



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 07:48 AM EDT

PDB ID : 1F1X / pdb_00001f1x
Title : CRYSTAL STRUCTURE OF HOMOPROTOCATECHUATE 2,3-DIOXYGENASE FROM BREVIBACTERIUM FUSCUM
Authors : Vetting, M.W.; Lipscomb, J.D.; Wackett, L.P.; Que Jr., L.; Ohlendorf, D.H.
Deposited on : 2000-05-20
Resolution : 1.60 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

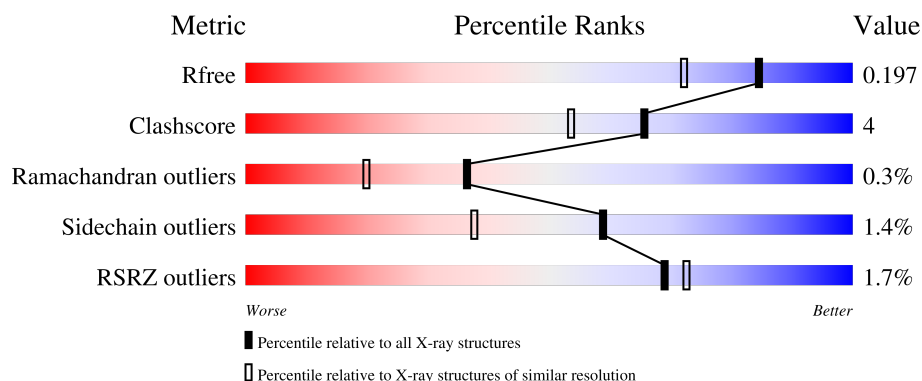
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

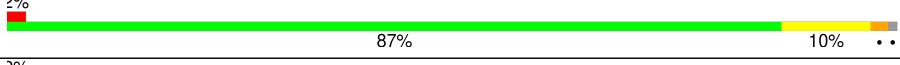
The reported resolution of this entry is 1.60 Å.

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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	322	
1	B	322	
1	C	322	
1	D	322	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11541 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 HOMOPROTOCATECHUATE 2,3-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	1	0
			2608	1651	460	489	8			
1	B	319	Total	C	N	O	S	0	1	0
			2608	1651	460	489	8			
1	C	319	Total	C	N	O	S	0	1	0
			2608	1651	460	489	8			
1	D	319	Total	C	N	O	S	0	1	0
			2608	1651	460	489	8			

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		
2	D	1	Total	Fe	0	0
			1	1		

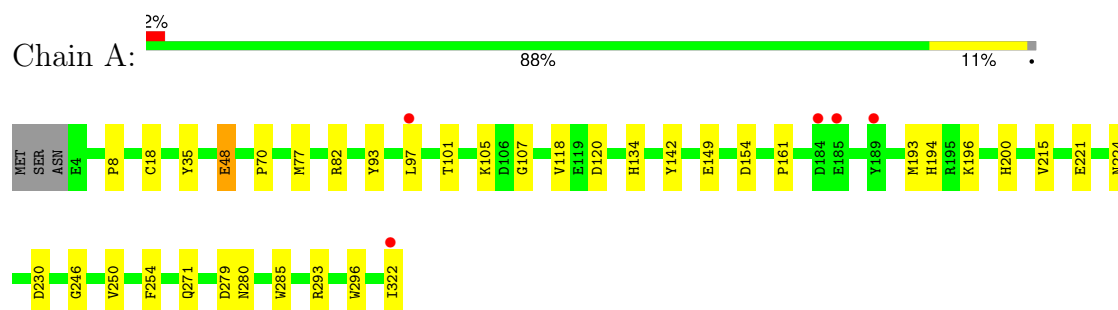
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	276	Total	O	0	0
			276	276		
3	B	278	Total	O	0	0
			278	278		
3	C	270	Total	O	0	0
			270	270		
3	D	281	Total	O	0	0
			281	281		

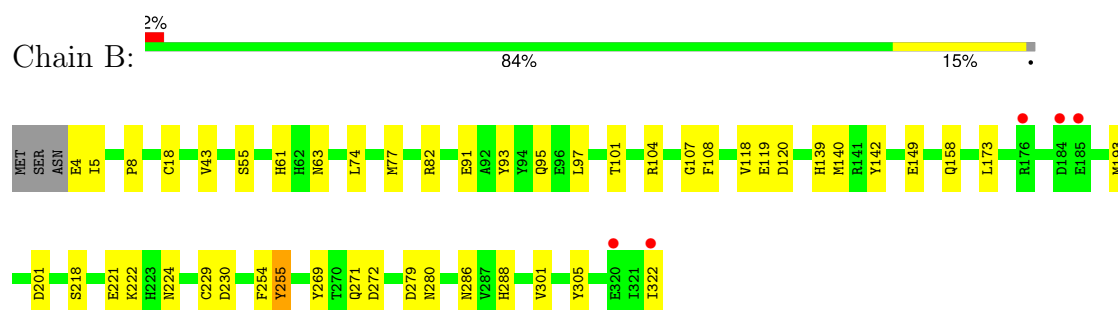
3 Residue-property plots

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.

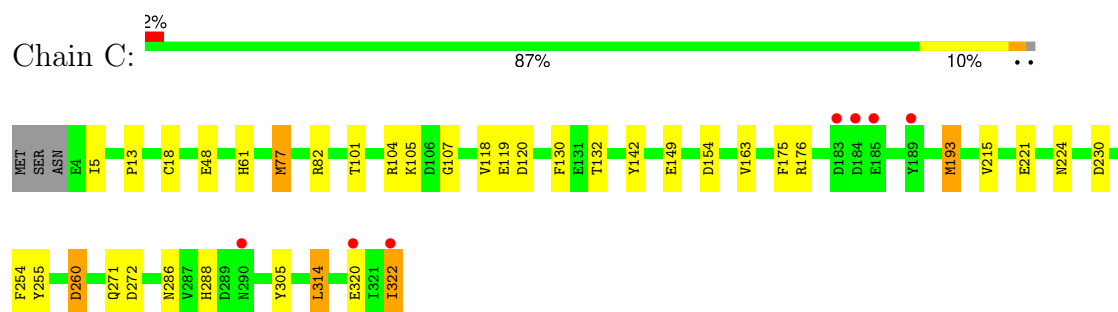
• Molecule 1: HOMOPROTOCATECHUATE 2,3-DIOXYGENASE



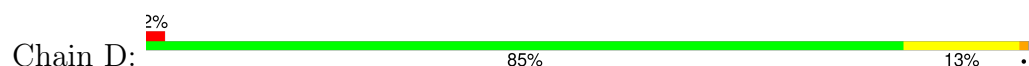
• Molecule 1: HOMOPROTOCATECHUATE 2,3-DIOXYGENASE

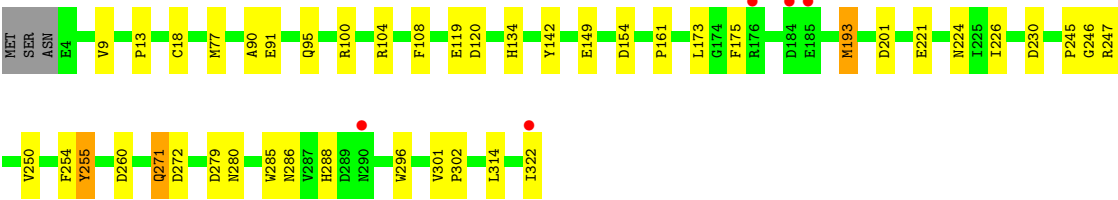


• Molecule 1: HOMOPROTOCATECHUATE 2,3-DIOXYGENASE



• Molecule 1: HOMOPROTOCATECHUATE 2,3-DIOXYGENASE





4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	157.10Å 157.10Å 121.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.60 30.00 – 1.60	Depositor EDS
% Data completeness (in resolution range)	94.1 (30.00-1.60) 94.1 (30.00-1.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.74 (at 1.50Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.168 , 0.195 0.170 , 0.197	Depositor DCC
R_{free} test set	21491 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11541	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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: FE

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	1.26	3/2679 (0.1%)	1.25	10/3642 (0.3%)
1	B	1.18	3/2679 (0.1%)	1.22	16/3642 (0.4%)
1	C	1.35	5/2679 (0.2%)	1.25	9/3642 (0.2%)
1	D	1.20	4/2679 (0.1%)	1.23	11/3642 (0.3%)
All	All	1.25	15/10716 (0.1%)	1.23	46/14568 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
All	All	0	2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	322	ILE	C-OXT	21.81	1.67	1.23
1	C	77	MET	SD-CE	-11.79	1.50	1.79
1	D	193	MET	SD-CE	9.81	2.04	1.79
1	A	77	MET	SD-CE	-9.71	1.55	1.79
1	D	77	MET	SD-CE	-9.10	1.56	1.79
1	B	193	MET	SD-CE	8.46	2.00	1.79
1	B	301	VAL	CA-C	7.17	1.59	1.53
1	D	90	ALA	CA-CB	6.43	1.63	1.53
1	C	193	MET	SD-CE	6.29	1.95	1.79
1	A	193	MET	SD-CE	5.95	1.94	1.79
1	B	140	MET	SD-CE	-5.75	1.65	1.79
1	A	254	PHE	CA-C	5.47	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	301	VAL	CA-C	5.32	1.57	1.53
1	C	163	VAL	CA-CB	5.19	1.60	1.54
1	C	132	THR	CA-CB	5.05	1.62	1.53

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	322	ILE	CA-C-O	10.58	152.75	121.00
1	B	4	GLU	CA-C-N	-9.52	115.74	122.59
1	B	4	GLU	C-N-CA	-9.52	115.74	122.59
1	C	5	ILE	N-CA-C	-7.54	100.15	107.76
1	A	82	ARG	N-CA-C	7.48	120.50	111.82
1	C	107	GLY	N-CA-C	7.03	121.78	112.65
1	D	9	VAL	N-CA-C	-6.99	103.38	111.00
1	A	149	GLU	N-CA-C	6.86	120.33	110.24
1	B	149	GLU	N-CA-C	6.77	120.20	110.24
1	C	149	GLU	N-CA-C	6.76	120.18	110.24
1	B	5	ILE	N-CA-C	-6.75	100.94	107.76
1	B	82	ARG	N-CA-C	6.72	118.69	111.36
1	C	82	ARG	N-CA-C	6.42	119.27	111.82
1	A	70	PRO	N-CA-C	6.41	122.00	113.40
1	B	61	HIS	N-CA-C	6.38	118.23	111.28
1	A	196	LYS	N-CA-C	6.33	121.00	113.16
1	B	254	PHE	N-CA-C	-6.29	98.95	108.96
1	D	149	GLU	N-CA-C	6.28	119.47	110.24
1	C	215	VAL	N-CA-C	-5.99	99.85	108.48
1	B	201	ASP	N-CA-C	-5.95	106.56	113.88
1	C	61	HIS	N-CA-C	5.92	117.73	111.28
1	D	201	ASP	N-CA-C	-5.73	106.83	113.88
1	B	139	HIS	N-CA-C	5.71	119.34	112.38
1	D	255	TYR	N-CA-C	5.67	118.03	109.41
1	A	254	PHE	N-CA-C	-5.62	100.03	108.96
1	B	43	VAL	N-CA-C	5.59	116.81	108.54
1	C	13	PRO	N-CA-C	-5.58	102.51	111.38
1	D	161	PRO	N-CA-C	5.48	120.75	113.57
1	C	254	PHE	N-CA-C	-5.42	100.35	108.96
1	A	194	HIS	N-CA-C	5.39	117.87	109.52
1	B	5	ILE	CA-C-O	5.33	122.29	119.15
1	D	119	GLU	N-CA-C	-5.23	98.03	107.75
1	D	13	PRO	N-CA-C	-5.22	103.08	111.38
1	A	215	VAL	N-CA-C	-5.21	100.82	108.85
1	D	77	MET	N-CA-C	-5.21	99.92	108.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	130	PHE	N-CA-C	-5.20	106.01	112.93
1	B	107	GLY	N-CA-C	5.19	119.22	112.68
1	B	18[A]	CYS	N-CA-C	-5.18	102.20	109.96
1	B	18[B]	CYS	N-CA-C	-5.18	102.20	109.96
1	D	254	PHE	N-CA-C	-5.10	100.84	108.96
1	B	255	TYR	N-CA-C	5.05	117.83	109.85
1	A	200	HIS	N-CA-C	5.04	116.51	108.79
1	B	119	GLU	N-CA-C	-5.04	98.38	107.75
1	A	107	GLY	N-CA-C	5.03	120.66	112.61
1	A	35	TYR	N-CA-C	5.02	117.64	111.82
1	D	302	PRO	N-CA-C	5.00	121.06	113.81

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	305	TYR	Sidechain
1	C	305	TYR	Sidechain

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	2608	0	2489	21	0
1	B	2608	0	2489	23	0
1	C	2608	0	2489	17	0
1	D	2608	0	2489	22	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
3	A	276	0	0	4	0
3	B	278	0	0	0	0
3	C	270	0	0	3	0
3	D	281	0	0	1	0
All	All	11541	0	9956	77	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 4.

All (77) 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:D:193:MET:SD	1:D:193:MET:CE	2.04	1.42
1:C:322:ILE:OXT	1:C:322:ILE:C	1.67	1.35
1:B:8:PRO:HG3	1:B:97:LEU:HD11	1.30	1.09
1:B:74:LEU:HD21	1:B:77:MET:HG3	1.42	1.01
1:B:8:PRO:HG3	1:B:97:LEU:CD1	1.93	0.99
1:B:91:GLU:O	1:B:95:GLN:HG2	1.64	0.96
1:A:48:GLU:H	1:A:48:GLU:CD	1.70	0.94
1:C:48:GLU:CD	1:C:48:GLU:H	1.81	0.87
1:A:8:PRO:CG	1:A:97:LEU:HD11	2.05	0.86
1:A:8:PRO:HG3	1:A:97:LEU:HD11	1.57	0.84
1:A:161:PRO:HG3	1:A:322:ILE:OXT	1.80	0.81
1:A:93:TYR:O	1:A:97:LEU:HD13	1.83	0.78
1:B:8:PRO:CG	1:B:97:LEU:HD11	2.14	0.74
1:A:8:PRO:HG3	1:A:97:LEU:CD1	2.17	0.74
1:A:105:LYS:HG2	3:A:1467:HOH:O	1.87	0.73
1:C:105:LYS:HG2	3:C:1460:HOH:O	1.90	0.70
1:A:8:PRO:HG2	1:A:97:LEU:HD11	1.79	0.64
1:A:48:GLU:CD	1:A:48:GLU:N	2.49	0.62
1:D:193:MET:CE	1:D:193:MET:CG	2.78	0.61
1:A:221:GLU:H	1:A:224:ASN:HD22	1.46	0.61
1:B:74:LEU:HD21	1:B:77:MET:CG	2.26	0.60
1:B:221:GLU:H	1:B:224:ASN:HD22	1.50	0.59
1:D:286:ASN:ND2	1:D:288:HIS:H	2.01	0.58
1:C:286:ASN:ND2	1:C:288:HIS:H	2.01	0.57
1:D:91:GLU:O	1:D:95:GLN:HG3	2.04	0.57
1:B:322:ILE:HG22	1:B:322:ILE:O	2.06	0.56
1:B:104:ARG:HD2	1:B:108:PHE:CE2	2.41	0.55
1:C:48:GLU:CD	1:C:48:GLU:N	2.59	0.55
1:D:286:ASN:HD22	1:D:288:HIS:H	1.55	0.55
1:C:101:THR:HG22	1:C:118:VAL:HG12	1.88	0.54
1:B:101:THR:HG22	1:B:118:VAL:HG12	1.90	0.53
1:B:222:LYS:HD2	1:D:226:ILE:HD13	1.91	0.53
1:B:55:SER:H	1:B:63:ASN:HD22	1.56	0.53
1:C:221:GLU:H	1:C:224:ASN:HD22	1.56	0.52
1:B:93:TYR:O	1:B:97:LEU:HD13	2.11	0.51
1:D:91:GLU:O	1:D:95:GLN:CG	2.59	0.51
1:B:230:ASP:HB3	1:C:142:TYR:CG	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:HIS:HD2	3:A:1396:HOH:O	1.94	0.50
1:A:142:TYR:CG	1:D:230:ASP:HB3	2.47	0.50
1:B:286:ASN:ND2	1:B:288:HIS:H	2.09	0.50
1:A:230:ASP:HB3	1:D:142:TYR:CG	2.48	0.49
1:A:250:VAL:HG22	1:A:285:TRP:CD1	2.48	0.49
1:A:293:ARG:NH2	3:A:1237:HOH:O	2.46	0.49
1:C:322:ILE:OXT	1:C:322:ILE:O	0.49	0.49
1:D:250:VAL:HG22	1:D:285:TRP:CD1	2.48	0.48
1:B:142:TYR:CG	1:C:230:ASP:HB3	2.50	0.47
1:B:104:ARG:HD2	1:B:108:PHE:CD2	2.50	0.47
1:D:221:GLU:H	1:D:224:ASN:HD22	1.61	0.46
1:A:101:THR:HG22	1:A:118:VAL:HG12	1.98	0.46
1:B:8:PRO:HG2	1:B:93:TYR:CE1	2.51	0.45
1:B:229:CYS:HB3	1:D:296:TRP:CD1	2.52	0.45
1:C:119:GLU:HG3	1:C:314:LEU:HD22	1.98	0.45
1:D:100:ARG:HG2	1:D:314:LEU:HD12	1.97	0.45
1:C:18[A]:CYS:SG	1:C:154:ASP:O	2.75	0.45
1:A:105:LYS:HG3	3:A:1501:HOH:O	2.16	0.45
1:A:18[A]:CYS:SG	1:A:154:ASP:O	2.74	0.44
1:B:218:SER:HA	1:B:269:TYR:O	2.18	0.44
1:C:255:TYR:CD1	1:C:255:TYR:C	2.96	0.44
1:A:97:LEU:CD1	1:A:97:LEU:N	2.80	0.44
1:D:134:HIS:HD2	3:D:1213:HOH:O	2.00	0.44
1:D:175:PHE:HB3	1:D:193:MET:HB2	1.99	0.44
1:A:246:GLY:HA2	1:A:296:TRP:CZ3	2.53	0.43
1:C:320:GLU:CB	3:C:1405:HOH:O	2.66	0.43
1:B:279:ASP:O	1:B:280:ASN:C	2.62	0.43
1:D:255:TYR:CD1	1:D:255:TYR:C	2.97	0.43
1:D:245:PRO:HA	1:D:255:TYR:O	2.19	0.42
1:C:175:PHE:HB3	1:C:193:MET:HB2	2.01	0.42
1:B:255:TYR:CD1	1:B:255:TYR:C	2.97	0.42
1:C:104:ARG:NE	3:C:1643:HOH:O	2.36	0.42
1:D:279:ASP:O	1:D:280:ASN:C	2.62	0.42
1:A:279:ASP:O	1:A:280:ASN:C	2.63	0.42
1:D:104:ARG:HG3	1:D:108:PHE:CZ	2.54	0.41
1:D:247:ARG:HH12	1:D:271:GLN:NE2	2.17	0.41
1:D:246:GLY:HA2	1:D:296:TRP:CZ3	2.56	0.40
1:D:18[A]:CYS:SG	1:D:154:ASP:O	2.80	0.40
1:C:260:ASP:OD1	1:C:260:ASP:C	2.64	0.40
1:B:77:MET:HE1	1:B:158:GLN:NE2	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	318/322 (99%)	311 (98%)	6 (2%)	1 (0%)	36	20
1	B	318/322 (99%)	312 (98%)	5 (2%)	1 (0%)	36	20
1	C	318/322 (99%)	313 (98%)	4 (1%)	1 (0%)	36	20
1	D	318/322 (99%)	314 (99%)	3 (1%)	1 (0%)	36	20
All	All	1272/1288 (99%)	1250 (98%)	18 (1%)	4 (0%)	36	20

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	271	GLN
1	B	271	GLN
1	C	271	GLN
1	D	271	GLN

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	278/280 (99%)	276 (99%)	2 (1%)	76	63
1	B	278/280 (99%)	275 (99%)	3 (1%)	65	46
1	C	278/280 (99%)	272 (98%)	6 (2%)	45	22
1	D	278/280 (99%)	274 (99%)	4 (1%)	59	38
All	All	1112/1120 (99%)	1097 (99%)	15 (1%)	59	40

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	GLU
1	A	120	ASP
1	B	120	ASP
1	B	173	LEU
1	B	272	ASP
1	C	77	MET
1	C	120	ASP
1	C	176	ARG
1	C	260	ASP
1	C	272	ASP
1	C	314	LEU
1	D	120	ASP
1	D	173	LEU
1	D	260	ASP
1	D	272	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	95	GLN
1	A	134	HIS
1	A	182	GLN
1	A	224	ASN
1	B	33	ASN
1	B	63	ASN
1	B	134	HIS
1	B	224	ASN
1	B	271	GLN
1	B	286	ASN
1	B	288	HIS
1	C	95	GLN
1	C	224	ASN
1	C	286	ASN
1	C	288	HIS
1	D	33	ASN
1	D	134	HIS
1	D	224	ASN
1	D	271	GLN
1	D	286	ASN

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 4 ligands modelled in this entry, 4 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	319/322 (99%)	-0.21	5 (1%) 70 74	7, 16, 26, 39	1 (0%)
1	B	319/322 (99%)	-0.30	5 (1%) 70 74	7, 16, 28, 40	1 (0%)
1	C	319/322 (99%)	-0.23	7 (2%) 62 66	6, 15, 26, 40	1 (0%)
1	D	319/322 (99%)	-0.28	5 (1%) 70 74	7, 16, 28, 39	1 (0%)
All	All	1276/1288 (99%)	-0.25	22 (1%) 69 72	6, 16, 27, 40	4 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	322	ILE	7.3
1	C	322	ILE	6.6
1	D	322	ILE	5.1
1	C	189	TYR	4.2
1	A	322	ILE	3.8
1	D	184	ASP	3.8
1	C	184	ASP	3.7
1	C	185	GLU	3.3
1	A	184	ASP	3.2
1	A	185	GLU	2.8
1	B	184	ASP	2.7
1	B	320	GLU	2.5
1	B	185	GLU	2.4
1	D	185	GLU	2.4
1	D	290	ASN	2.4
1	C	320	GLU	2.3
1	A	189	TYR	2.2
1	B	176	ARG	2.1
1	D	176	ARG	2.1
1	A	97	LEU	2.1
1	C	290	ASN	2.1
1	C	183	ASP	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($\text{\AA}^2$)	Q<0.9
2	FE	A	323	1/1	0.99	0.17	23,23,23,23	0
2	FE	C	323	1/1	0.99	0.15	22,22,22,22	0
2	FE	D	323	1/1	0.99	0.17	23,23,23,23	0
2	FE	B	323	1/1	1.00	0.13	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.