



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 26, 2020 – 12:08 PM BST

PDB ID : 5MHN
Title : FXIIIa in complex with the inhibitor ZED2360
Authors : Stieler, M.; Heine, A.; Klebe, G.
Deposited on : 2016-11-24
Resolution : 2.48 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13

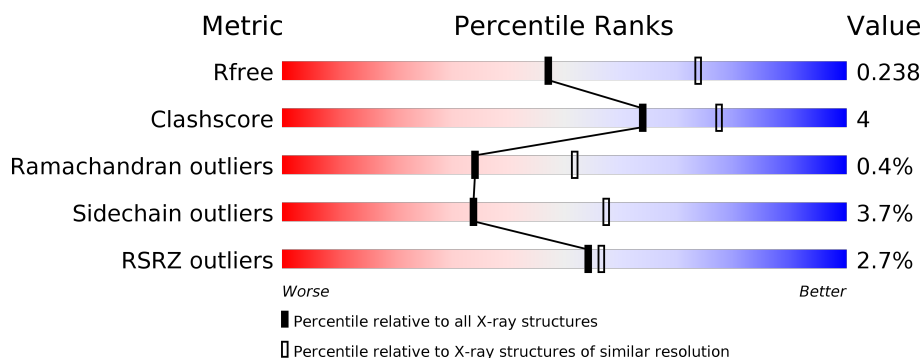
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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}	130704	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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 on 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	738	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>12%</div> <div>7%</div> </div> </div>
1	B	738	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>7%</div> </div> </div>
2	H	8	<div> <div></div> <div> <div>63%</div> <div>25%</div> <div>13%</div> </div> </div>
2	I	8	<div> <div>13%</div> <div> <div></div> <div>75%</div> <div>25%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10991 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 Coagulation factor XIII A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	688	Total	C	N	O	S	0	0	0
			5283	3383	876	999	25			
1	B	685	Total	C	N	O	S	0	0	0
			5326	3410	891	1000	25			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP P00488
A	-5	HIS	-	expression tag	UNP P00488
A	-4	HIS	-	expression tag	UNP P00488
A	-3	HIS	-	expression tag	UNP P00488
A	-2	HIS	-	expression tag	UNP P00488
A	-1	HIS	-	expression tag	UNP P00488
A	0	HIS	-	expression tag	UNP P00488
A	649	ILE	THR	engineered mutation	UNP P00488
A	651	GLU	GLN	engineered mutation	UNP P00488
B	-6	MET	-	initiating methionine	UNP P00488
B	-5	HIS	-	expression tag	UNP P00488
B	-4	HIS	-	expression tag	UNP P00488
B	-3	HIS	-	expression tag	UNP P00488
B	-2	HIS	-	expression tag	UNP P00488
B	-1	HIS	-	expression tag	UNP P00488
B	0	HIS	-	expression tag	UNP P00488
B	649	ILE	THR	engineered mutation	UNP P00488
B	651	GLU	GLN	engineered mutation	UNP P00488

- Molecule 2 is a protein called inhibitor ZED2360.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	8	Total	C	N	O	S	0	0	0
			75	54	9	11	1			

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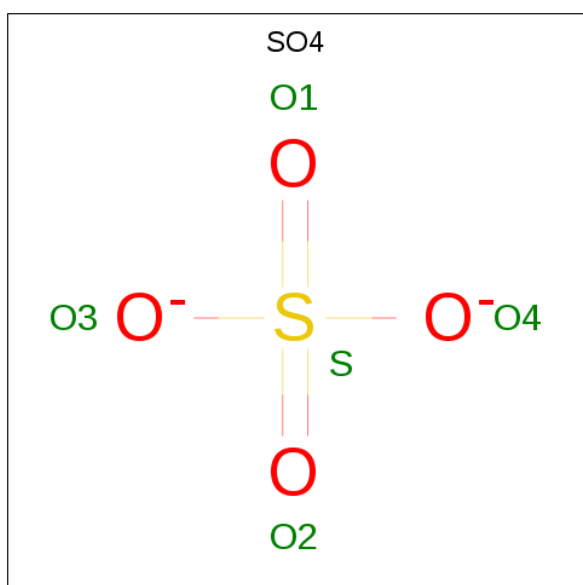
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	8	Total	C	N	O	S	0	0	0
			65	44	9	11	1			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Ca	0	0
			3	3		
3	A	3	Total	Ca	0	0
			3	3		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

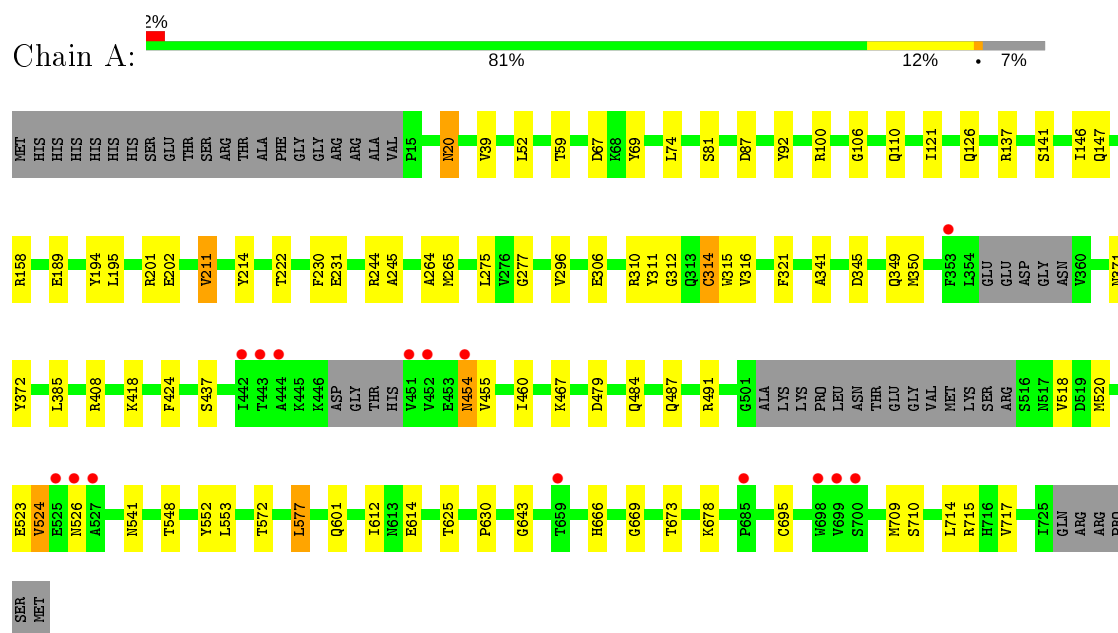
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	95	Total	O	0	0
			95	95		
6	B	98	Total	O	0	0
			98	98		

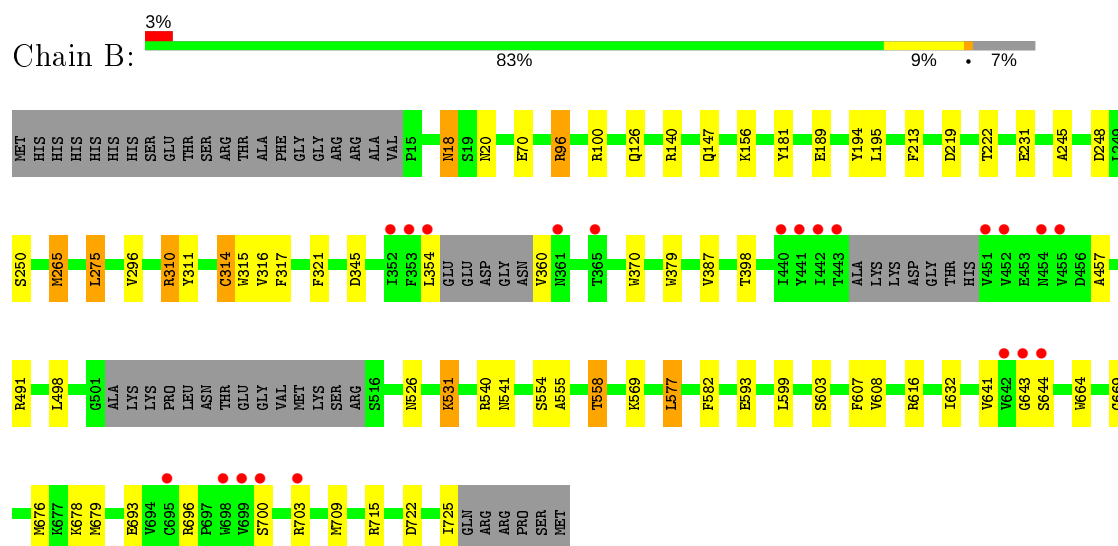
3 Residue-property plots [i](#)

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: Coagulation factor XIII A chain



• Molecule 1: Coagulation factor XIII A chain




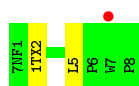
• Molecule 2: inhibitor ZED2360

Chain H:  63% 25% 13%



● Molecule 2: inhibitor ZED2360

Chain I:  13% 75% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	56.61Å 80.51Å 103.11Å 87.98° 77.01° 82.26°	Depositor
Resolution (Å)	48.12 – 2.48 48.12 – 2.48	Depositor EDS
% Data completeness (in resolution range)	97.4 (48.12-2.48) 97.5 (48.12-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.48Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.180 , 0.238 0.180 , 0.238	Depositor DCC
R_{free} test set	3045 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	39.8	Xtriage
Anisotropy	0.777	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10991	wwPDB-VP
Average B, all atoms (Å ²)	54.0	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 38.16 % 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 3.8462e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: GOL, CA, 7NF, SO4, 1TX

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	0.42	1/5411 (0.0%)	0.59	0/7383
1	B	0.43	1/5455 (0.0%)	0.59	0/7432
2	H	0.28	0/54	0.54	0/76
2	I	0.29	0/45	0.42	0/63
All	All	0.42	2/10965 (0.0%)	0.59	0/14954

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	314	CYS	CB-SG	-6.43	1.71	1.82
1	A	314	CYS	CB-SG	-5.46	1.73	1.81

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	5283	0	4904	50	0
1	B	5326	0	5017	37	0
2	H	75	0	67	4	0
2	I	65	0	42	4	0
3	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	0	0	0
4	A	10	0	0	0	0
4	B	15	0	0	0	0
5	A	12	0	16	2	0
5	B	6	0	8	0	0
6	A	95	0	0	5	0
6	B	98	0	0	0	0
All	All	10991	0	10054	87	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 (87) 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:398:THR:HG21	2:I:2:1TX:H11	1.69	0.75
1:B:314:CYS:SG	1:B:315:TRP:N	2.61	0.74
1:B:245:ALA:HB2	1:B:265:MET:HG2	1.70	0.73
1:A:314:CYS:HB3	2:H:2:1TX:C25	2.16	0.70
1:B:345:ASP:OD2	1:B:345:ASP:N	2.26	0.68
1:A:92:TYR:O	1:A:137:ARG:NH2	2.27	0.66
1:A:630:PRO:HB2	1:A:717:VAL:HG11	1.78	0.65
1:A:541:ASN:HB2	1:A:577:LEU:HD13	1.79	0.64
1:A:231:GLU:HG3	1:A:296:VAL:HG21	1.80	0.62
1:B:641:VAL:O	1:B:643:GLY:HA2	2.00	0.62
1:B:231:GLU:HG3	1:B:296:VAL:HG21	1.81	0.61
1:A:189:GLU:HA	1:A:194:TYR:CG	2.38	0.58
1:B:354:LEU:HA	1:B:360:VAL:HA	1.84	0.58
1:B:558:THR:HG23	1:B:603:SER:HB3	1.87	0.57
1:A:345:ASP:N	1:A:345:ASP:OD1	2.40	0.55
1:B:700:SER:HA	1:B:725:ILE:HB	1.88	0.55
1:B:96:ARG:HH11	1:B:96:ARG:HB2	1.71	0.55
1:A:666:HIS:HB2	6:A:984:HOH:O	2.07	0.55
1:B:189:GLU:HA	1:B:194:TYR:CG	2.42	0.54
1:A:92:TYR:HD2	1:A:137:ARG:HH12	1.55	0.54
1:A:87:ASP:OD1	1:A:141:SER:HB3	2.08	0.54
1:A:195:LEU:O	1:A:201:ARG:NH1	2.42	0.53
1:B:540:ARG:HD3	1:B:582:PHE:CZ	2.44	0.52
1:A:385:LEU:HD22	1:A:424:PHE:HB3	1.92	0.52
1:B:632:ILE:HD11	1:B:709:MET:HB3	1.92	0.52
1:B:554:SER:HB3	1:B:607:PHE:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:467:LYS:NZ	6:A:904:HOH:O	2.43	0.50
1:B:310:ARG:HB3	1:B:311:TYR:CD2	2.46	0.50
1:A:484:GLN:HB2	1:A:487:GLN:HG3	1.95	0.49
1:B:664:TRP:CE2	1:B:679:MET:HG3	2.48	0.49
1:A:275:LEU:HD11	1:A:316:VAL:HG12	1.94	0.48
1:B:126:GLN:O	1:B:147:GLN:NE2	2.46	0.48
1:B:314:CYS:HB3	2:I:2:1TX:O14	2.15	0.47
1:B:275:LEU:HB3	1:B:317:PHE:CE1	2.48	0.47
1:A:106:GLY:O	1:A:158:ARG:NH2	2.47	0.47
1:B:275:LEU:HD21	1:B:316:VAL:HG12	1.97	0.47
1:A:709:MET:HE1	1:A:714:LEU:HG	1.97	0.47
1:B:555:ALA:HB3	1:B:569:LYS:HB3	1.97	0.47
1:B:310:ARG:HB3	1:B:311:TYR:CE2	2.50	0.46
1:A:20:ASN:HB3	6:A:918:HOH:O	2.15	0.46
1:A:121:ILE:HB	6:A:947:HOH:O	2.16	0.46
1:A:673:THR:HB	1:A:695:CYS:SG	2.55	0.46
1:B:541:ASN:HB2	1:B:577:LEU:HD22	1.98	0.46
1:A:69:TYR:HA	1:A:230:PHE:HB3	1.98	0.45
1:B:457:ALA:HB1	1:B:491:ARG:NH2	2.31	0.45
1:A:245:ALA:HB2	1:A:265:MET:HG3	1.99	0.45
1:A:552:TYR:HA	1:A:572:THR:HA	1.98	0.45
1:A:214:TYR:HB2	1:A:372:TYR:CZ	2.51	0.45
1:A:211:VAL:HG13	1:A:222:THR:HG23	1.99	0.45
1:A:277:GLY:HA2	1:A:312:GLY:O	2.17	0.45
1:A:126:GLN:O	1:A:147:GLN:NE2	2.49	0.44
1:A:454:ASN:HD22	1:A:455:VAL:H	1.65	0.44
1:B:248:ASP:OD2	1:B:250:SER:OG	2.28	0.44
1:B:156:LYS:HE3	1:B:181:TYR:OH	2.18	0.44
1:B:310:ARG:HA	1:B:311:TYR:HA	1.82	0.44
1:A:710:SER:HA	1:A:715:ARG:HA	1.99	0.44
1:B:18:ASN:HD22	1:B:18:ASN:C	2.20	0.44
1:A:341:ALA:HB2	1:A:460:ILE:HD12	1.99	0.44
1:A:244:ARG:NH2	1:A:306:GLU:O	2.50	0.44
1:B:398:THR:CG2	2:I:2:1TX:H11	2.44	0.43
1:A:194:TYR:CD2	5:A:806:GOL:H31	2.53	0.43
1:B:676:MET:SD	1:B:693:GLU:HG2	2.58	0.43
1:A:518:VAL:HB	1:A:612:ILE:HD11	1.99	0.43
1:A:524:VAL:HG11	1:A:625:THR:HG21	2.00	0.42
1:A:194:TYR:HD2	5:A:806:GOL:H31	1.84	0.42
1:A:310:ARG:HA	1:A:311:TYR:HA	1.86	0.42
1:A:52:LEU:HB3	1:A:74:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:ASP:OD1	1:A:67:ASP:N	2.52	0.42
1:B:213:PHE:CD1	1:B:222:THR:HG22	2.55	0.42
1:A:349:GLN:HA	1:A:437:SER:HB2	2.02	0.42
1:A:418:LYS:NZ	1:A:479:ASP:O	2.44	0.41
1:B:195:LEU:HD13	1:B:379:TRP:CE2	2.55	0.41
1:A:341:ALA:HB1	1:A:350:MET:SD	2.61	0.41
1:A:371:ASN:HB3	2:H:5:LEU:HD13	2.03	0.41
1:A:245:ALA:HB2	1:A:265:MET:CG	2.50	0.41
1:B:644:SER:O	1:B:696:ARG:HA	2.21	0.41
1:B:370:TRP:CD2	2:I:2:1TX:O13	2.73	0.41
1:B:569:LYS:HD3	1:B:593:GLU:OE2	2.21	0.41
1:A:315:TRP:CD2	2:H:1:7NF:C52	3.03	0.41
1:A:81:SER:HA	1:A:146:ILE:O	2.21	0.41
1:A:424:PHE:HA	6:A:976:HOH:O	2.20	0.40
1:A:548:THR:OG1	1:A:614:GLU:OE2	2.27	0.40
1:B:531:LYS:NZ	1:B:531:LYS:HA	2.36	0.40
1:A:264:ALA:HB2	1:A:408:ARG:HB3	2.03	0.40
1:B:703:ARG:HG3	1:B:725:ILE:HG13	2.04	0.40
1:A:189:GLU:HA	1:A:194:TYR:CD1	2.57	0.40
1:A:371:ASN:HA	2:H:5:LEU:HD22	2.03	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	680/738 (92%)	653 (96%)	24 (4%)	3 (0%)	34	52
1	B	677/738 (92%)	650 (96%)	24 (4%)	3 (0%)	34	52
2	H	4/8 (50%)	4 (100%)	0	0	100	100
2	I	4/8 (50%)	4 (100%)	0	0	100	100
All	All	1365/1492 (92%)	1311 (96%)	48 (4%)	6 (0%)	34	52

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	526	ASN
1	A	643	GLY
1	B	219	ASP
1	B	526	ASN
1	A	669	GLY
1	B	669	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	535/651 (82%)	518 (97%)	17 (3%)	39	63
1	B	549/651 (84%)	528 (96%)	21 (4%)	33	56
2	H	6/6 (100%)	5 (83%)	1 (17%)	2	3
2	I	3/6 (50%)	2 (67%)	1 (33%)	0	0
All	All	1093/1314 (83%)	1053 (96%)	40 (4%)	34	57

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	39	VAL
1	A	59	THR
1	A	100	ARG
1	A	110	GLN
1	A	202	GLU
1	A	211	VAL
1	A	321	PHE
1	A	454	ASN
1	A	491	ARG
1	A	520	MET
1	A	523	GLU
1	A	524	VAL
1	A	553	LEU

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Mol	Chain	Res	Type
1	A	577	LEU
1	A	601	GLN
1	A	678	LYS
1	B	18	ASN
1	B	20	ASN
1	B	70	GLU
1	B	96	ARG
1	B	100	ARG
1	B	140	ARG
1	B	265	MET
1	B	275	LEU
1	B	310	ARG
1	B	321	PHE
1	B	387	VAL
1	B	498	LEU
1	B	531	LYS
1	B	558	THR
1	B	577	LEU
1	B	599	LEU
1	B	608	VAL
1	B	616	ARG
1	B	678	LYS
1	B	715	ARG
1	B	722	ASP
2	H	5	LEU
2	I	5	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	454	ASN
1	B	18	ASN
1	B	112	ASN
1	B	344	ASN
1	B	459	HIS
1	B	468	GLN

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	$\# Z > 2$
2	1TX	H	2	1,2	10,11,12	0.52	0	7,12,14	0.44	0
2	1TX	I	2	1,2	10,11,12	0.57	0	7,12,14	0.40	0

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
2	1TX	H	2	1,2	-	1/10/11/13	-
2	1TX	I	2	1,2	-	1/10/11/13	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	2	1TX	C22-C23-C24-C25
2	I	2	1TX	C22-C23-C24-C25

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	2	1TX	1	0
2	I	2	1TX	4	0

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 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	SO4	A	805	-	4,4,4	0.17	0	6,6,6	0.37	0
4	SO4	B	805	-	4,4,4	0.10	0	6,6,6	0.54	0
4	SO4	B	806	-	4,4,4	0.15	0	6,6,6	0.29	0
5	GOL	B	807	-	5,5,5	0.33	0	5,5,5	0.40	0
4	SO4	A	804	-	4,4,4	0.22	0	6,6,6	0.40	0
4	SO4	B	804	-	4,4,4	0.12	0	6,6,6	0.24	0
5	GOL	A	806	-	5,5,5	0.46	0	5,5,5	0.44	0
5	GOL	A	807	-	5,5,5	0.34	0	5,5,5	0.45	0

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
5	GOL	A	806	-	-	2/4/4/4	-
5	GOL	B	807	-	-	2/4/4/4	-
5	GOL	A	807	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	807	GOL	O1-C1-C2-C3
5	A	806	GOL	O1-C1-C2-C3
5	B	807	GOL	O1-C1-C2-O2
5	A	806	GOL	O1-C1-C2-O2
5	A	807	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	806	GOL	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 ⓘ

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	688/738 (93%)	-0.00	15 (2%) 62 64	30, 51, 84, 115	0
1	B	685/738 (92%)	0.05	21 (3%) 49 51	32, 55, 82, 114	0
2	H	6/8 (75%)	0.31	0 100 100	45, 55, 72, 82	0
2	I	6/8 (75%)	0.35	1 (16%) 1 1	50, 66, 78, 81	0
All	All	1385/1492 (92%)	0.03	37 (2%) 54 56	30, 53, 83, 115	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	444	ALA	5.1
1	A	699	VAL	5.1
1	B	700	SER	4.7
1	B	699	VAL	3.9
1	A	442	ILE	3.9
1	B	353	PHE	3.8
1	B	643	GLY	3.7
1	B	452	VAL	3.6
1	B	451	VAL	3.6
1	B	354	LEU	3.4
1	B	443	THR	3.3
1	A	452	VAL	3.2
1	A	353	PHE	3.0
1	A	443	THR	3.0
1	B	352	ILE	3.0
1	B	440	ILE	2.9
1	B	642	VAL	2.9
1	A	527	ALA	2.7
1	B	695	CYS	2.7
1	A	700	SER	2.5
1	A	698	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
2	I	7	TRP	2.5
1	B	442	ILE	2.4
1	B	361	ASN	2.4
1	A	685	PRO	2.4
1	A	526	ASN	2.4
1	B	698	TRP	2.4
1	B	441	TYR	2.3
1	A	659	THR	2.3
1	A	525	GLU	2.2
1	B	365	THR	2.2
1	B	454	ASN	2.2
1	A	451	VAL	2.1
1	B	644	SER	2.1
1	A	454	ASN	2.1
1	B	455	VAL	2.1
1	B	703	ARG	2.1

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(Å ²)	Q<0.9
2	1TX	I	2	12/13	0.94	0.18	33,52,60,65	0
2	1TX	H	2	12/13	0.97	0.16	37,48,64,68	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
3	CA	A	801	1/1	0.56	0.11	82,82,82,82	0
5	GOL	A	807	6/6	0.93	0.28	56,57,57,58	0
3	CA	A	802	1/1	0.95	0.09	60,60,60,60	0
3	CA	B	803	1/1	0.95	0.07	59,59,59,59	0
4	SO4	B	805	5/5	0.95	0.15	47,57,57,65	5
5	GOL	B	807	6/6	0.95	0.20	49,59,61,65	0
5	GOL	A	806	6/6	0.96	0.23	46,54,61,65	0
4	SO4	A	804	5/5	0.96	0.12	34,37,48,57	5
4	SO4	B	804	5/5	0.97	0.10	62,66,76,78	0
4	SO4	B	806	5/5	0.97	0.19	52,57,59,61	5
4	SO4	A	805	5/5	0.97	0.14	52,55,62,65	5
3	CA	B	802	1/1	0.98	0.05	68,68,68,68	0
3	CA	B	801	1/1	0.98	0.08	38,38,38,38	0
3	CA	A	803	1/1	0.99	0.05	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.