 (97%)	-0.51	28 (2%) 61 60	3, 14, 37, 113	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	52	GLY	6.1
1	A	53	SER	5.7
1	B	627	ALA	5.4
1	B	51	ALA	4.8
1	A	628	ASN	4.5
1	A	51	ALA	4.4
1	B	628	ASN	4.3
1	A	52	GLY	4.0
1	A	50	GLY	4.0
1	B	54	GLU	3.9
1	A	34	GLY	3.8
1	A	48	ALA	3.6
1	B	55	ALA	3.6
1	A	9	ALA	3.4
1	A	49	ARG	3.3
1	A	55	ALA	2.9
1	A	68	SER	2.9
1	B	9	ALA	2.6
1	A	35	PRO	2.6
1	A	33	LEU	2.5
1	B	315	CYS	2.4
1	B	53	SER	2.4
1	A	314	GLY	2.3
1	A	56	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	106	GLU	2.2
1	A	54	GLU	2.1
1	A	105	PHE	2.1
1	A	266	ASP	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, 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
1	TPQ	A	382	14/15	0.90	0.10	8,21,29,33	0
1	TPQ	B	382	14/15	0.90	0.12	7,27,41,51	0

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	CO	A	701	1/1	0.99	0.01	10,10,10,10	0
2	CO	B	701	1/1	0.99	0.02	9,9,9,9	0

6.5 Other polymers [i](#)

There are no such residues in this entry.