



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:02 AM UTC

PDB ID : 6K31 / pdb_00006k31
Title : Crystal structure of pyrophosphate-dependent phosphoenolpyruvate carboxykinase (PPi-PEPCK)
Authors : Chiba, Y.; Miyakawa, T.; Tanokura, M.
Deposited on : 2019-05-15
Resolution : 2.60 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

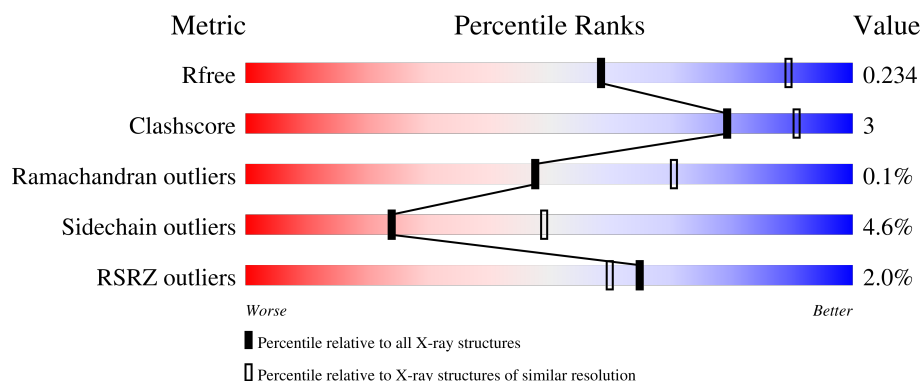
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	1153	% 89% 7% . .
1	B	1153	3% 86% 9% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17477 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 AiPEPCK.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1109	Total	C	N	O	S	Se	0	0	0
			8568	5401	1519	1624	8	16			
1	B	1108	Total	C	N	O	S	Se	0	0	0
			8552	5391	1517	1620	8	16			

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co) (labeled as "Ligand of Interest" by depositor).

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

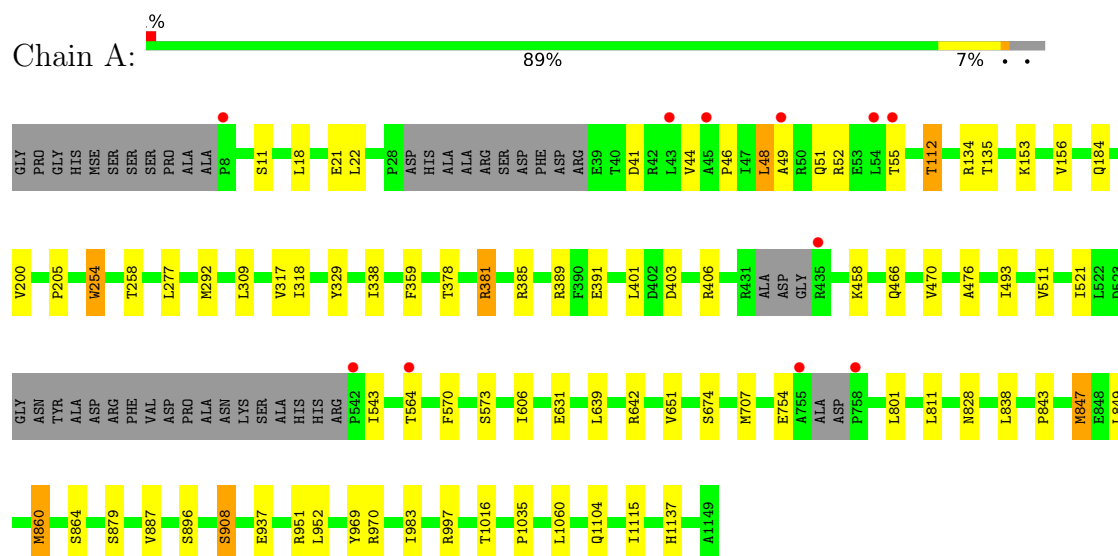
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	216	Total	O	0	0
			216	216		
3	B	139	Total	O	0	0
			139	139		

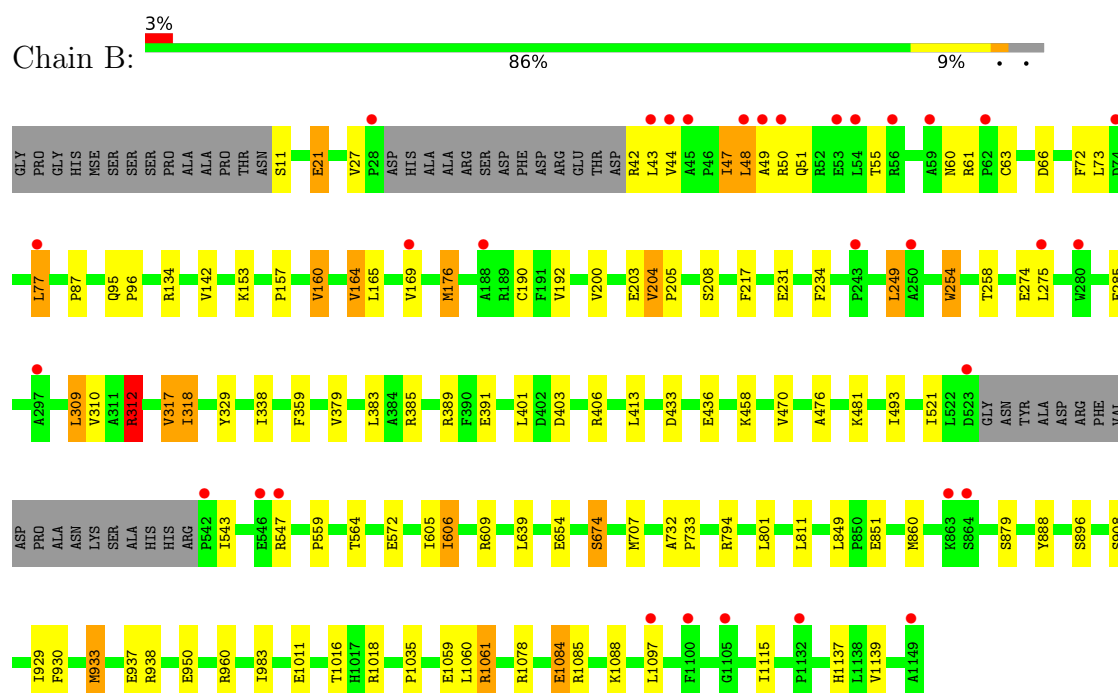
3 Residue-property plots [i](#)

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: AiPEPCK



• Molecule 1: AiPEPCK



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.44Å 160.44Å 200.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.12 – 2.60 48.12 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.12-2.60) 99.9 (48.12-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.60 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.196 , 0.241 0.195 , 0.234	Depositor DCC
R_{free} test set	4595 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.043 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17477	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% 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:
CO

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	1.00	3/8750 (0.0%)	1.05	12/11879 (0.1%)
1	B	0.96	1/8735 (0.0%)	1.05	13/11862 (0.1%)
All	All	0.98	4/17485 (0.0%)	1.05	25/23741 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	864	SER	C-O	-6.45	1.21	1.23
1	A	952	LEU	CA-C	-6.14	1.45	1.52
1	B	481	LYS	CA-C	-5.23	1.47	1.52
1	A	838	LEU	CA-C	-5.21	1.47	1.53

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	933	MSE	CG-SE-CE	8.39	117.38	98.92
1	A	847	MSE	CG-SE-CE	-8.35	80.56	98.92
1	B	543	ILE	N-CA-C	7.62	118.42	110.72
1	A	983	ILE	CB-CA-C	-7.42	104.39	111.44
1	B	983	ILE	CB-CA-C	-7.28	104.52	111.44
1	A	543	ILE	N-CA-C	7.13	117.90	110.62
1	B	707	MSE	CA-CB-CG	-6.90	100.30	114.10
1	B	312	ARG	NE-CZ-NH2	6.65	125.18	119.20
1	A	707	MSE	CA-CB-CG	-6.50	101.10	114.10
1	A	1035	PRO	N-CA-C	6.45	118.56	110.70
1	B	1035	PRO	N-CA-C	6.05	118.08	110.70
1	A	754	GLU	N-CA-C	5.62	117.33	110.41
1	A	112	THR	CB-CA-C	5.58	119.42	109.65
1	B	929	ILE	CB-CA-C	-5.51	104.82	112.04
1	B	164	VAL	N-CA-CB	5.50	118.82	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	PHE	N-CA-C	5.49	119.67	112.92
1	B	888	TYR	N-CA-C	-5.49	105.22	111.14
1	A	860	MSE	N-CA-CB	-5.40	102.08	110.29
1	B	254	TRP	N-CA-C	5.37	117.57	109.41
1	B	312	ARG	NE-CZ-NH1	-5.36	116.14	121.50
1	A	937	GLU	N-CA-C	5.33	117.09	111.28
1	A	254	TRP	N-CA-C	5.32	117.76	109.52
1	B	937	GLU	N-CA-C	5.15	116.90	111.28
1	A	887	VAL	CB-CA-C	-5.13	104.55	112.05
1	A	511	VAL	N-CA-C	5.02	115.74	110.62

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	8568	0	8433	28	0
1	B	8552	0	8417	62	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	216	0	0	1	0
3	B	139	0	0	5	0
All	All	17477	0	16850	90	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 3.

All (90) 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:73:LEU:HD21	1:B:165:LEU:HD21	1.61	0.83
1:A:18:LEU:C	1:A:18:LEU:HD23	2.11	0.75
1:B:860:MSE:HG3	1:B:1016:THR:HG21	1.72	0.71
1:A:860:MSE:HG3	1:A:1016:THR:HG21	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:933:MSE:HE3	1:B:938:ARG:CB	2.25	0.67
1:B:310:VAL:CG1	1:B:318:ILE:HD11	2.26	0.66
1:B:176:MSE:HE1	1:B:190:CYS:C	2.22	0.64
1:B:176:MSE:CE	1:B:190:CYS:O	2.45	0.64
1:B:204:VAL:HG23	1:B:208:SER:OG	1.99	0.63
1:B:960:ARG:NH1	1:B:1011:GLU:OE1	2.33	0.62
1:A:951:ARG:HD3	1:A:969:TYR:CZ	2.35	0.61
1:B:310:VAL:HG13	1:B:318:ILE:HD11	1.81	0.61
1:B:933:MSE:HE3	1:B:938:ARG:HB2	1.83	0.60
1:B:930:PHE:CD1	1:B:933:MSE:HE2	2.37	0.59
1:B:51:GLN:O	1:B:55:THR:HG23	2.03	0.58
1:A:51:GLN:O	1:A:55:THR:HG23	2.02	0.58
1:B:164:VAL:HG21	1:B:309:LEU:CD1	2.33	0.57
1:B:176:MSE:CE	1:B:190:CYS:C	2.78	0.56
1:B:609:ARG:NH2	3:B:1306:HOH:O	2.37	0.56
1:B:21:GLU:HB3	1:B:48:LEU:HD11	1.87	0.56
1:B:933:MSE:HE3	1:B:938:ARG:HB3	1.88	0.56
1:B:63:CYS:SG	1:B:66:ASP:OD1	2.58	0.55
1:B:72:PHE:CG	1:B:317:VAL:HG22	2.43	0.54
1:B:61:ARG:O	1:B:61:ARG:HD2	2.08	0.53
1:B:458:LYS:HD3	1:B:470:VAL:HG21	1.90	0.53
1:A:458:LYS:HD3	1:A:470:VAL:HG21	1.90	0.53
1:B:1078:ARG:NH2	3:B:1303:HOH:O	2.32	0.52
1:B:157:PRO:HD2	1:B:160:VAL:HG11	1.91	0.52
1:B:801:LEU:HD12	1:B:811:LEU:HD21	1.92	0.51
1:B:606:ILE:HD12	1:B:606:ILE:N	2.26	0.51
1:B:44:VAL:O	1:B:44:VAL:HG12	2.11	0.51
1:A:134:ARG:HG3	1:A:329:TYR:CE1	2.47	0.50
1:A:277:LEU:HD21	1:A:292:MSE:HE3	1.94	0.50
1:B:164:VAL:HG21	1:B:309:LEU:HD12	1.93	0.50
1:A:801:LEU:HD12	1:A:811:LEU:HD21	1.95	0.49
1:B:930:PHE:HA	1:B:933:MSE:HE2	1.95	0.49
1:A:156:VAL:HA	1:A:292:MSE:HE2	1.94	0.49
1:B:96:PRO:HA	1:B:231:GLU:OE2	2.13	0.48
1:B:258:THR:O	1:B:317:VAL:HA	2.12	0.48
1:B:310:VAL:CG1	1:B:318:ILE:CD1	2.91	0.48
1:A:153:LYS:NZ	1:A:879:SER:O	2.37	0.47
1:A:606:ILE:HD12	1:A:606:ILE:N	2.28	0.47
1:B:930:PHE:CD1	1:B:933:MSE:CE	2.97	0.47
1:A:378:THR:HG23	1:A:381:ARG:H	1.78	0.47
1:A:258:THR:O	1:A:317:VAL:HA	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:PRO:HD3	1:B:169:VAL:HG13	1.97	0.46
1:A:970:ARG:NH2	1:A:997:ARG:HD2	2.30	0.46
1:A:18:LEU:C	1:A:18:LEU:CD2	2.85	0.46
1:A:277:LEU:HD21	1:A:292:MSE:CE	2.46	0.46
1:B:160:VAL:HG23	1:B:275:LEU:HB3	1.96	0.46
1:A:18:LEU:HD23	1:A:22:LEU:HD12	1.98	0.46
1:B:134:ARG:HG3	1:B:329:TYR:CE1	2.51	0.46
1:B:153:LYS:NZ	1:B:879:SER:O	2.38	0.46
1:B:379:VAL:O	1:B:383:LEU:HD13	2.16	0.45
1:A:48:LEU:HD23	1:A:49:ALA:N	2.32	0.45
1:A:359:PHE:CE2	1:A:476:ALA:HB2	2.52	0.45
1:B:48:LEU:HD23	1:B:49:ALA:N	2.32	0.44
1:A:570:PHE:O	1:A:573:SER:OG	2.27	0.44
1:B:27:VAL:HG11	1:B:42:ARG:HH12	1.83	0.44
1:B:47:ILE:HA	1:B:50:ARG:HG3	2.00	0.44
1:B:176:MSE:HE1	1:B:190:CYS:O	2.14	0.44
1:B:200:VAL:HG22	1:B:338:ILE:HG23	1.99	0.44
1:B:249:LEU:HD12	1:B:1097:LEU:HD23	1.99	0.44
1:A:18:LEU:HD23	1:A:18:LEU:O	2.17	0.43
1:A:200:VAL:HG22	1:A:338:ILE:HG23	2.01	0.43
1:A:292:MSE:HE3	1:A:292:MSE:HB3	1.83	0.43
1:A:277:LEU:CD2	1:A:292:MSE:HE3	2.48	0.43
1:B:72:PHE:CG	1:B:317:VAL:CG2	3.02	0.43
1:B:47:ILE:H	1:B:47:ILE:HG13	1.48	0.43
1:B:960:ARG:NH1	1:B:1011:GLU:CD	2.76	0.43
1:B:605:ILE:HD12	1:B:605:ILE:N	2.34	0.42
1:B:157:PRO:HD2	1:B:160:VAL:CG1	2.49	0.42
1:B:1084:GLU:OE1	1:B:1088:LYS:HE3	2.20	0.42
1:A:391:GLU:HB2	1:A:401:LEU:HD21	2.02	0.42
1:B:732:ALA:N	1:B:733:PRO:CD	2.83	0.42
1:B:72:PHE:CD2	1:B:317:VAL:CG2	3.02	0.42
1:B:359:PHE:CE2	1:B:476:ALA:HB2	2.55	0.42
1:B:654:GLU:OE2	3:B:1302:HOH:O	2.22	0.42
1:A:828:ASN:ND2	1:A:908:SER:OG	2.53	0.42
1:B:142:VAL:CG1	1:B:312:ARG:NH1	2.83	0.42
1:B:559:PRO:HG3	1:B:572:GLU:OE2	2.20	0.42
1:B:391:GLU:HB2	1:B:401:LEU:HD21	2.02	0.41
1:B:851:GLU:OE2	1:B:1061:ARG:NH2	2.50	0.41
1:A:466:GLN:NE2	3:A:1333:HOH:O	2.53	0.41
1:B:176:MSE:HE3	1:B:176:MSE:HA	2.02	0.41
1:B:674:SER:O	3:B:1301:HOH:O	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1085:ARG:HG2	3:B:1384:HOH:O	2.21	0.41
1:A:21:GLU:HB3	1:A:48:LEU:HD11	2.03	0.40
1:B:73:LEU:HD21	1:B:165:LEU:CD2	2.43	0.40
1:B:77:LEU:N	1:B:77:LEU:HD23	2.36	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	1099/1153 (95%)	1054 (96%)	44 (4%)	1 (0%)	48	70
1	B	1102/1153 (96%)	1052 (96%)	49 (4%)	1 (0%)	48	70
All	All	2201/2306 (95%)	2106 (96%)	93 (4%)	2 (0%)	48	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	436	GLU
1	A	46	PRO

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	895/909 (98%)	861 (96%)	34 (4%)	29	56
1	B	891/909 (98%)	842 (94%)	49 (6%)	19	41
All	All	1786/1818 (98%)	1703 (95%)	83 (5%)	24	49

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	41	ASP
1	A	44	VAL
1	A	48	LEU
1	A	52	ARG
1	A	112	THR
1	A	135	THR
1	A	184	GLN
1	A	205	PRO
1	A	254	TRP
1	A	309	LEU
1	A	318	ILE
1	A	381	ARG
1	A	385	ARG
1	A	389	ARG
1	A	403	ASP
1	A	406	ARG
1	A	493	ILE
1	A	521	ILE
1	A	564	THR
1	A	631	GLU
1	A	639	LEU
1	A	642	ARG
1	A	651	VAL
1	A	674	SER
1	A	843	PRO
1	A	847	MSE
1	A	849	LEU
1	A	896	SER
1	A	908	SER
1	A	1060	LEU
1	A	1104	GLN

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Mol	Chain	Res	Type
1	A	1115	ILE
1	A	1137	HIS
1	B	11	SER
1	B	21	GLU
1	B	43	LEU
1	B	47	ILE
1	B	48	LEU
1	B	60	ASN
1	B	77	LEU
1	B	95	GLN
1	B	160	VAL
1	B	176	MSE
1	B	192	VAL
1	B	203	GLU
1	B	204	VAL
1	B	205	PRO
1	B	217	PHE
1	B	249	LEU
1	B	254	TRP
1	B	274	GLU
1	B	285	GLU
1	B	309	LEU
1	B	312	ARG
1	B	317	VAL
1	B	318	ILE
1	B	385	ARG
1	B	389	ARG
1	B	403	ASP
1	B	406	ARG
1	B	413	LEU
1	B	433	ASP
1	B	493	ILE
1	B	521	ILE
1	B	547	ARG
1	B	564	THR
1	B	606	ILE
1	B	639	LEU
1	B	674	SER
1	B	794	ARG
1	B	849	LEU
1	B	896	SER
1	B	908	SER

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Mol	Chain	Res	Type
1	B	950	GLU
1	B	1018	ARG
1	B	1059	GLU
1	B	1060	LEU
1	B	1061	ARG
1	B	1084	GLU
1	B	1115	ILE
1	B	1137	HIS
1	B	1139	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	828	ASN
1	A	957	HIS
1	B	51	GLN
1	B	95	GLN
1	B	257	HIS
1	B	302	ASN
1	B	607	ASN
1	B	957	HIS

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 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 [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	1093/1153 (94%)	-0.32	11 (1%) 79 76	26, 44, 82, 133	0
1	B	1092/1153 (94%)	0.18	32 (2%) 53 48	30, 57, 99, 152	0
All	All	2185/2306 (94%)	-0.07	43 (1%) 65 60	26, 50, 91, 152	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	542	PRO	4.5
1	B	50	ARG	4.0
1	B	547	ARG	4.0
1	B	43	LEU	3.8
1	A	758	PRO	3.7
1	B	1149	ALA	3.5
1	B	54	LEU	3.3
1	A	542	PRO	3.3
1	B	1100	PHE	3.1
1	A	8	PRO	3.0
1	A	755	ALA	3.0
1	B	28	PRO	3.0
1	A	54	LEU	2.9
1	A	43	LEU	2.8
1	B	48	LEU	2.8
1	B	53	GLU	2.8
1	B	62	PRO	2.7
1	B	49	ALA	2.7
1	B	523	ASP	2.7
1	A	45	ALA	2.6
1	B	44	VAL	2.6
1	B	45	ALA	2.6
1	B	1097	LEU	2.5
1	B	250	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	77	LEU	2.3
1	B	864	SER	2.3
1	B	280	TRP	2.3
1	B	56	ARG	2.3
1	B	243	PRO	2.3
1	A	49	ALA	2.2
1	B	169	VAL	2.2
1	B	546	GLU	2.2
1	B	863	LYS	2.2
1	B	1105	GLY	2.1
1	B	297	ALA	2.1
1	B	74	ASP	2.1
1	B	59	ALA	2.1
1	A	55	THR	2.1
1	A	564	THR	2.0
1	B	1132	PRO	2.0
1	B	188	ALA	2.0
1	B	275	LEU	2.0
1	A	435	ARG	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.

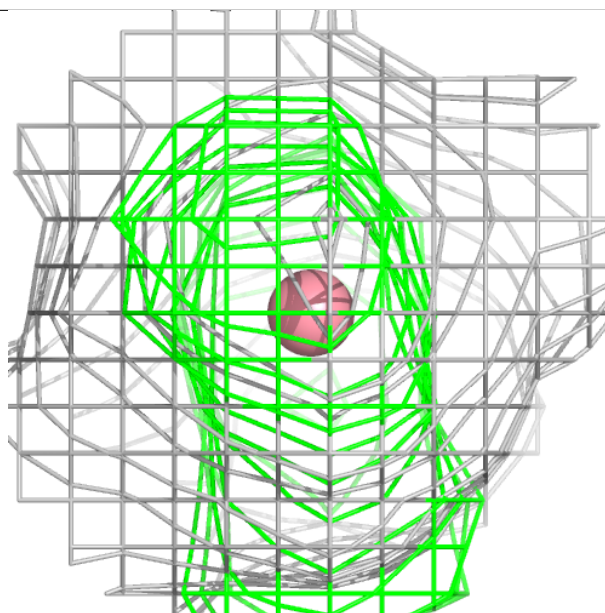
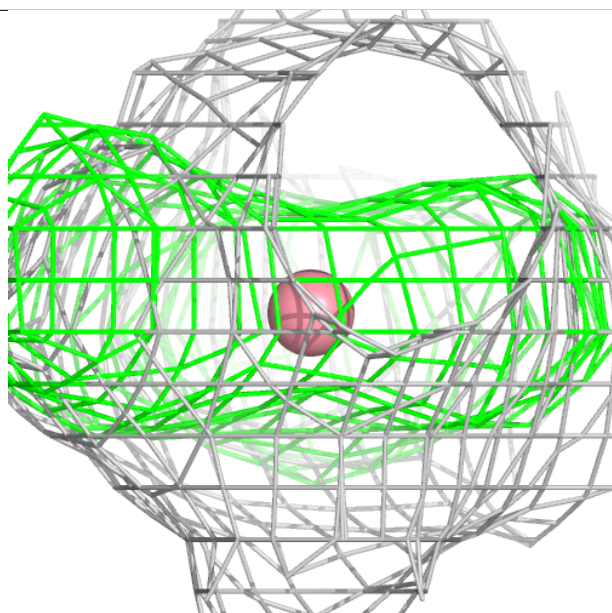
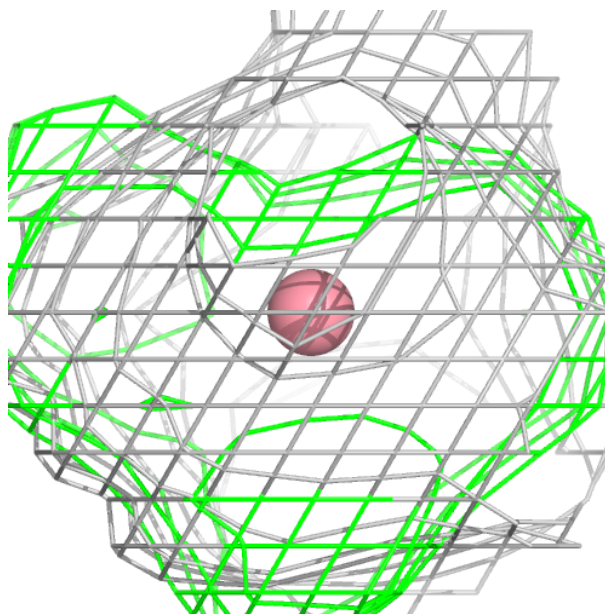
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CO	A	1201	1/1	0.98	0.08	37,37,37,37	0
2	CO	B	1201	1/1	0.98	0.10	45,45,45,45	0

The following is a graphical depiction of the model fit to experimental electron density of all

instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

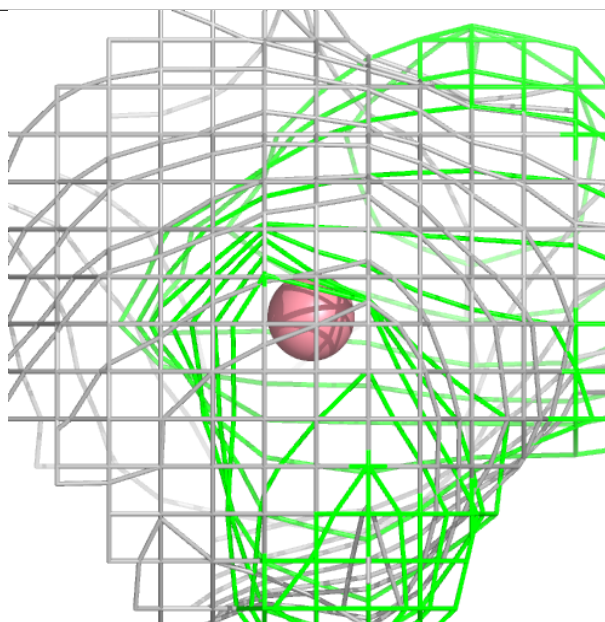
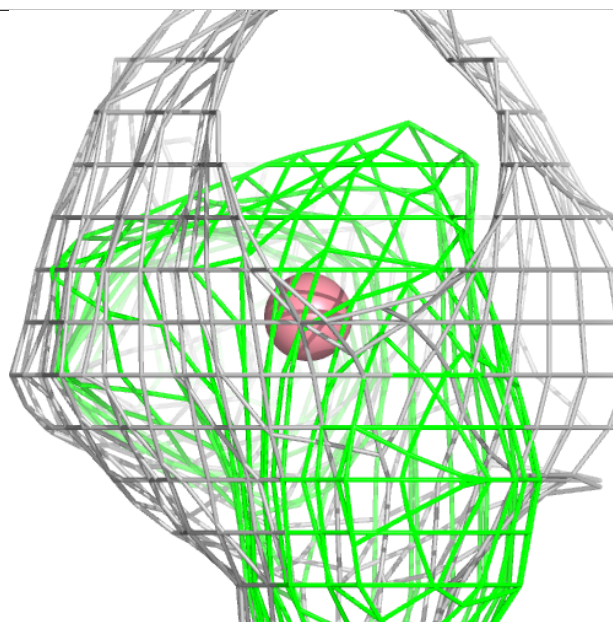
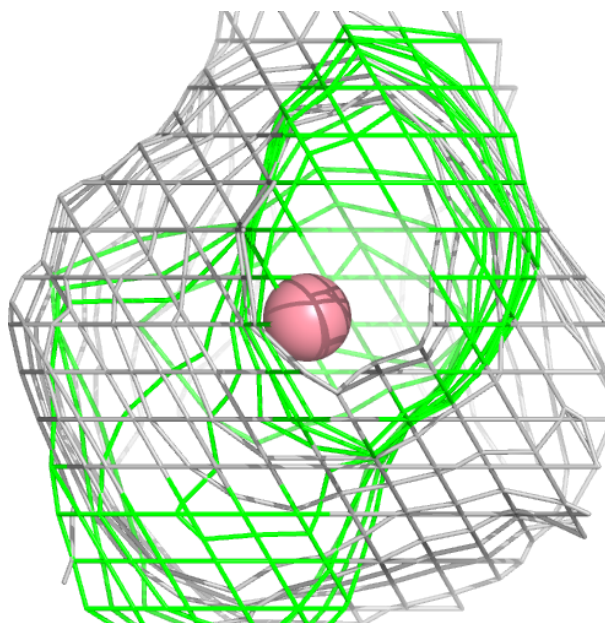
Electron density around CO A 1201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CO B 1201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.