



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 15, 2026 – 12:16 AM JST

PDB ID : 8YXS / pdb_00008yxs
Title : X-ray structure of non-heme iron dioxygenase from *Aspergillus brunneoviolaceus*
Authors : Lv, X.; Ma, X.
Deposited on : 2024-04-02
Resolution : 3.62 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	1.8.5 (274361), CSD as541be (2020)
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

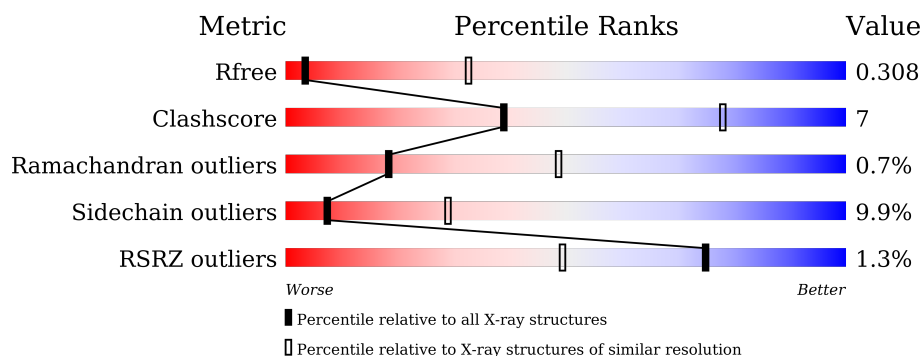
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.62 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	1062 (3.72-3.52)
Clashscore	190562	1092 (3.72-3.52)
Ramachandran outliers	187476	1057 (3.72-3.52)
Sidechain outliers	187428	1055 (3.72-3.52)
RSRZ outliers	180081	1060 (3.72-3.52)

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	456	2% 72% 24% ..
1	B	456	77% 20% ..
1	C	456	71% 24% ..
1	D	456	3% 73% 23% ..
1	E	456	% 77% 19% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17736 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 Oxidoreductase AflY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	0	0
			3546	2250	630	649	17			
1	B	446	Total	C	N	O	S	0	0	0
			3546	2250	630	649	17			
1	C	446	Total	C	N	O	S	0	0	0
			3546	2250	630	649	17			
1	D	446	Total	C	N	O	S	0	0	0
			3546	2250	630	649	17			
1	E	446	Total	C	N	O	S	0	0	0
			3546	2250	630	649	17			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	VAL	ALA	conflict	UNP A0A8G1RKM4
A	251	VAL	LEU	conflict	UNP A0A8G1RKM4
A	441	MET	ASN	engineered mutation	UNP A0A8G1RKM4
B	31	VAL	ALA	conflict	UNP A0A8G1RKM4
B	251	VAL	LEU	conflict	UNP A0A8G1RKM4
B	441	MET	ASN	engineered mutation	UNP A0A8G1RKM4
C	31	VAL	ALA	conflict	UNP A0A8G1RKM4
C	251	VAL	LEU	conflict	UNP A0A8G1RKM4
C	441	MET	ASN	engineered mutation	UNP A0A8G1RKM4
D	31	VAL	ALA	conflict	UNP A0A8G1RKM4
D	251	VAL	LEU	conflict	UNP A0A8G1RKM4
D	441	MET	ASN	engineered mutation	UNP A0A8G1RKM4
E	31	VAL	ALA	conflict	UNP A0A8G1RKM4
E	251	VAL	LEU	conflict	UNP A0A8G1RKM4
E	441	MET	ASN	engineered mutation	UNP A0A8G1RKM4

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

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

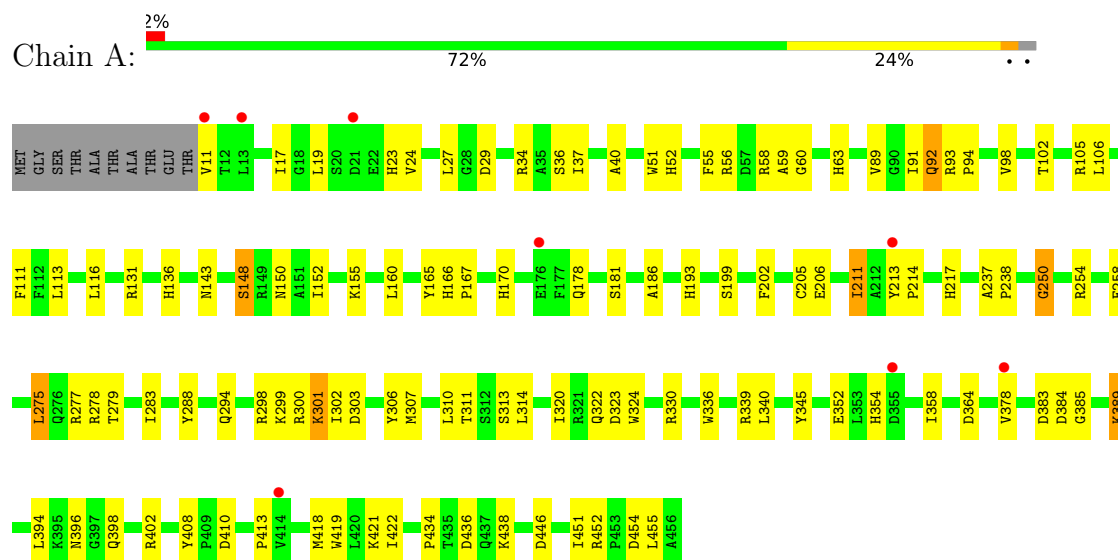
- Molecule 3 is water.

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

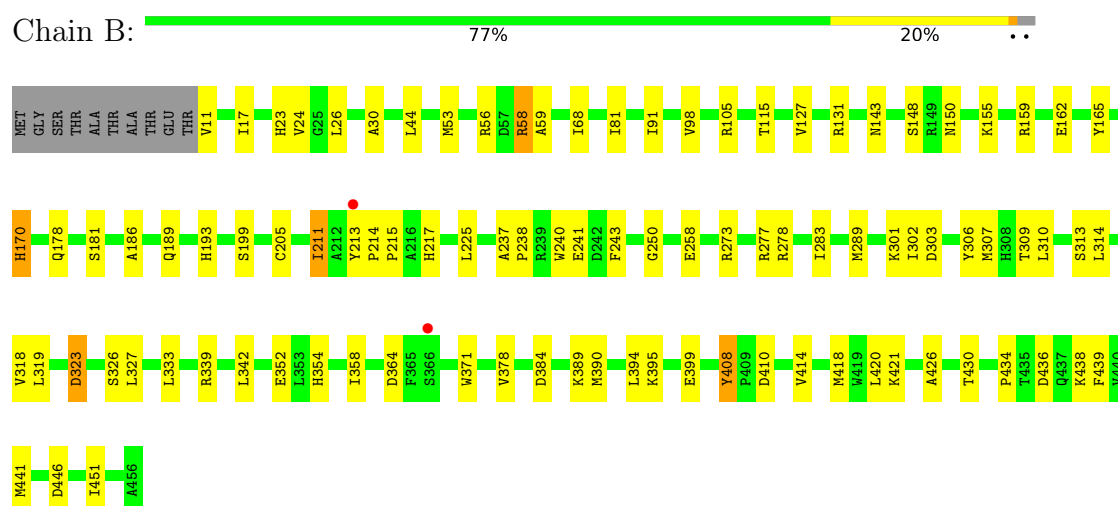
3 Residue-property plots [i](#)

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: Oxidoreductase Afly

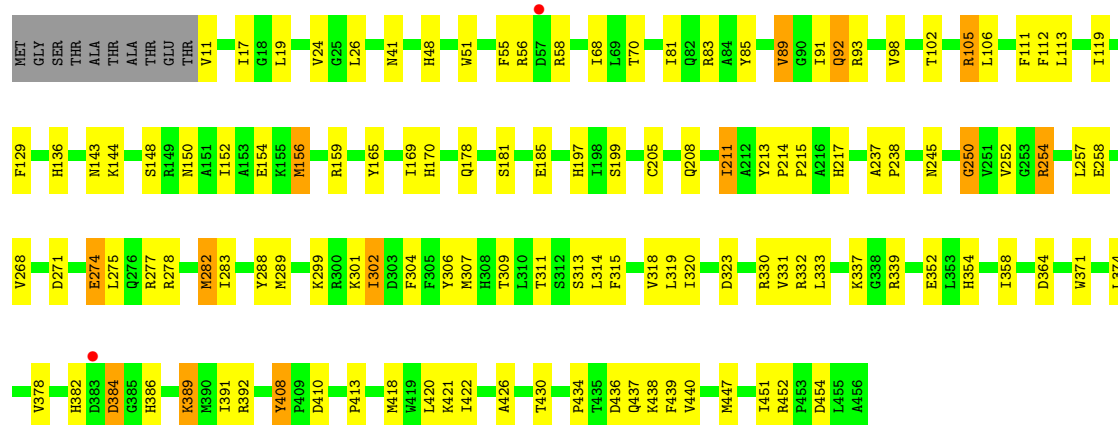


• Molecule 1: Oxidoreductase Afly

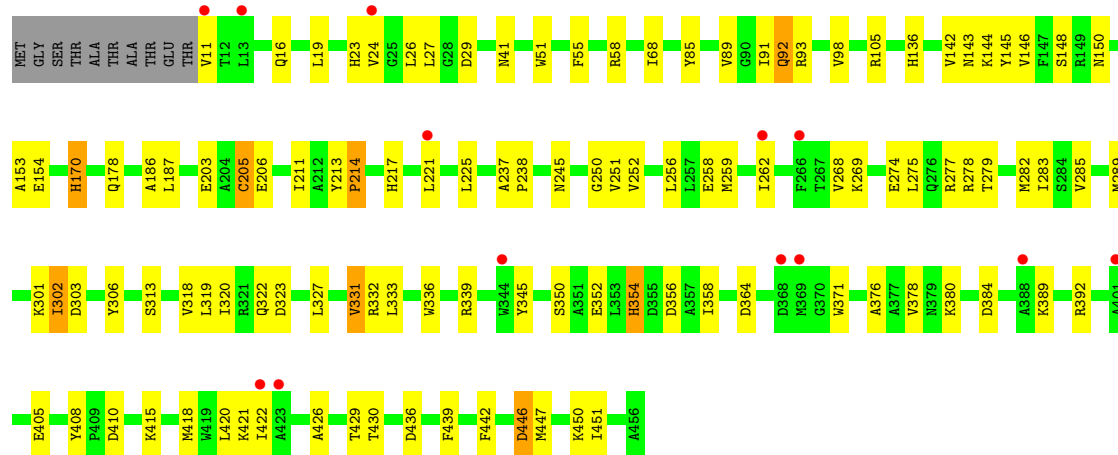
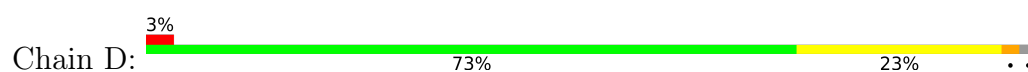


• Molecule 1: Oxidoreductase Afly

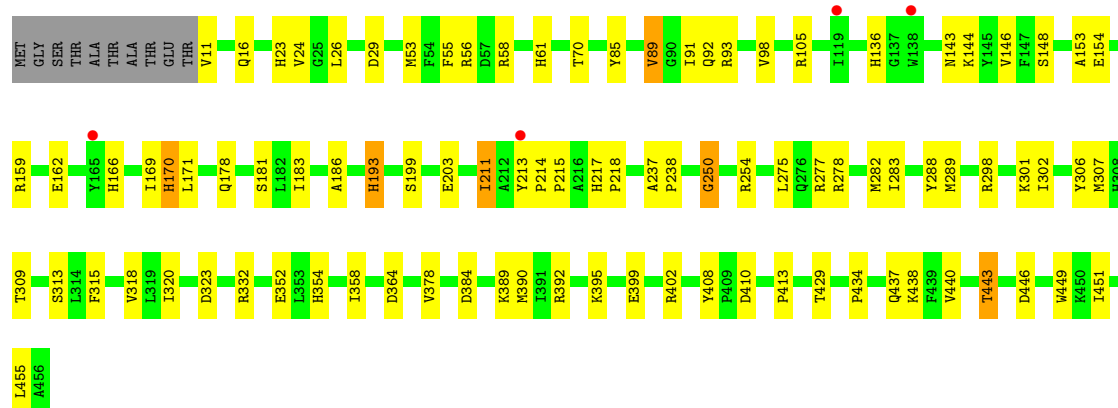
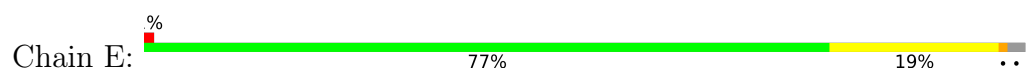




● Molecule 1: Oxidoreductase Afly



● Molecule 1: Oxidoreductase Afly



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	256.99Å 109.74Å 179.89Å 90.00° 93.39° 90.00°	Depositor
Resolution (Å)	71.59 – 3.62 71.59 – 3.62	Depositor EDS
% Data completeness (in resolution range)	99.8 (71.59-3.62) 99.7 (71.59-3.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 3.58Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.276 , 0.312 0.278 , 0.308	Depositor DCC
R_{free} test set	2894 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	99.2	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	17736	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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, KCX

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	0.16	0/3620	0.33	0/4902
1	B	0.15	0/3620	0.31	0/4902
1	C	0.13	0/3620	0.30	0/4902
1	D	0.16	0/3620	0.32	0/4902
1	E	0.14	0/3620	0.31	0/4902
All	All	0.15	0/18100	0.32	0/24510

There are no bond length outliers.

There are no bond angle outliers.

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	3546	0	3451	54	0
1	B	3546	0	3451	43	0
1	C	3546	0	3451	63	0
1	D	3546	0	3451	48	0
1	E	3546	0	3451	37	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
2	E	1	0	0	0	0
3	A	1	0	0	2	0
All	All	17736	0	17255	239	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 7.

The worst 5 of 239 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:C:434:PRO:HD2	1:C:437:GLN:HB2	1.64	0.78
1:D:283:ILE:HG12	1:D:313:SER:HB2	1.68	0.76
1:B:148:SER:HG	1:B:150:ASN:HD22	1.36	0.72
1:D:252:VAL:HG13	1:D:256:LEU:HD13	1.70	0.71
1:A:63:HIS:CE1	3:A:601:HOH:O	2.44	0.70

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	443/456 (97%)	410 (93%)	31 (7%)	2 (0%)	24	55
1	B	443/456 (97%)	417 (94%)	23 (5%)	3 (1%)	18	49
1	C	443/456 (97%)	416 (94%)	24 (5%)	3 (1%)	18	49
1	D	443/456 (97%)	414 (94%)	25 (6%)	4 (1%)	14	44
1	E	443/456 (97%)	417 (94%)	23 (5%)	3 (1%)	18	49
All	All	2215/2280 (97%)	2074 (94%)	126 (6%)	15 (1%)	18	49

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	GLY
1	E	250	GLY
1	A	214	PRO
1	C	214	PRO
1	D	214	PRO

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	359/366 (98%)	324 (90%)	35 (10%)	8	29
1	B	359/366 (98%)	327 (91%)	32 (9%)	9	31
1	C	359/366 (98%)	322 (90%)	37 (10%)	7	28
1	D	359/366 (98%)	321 (89%)	38 (11%)	6	26
1	E	359/366 (98%)	324 (90%)	35 (10%)	8	29
All	All	1795/1830 (98%)	1618 (90%)	177 (10%)	7	29

5 of 177 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	136	HIS
1	E	16	GLN
1	D	203	GLU
1	D	352	GLU
1	E	92	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	193	HIS
1	E	139	GLN
1	D	14	ASN
1	E	437	GLN
1	E	14	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

5 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	KCX	D	389	1	9,11,12	0.95	0	5,12,14	1.49	1 (20%)
1	KCX	C	389	2,1	9,11,12	0.94	0	5,12,14	1.51	1 (20%)
1	KCX	E	389	2,1	9,11,12	1.13	1 (11%)	5,12,14	1.82	2 (40%)
1	KCX	B	389	2,1	9,11,12	1.20	1 (11%)	5,12,14	1.72	2 (40%)
1	KCX	A	389	2,1	9,11,12	0.92	0	5,12,14	1.43	1 (20%)

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	KCX	D	389	1	-	2/9/10/12	-
1	KCX	C	389	2,1	-	3/9/10/12	-
1	KCX	E	389	2,1	-	3/9/10/12	-
1	KCX	B	389	2,1	-	3/9/10/12	-
1	KCX	A	389	2,1	-	3/9/10/12	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	389	KCX	OQ1-CX	2.56	1.26	1.21
1	E	389	KCX	OQ1-CX	2.37	1.26	1.21

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	389	KCX	OQ1-CX-NZ	-3.33	119.79	124.96
1	C	389	KCX	OQ1-CX-NZ	-2.91	120.45	124.96
1	B	389	KCX	OQ1-CX-NZ	-2.86	120.53	124.96
1	D	389	KCX	OQ1-CX-NZ	-2.70	120.77	124.96
1	A	389	KCX	OQ1-CX-NZ	-2.56	120.99	124.96

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	389	KCX	O-C-CA-CB
1	E	389	KCX	CE-CD-CG-CB
1	E	389	KCX	CG-CD-CE-NZ
1	A	389	KCX	CE-CD-CG-CB
1	B	389	KCX	CE-CD-CG-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	389	KCX	1	0
1	A	389	KCX	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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	445/456 (97%)	0.07	8 (1%) 67 42	56, 88, 118, 149	0
1	B	445/456 (97%)	0.04	2 (0%) 88 71	58, 95, 130, 150	0
1	C	445/456 (97%)	-0.02	2 (0%) 88 71	58, 93, 131, 152	0
1	D	445/456 (97%)	0.38	13 (2%) 53 32	79, 109, 135, 154	0
1	E	445/456 (97%)	0.07	4 (0%) 81 58	79, 104, 134, 156	0
All	All	2225/2280 (97%)	0.11	29 (1%) 75 49	56, 99, 132, 156	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	213	TYR	6.1
1	D	262	ILE	3.3
1	A	11	VAL	3.2
1	D	368	ASP	3.1
1	D	422	ILE	3.0

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

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
1	KCX	B	389	12/13	0.93	0.23	78,90,105,115	0
1	KCX	A	389	12/13	0.95	0.12	63,76,81,82	0
1	KCX	D	389	12/13	0.95	0.17	97,106,113,114	0
1	KCX	E	389	12/13	0.96	0.11	87,95,103,110	0
1	KCX	C	389	12/13	0.98	0.10	66,71,78,79	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	FE	B	501	1/1	0.95	0.11	126,126,126,126	0
2	FE	D	501	1/1	0.95	0.07	83,83,83,83	0
2	FE	C	501	1/1	0.96	0.06	76,76,76,76	0
2	FE	E	501	1/1	0.98	0.09	117,117,117,117	0
2	FE	A	501	1/1	1.00	0.02	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.