



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:59 PM UTC

PDB ID : 1Z03 / pdb_00001z03
Title : 2-Oxoquinoline 8-Monooxygenase Component: Active site Modulation by
Rieske-[2Fe-2S] Center Oxidation/Reduction
Authors : Martins, B.M.; Svetlitchnaia, T.; Dobbek, H.
Deposited on : 2005-03-01
Resolution : 1.80 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

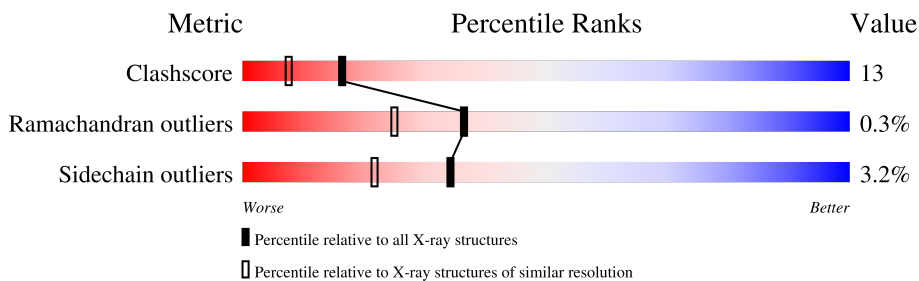
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	446	71% 21% . .
1	B	446	72% 22% . .
1	C	446	72% 22% . .
1	D	446	71% 23% . .
1	E	446	72% 21% . .
1	F	446	72% 21% . .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24453 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 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	0	0
			3454	2211	592	635	16			
1	B	427	Total	C	N	O	S	0	0	0
			3454	2211	592	635	16			
1	C	427	Total	C	N	O	S	0	0	0
			3454	2211	592	635	16			
1	D	427	Total	C	N	O	S	0	0	0
			3454	2211	592	635	16			
1	E	427	Total	C	N	O	S	0	0	0
			3454	2211	592	635	16			
1	F	427	Total	C	N	O	S	0	0	0
			3454	2211	592	635	16			

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

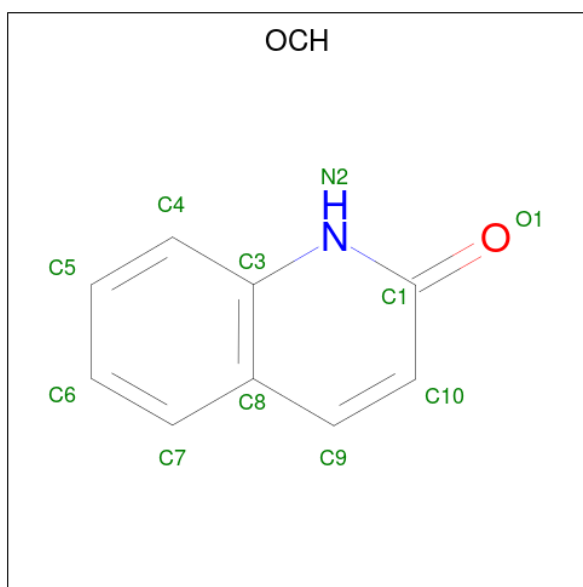
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		
2	D	1	Total	Fe	0	0
			1	1		
2	E	1	Total	Fe	0	0
			1	1		
2	F	1	Total	Fe	0	0
			1	1		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	C	1	Total	Fe	S	0	0
			4	2	2		
3	D	1	Total	Fe	S	0	0
			4	2	2		
3	E	1	Total	Fe	S	0	0
			4	2	2		
3	F	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 4 is QUINOLIN-2(1H)-ONE (CCD ID: OCH) (formula: C₉H₇NO).

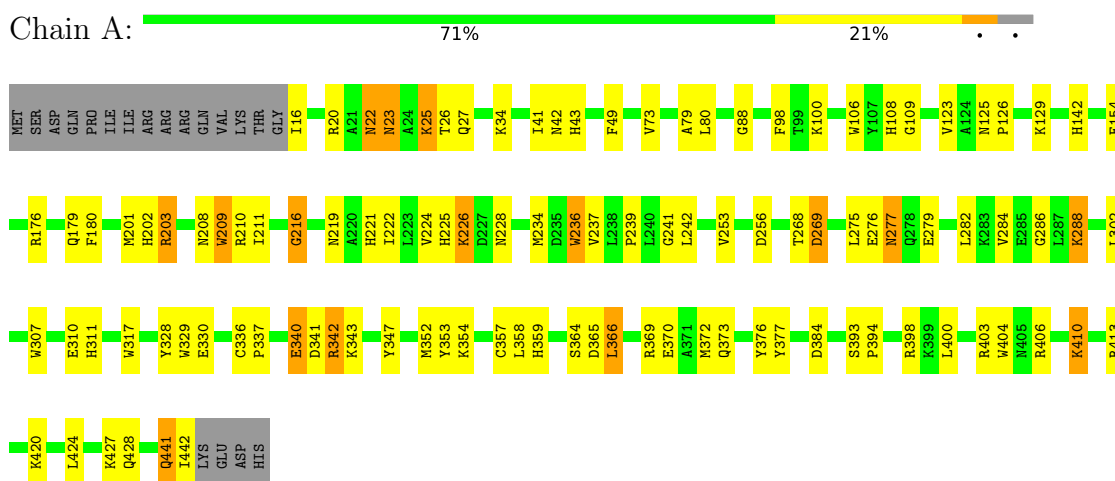


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	9	1	1		
4	B	1	Total	C	N	O	0	0
			11	9	1	1		
4	C	1	Total	C	N	O	0	0
			11	9	1	1		
4	D	1	Total	C	N	O	0	0
			11	9	1	1		
4	E	1	Total	C	N	O	0	0
			11	9	1	1		
4	F	1	Total	C	N	O	0	0
			11	9	1	1		

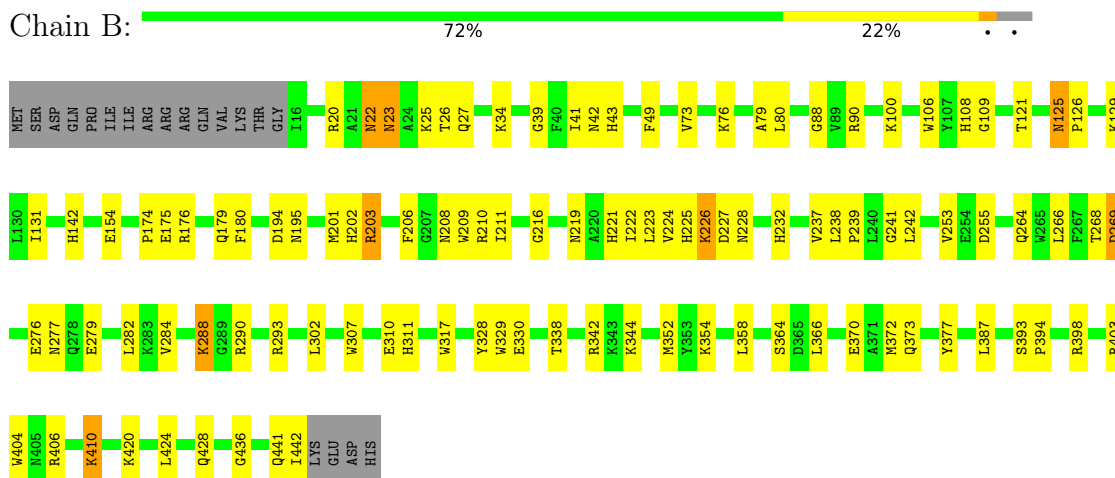
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	632	Total	O	0	0
			632	632		
5	B	611	Total	O	0	0
			611	611		
5	C	590	Total	O	0	0
			590	590		
5	D	638	Total	O	0	0
			638	638		
5	E	562	Total	O	0	0
			562	562		
5	F	600	Total	O	0	0
			600	600		

- Molecule 1: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component

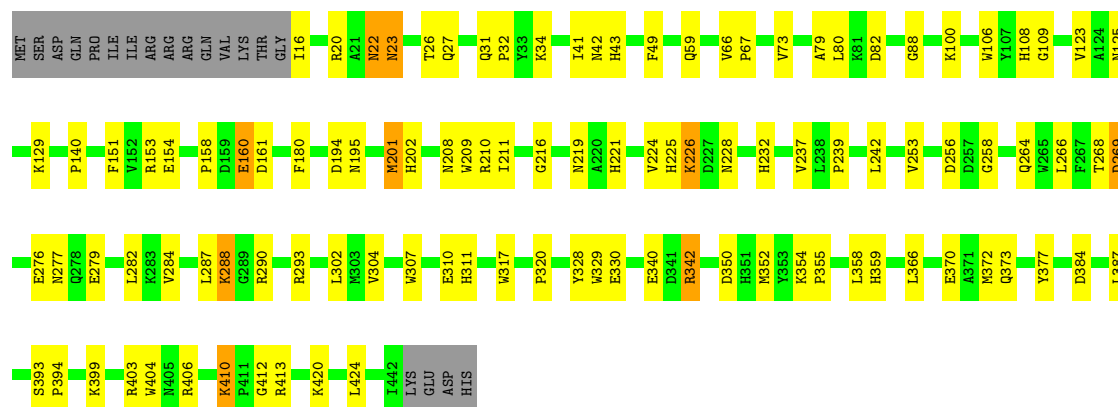


- Molecule 1: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component



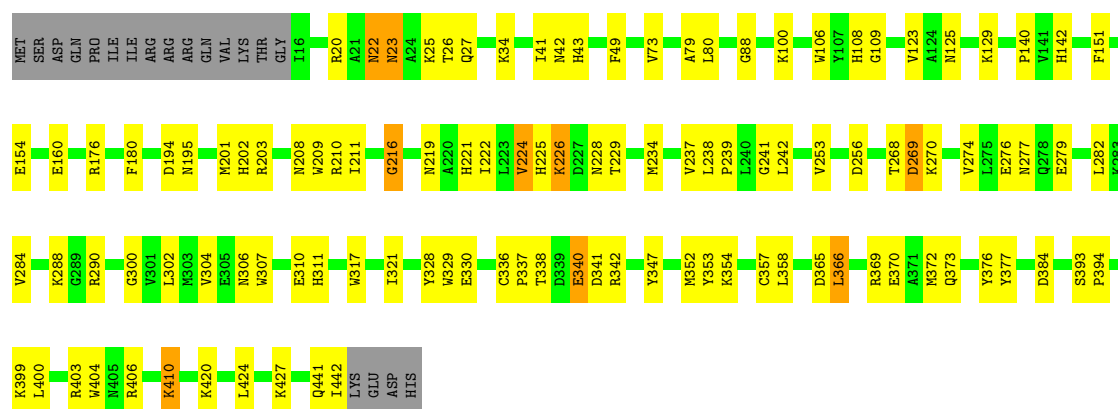
- Molecule 1: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component





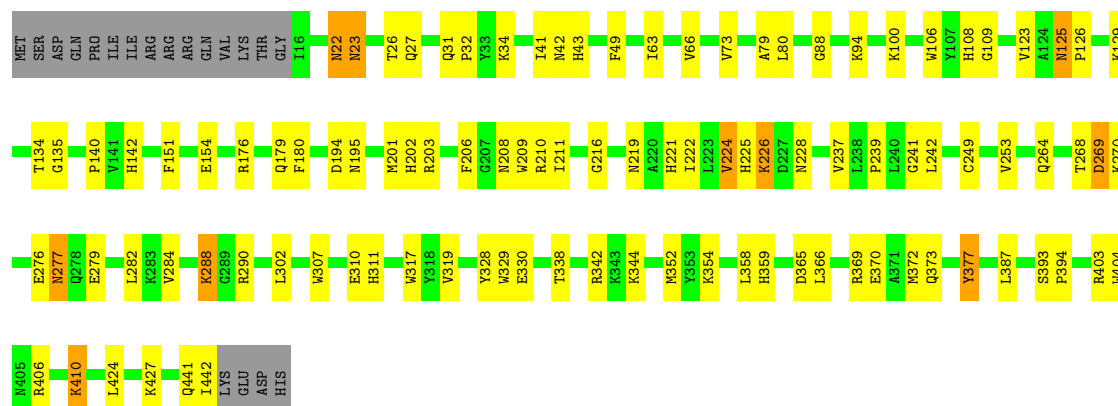
- Molecule 1: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component

Chain D: 71% 23%



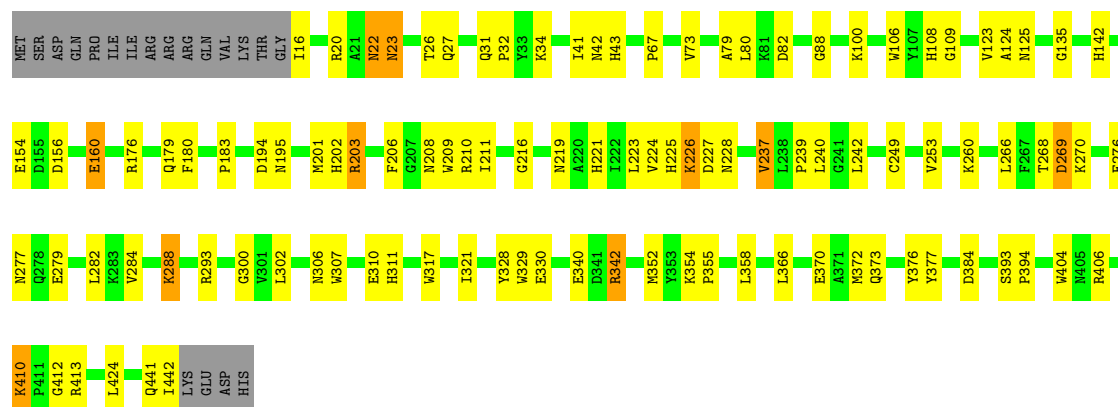
- Molecule 1: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component

Chain E: 72% 21%



- Molecule 1: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component

Chain F: 72% 21%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.53Å 166.94Å 173.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80	Depositor
% Data completeness (in resolution range)	98.2 (20.00-1.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.200 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	24453	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

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: FES, FE, OCH

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	0.40	0/3560	0.92	17/4853 (0.4%)
1	B	0.39	0/3560	0.91	12/4853 (0.2%)
1	C	0.41	1/3560 (0.0%)	0.89	13/4853 (0.3%)
1	D	0.40	0/3560	0.93	16/4853 (0.3%)
1	E	0.39	0/3560	0.91	11/4853 (0.2%)
1	F	0.40	0/3560	0.92	12/4853 (0.2%)
All	All	0.40	1/21360 (0.0%)	0.91	81/29118 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	201	MET	SD-CE	-7.18	1.61	1.79

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	321	ILE	N-CA-C	-9.52	102.53	111.48
1	F	321	ILE	N-CA-C	-9.28	102.76	111.48
1	F	88	GLY	N-CA-C	8.01	127.24	114.90
1	F	404	TRP	N-CA-C	7.59	122.73	113.17
1	A	216	GLY	N-CA-C	7.39	121.85	112.83

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	3454	0	3307	96	0
1	B	3454	0	3307	92	0
1	C	3454	0	3307	84	0
1	D	3454	0	3307	97	0
1	E	3454	0	3307	83	0
1	F	3454	0	3307	89	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
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	4	0	0	1	0
3	B	4	0	0	1	0
3	C	4	0	0	1	0
3	D	4	0	0	1	0
3	E	4	0	0	1	0
3	F	4	0	0	1	0
4	A	11	0	7	2	0
4	B	11	0	7	2	0
4	C	11	0	7	3	0
4	D	11	0	7	3	0
4	E	11	0	7	2	0
4	F	11	0	7	2	0
5	A	632	0	0	19	0
5	B	611	0	0	20	0
5	C	590	0	0	15	0
5	D	638	0	0	24	0
5	E	562	0	0	13	0
5	F	600	0	0	13	0
All	All	24453	0	19884	528	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 13.

The worst 5 of 528 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:F:225:HIS:HD1	1:F:228:ASN:HD21	1.02	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:225:HIS:HD1	1:E:228:ASN:HD21	1.07	0.99
1:C:232:HIS:HB2	5:C:5184:HOH:O	1.66	0.95
1:A:22:ASN:HD22	1:A:22:ASN:H	1.14	0.95
1:A:225:HIS:HD1	1:A:228:ASN:HD21	1.06	0.95

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	425/446 (95%)	402 (95%)	21 (5%)	2 (0%)	24	14
1	B	425/446 (95%)	403 (95%)	22 (5%)	0	100	100
1	C	425/446 (95%)	399 (94%)	25 (6%)	1 (0%)	43	31
1	D	425/446 (95%)	404 (95%)	19 (4%)	2 (0%)	24	14
1	E	425/446 (95%)	402 (95%)	22 (5%)	1 (0%)	43	31
1	F	425/446 (95%)	403 (95%)	20 (5%)	2 (0%)	24	14
All	All	2550/2676 (95%)	2413 (95%)	129 (5%)	8 (0%)	36	25

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	236	TRP
1	D	123	VAL
1	A	123	VAL
1	E	123	VAL
1	F	123	VAL

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	373/392 (95%)	360 (96%)	13 (4%)	32	19
1	B	373/392 (95%)	362 (97%)	11 (3%)	37	25
1	C	373/392 (95%)	361 (97%)	12 (3%)	34	22
1	D	373/392 (95%)	361 (97%)	12 (3%)	34	22
1	E	373/392 (95%)	362 (97%)	11 (3%)	37	25
1	F	373/392 (95%)	360 (96%)	13 (4%)	32	19
All	All	2238/2352 (95%)	2166 (97%)	72 (3%)	34	22

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	366	LEU
1	F	410	LYS
1	F	22	ASN
1	F	269	ASP
1	C	22	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	311	HIS
1	F	179	GLN
1	D	208	ASN
1	F	167	HIS
1	F	311	HIS

5.3.3 RNA ⓘ

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 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 for Mogul analysis.

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$
4	OCH	B	4601	-	12,12,12	2.75	5 (41%)	16,16,16	0.86	1 (6%)
4	OCH	E	4604	-	12,12,12	2.82	6 (50%)	16,16,16	0.75	1 (6%)
3	FES	C	500	1	0,4,4	-	-	-		
4	OCH	D	4603	-	12,12,12	3.05	6 (50%)	16,16,16	0.80	1 (6%)
3	FES	F	500	1	0,4,4	-	-	-		
4	OCH	A	4600	-	12,12,12	3.11	6 (50%)	16,16,16	0.81	1 (6%)
3	FES	D	500	1	0,4,4	-	-	-		
4	OCH	C	4602	-	12,12,12	2.90	6 (50%)	16,16,16	0.71	0
3	FES	B	500	1	0,4,4	-	-	-		
3	FES	A	500	1	0,4,4	-	-	-		
3	FES	E	500	1	0,4,4	-	-	-		
4	OCH	F	4605	-	12,12,12	3.07	6 (50%)	16,16,16	0.82	1 (6%)

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
4	OCH	B	4601	-	-	-	0/2/2/2
4	OCH	E	4604	-	-	-	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FES	C	500	1	-	-	0/1/1/1
4	OCH	D	4603	-	-	-	0/2/2/2
3	FES	F	500	1	-	-	0/1/1/1
4	OCH	A	4600	-	-	-	0/2/2/2
3	FES	D	500	1	-	-	0/1/1/1
4	OCH	C	4602	-	-	-	0/2/2/2
3	FES	B	500	1	-	-	0/1/1/1
3	FES	A	500	1	-	-	0/1/1/1
3	FES	E	500	1	-	-	0/1/1/1
4	OCH	F	4605	-	-	-	0/2/2/2

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	4605	OCH	C1-N2	7.33	1.46	1.37
4	A	4600	OCH	C1-N2	7.06	1.46	1.37
4	D	4603	OCH	C1-N2	6.88	1.45	1.37
4	C	4602	OCH	C1-N2	6.80	1.45	1.37
4	E	4604	OCH	C1-N2	6.61	1.45	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	4601	OCH	C10-C1-N2	-2.85	114.26	115.84
4	A	4600	OCH	C10-C1-N2	-2.21	114.62	115.84
4	E	4604	OCH	C10-C1-N2	-2.15	114.65	115.84
4	F	4605	OCH	C10-C1-N2	-2.15	114.66	115.84
4	D	4603	OCH	C10-C1-N2	-2.01	114.73	115.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	4601	OCH	2	0
4	E	4604	OCH	2	0
3	C	500	FES	1	0
4	D	4603	OCH	3	0
3	F	500	FES	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	4600	OCH	2	0
3	D	500	FES	1	0
4	C	4602	OCH	3	0
3	B	500	FES	1	0
3	A	500	FES	1	0
3	E	500	FES	1	0
4	F	4605	OCH	2	0

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.