



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:41 PM UTC

PDB ID : 5MHO / pdb_00005mho
Title : FXIIIa in complex with the inhibitor ZED2369
Authors : Stieler, M.; Heine, A.; Klebe, G.
Deposited on : 2016-11-24
Resolution : 2.92 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

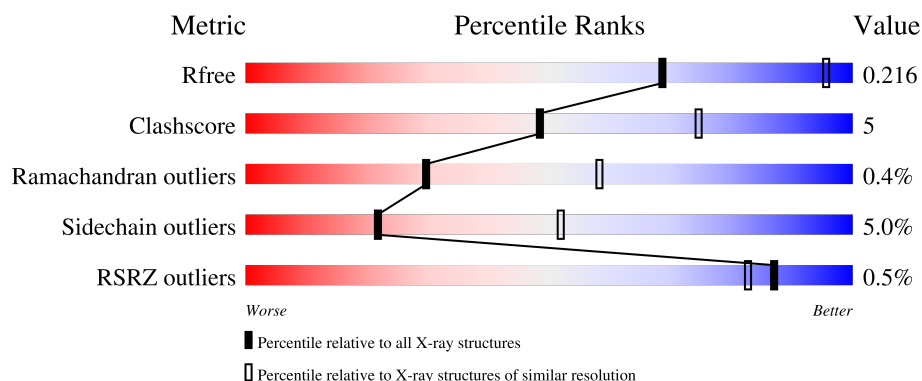
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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	738	76% 15% 8%
1	B	738	77% 14% 8%
2	G	9	44% 33% 11% 11%
2	H	9	44% 44% 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10661 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	678	Total	C	N	O	S	0	0	0
			5179	3312	866	976	25			
1	B	676	Total	C	N	O	S	0	1	0
			5222	3342	876	979	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 ZED2369.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	8	Total	C	N	O	0	0	1
			60	41	10	9			

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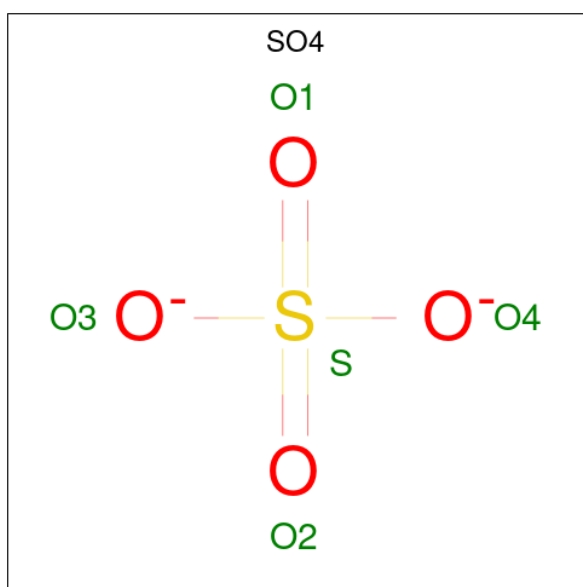
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	H	9	Total	C	N	O	0	0	1
			72	51	11	10			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	50	Total	O	0	0
			50	50		

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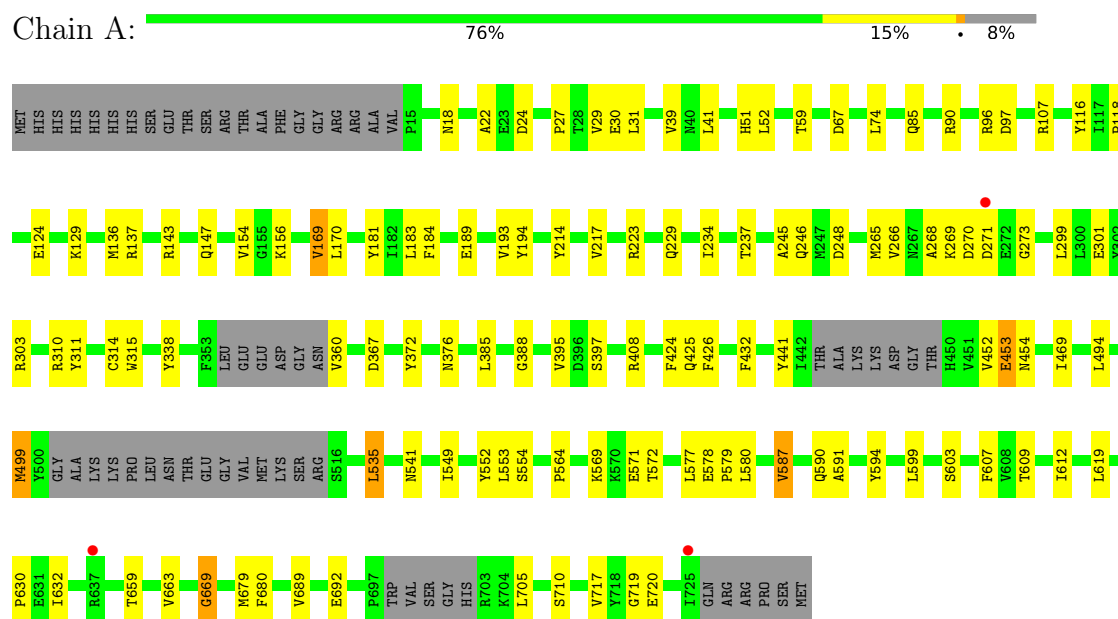
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	56	Total	O	0	0
			56	56		
5	G	1	Total	O	0	0
			1	1		

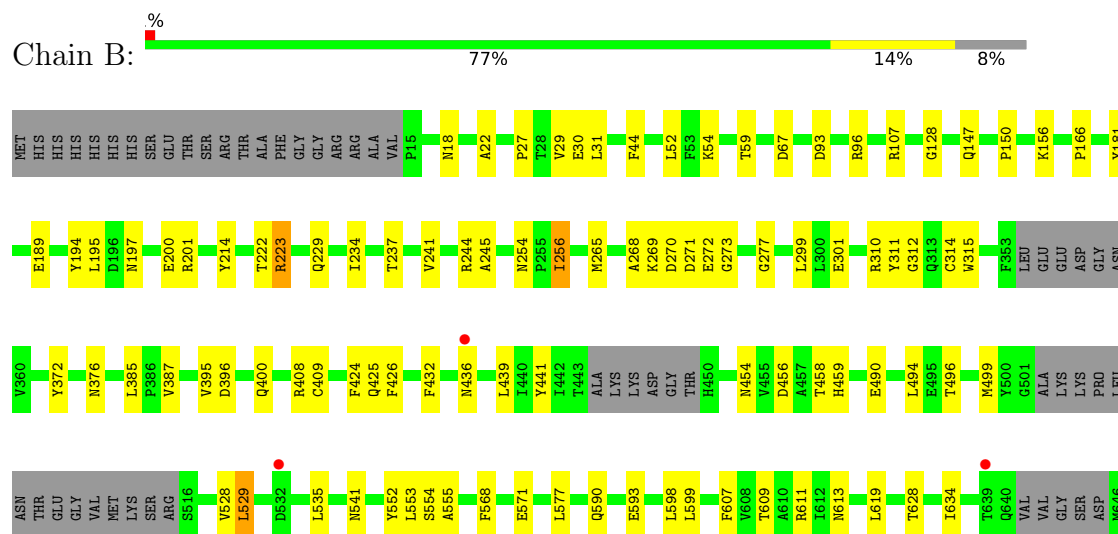
3 Residue-property plots [i](#)

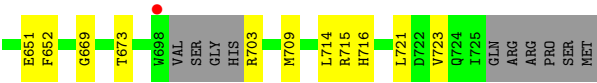
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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

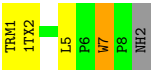


• Molecule 1: Coagulation factor XIII A chain





● Molecule 2: inhibitor ZED2369



● Molecule 2: inhibitor ZED2369



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	56.55Å 80.51Å 102.90Å 88.20° 76.91° 82.23°	Depositor
Resolution (Å)	17.71 – 2.92 17.71 – 2.92	Depositor EDS
% Data completeness (in resolution range)	95.9 (17.71-2.92) 95.7 (17.71-2.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.217 , 0.248 (Not available) , 0.216	Depositor DCC
R_{free} test set	1780 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.607	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10661	wwPDB-VP
Average B, all atoms (Å ²)	47.0	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 44.74 % 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 1.4611e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: TRM, 1TX, SO4, NH2, CA

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	0.11	0/5302	0.31	0/7233
1	B	0.12	0/5347	0.31	0/7287
2	G	0.43	0/38	0.57	0/52
2	H	0.51	0/51	0.62	0/72
All	All	0.12	0/10738	0.32	0/14644

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	5179	0	4775	55	0
1	B	5222	0	4834	55	0
2	G	60	0	43	5	0
2	H	72	0	55	6	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	5	0	0	0	0
4	B	10	0	0	0	0
5	A	50	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	56	0	0	0	0
5	G	1	0	0	0	0
All	All	10661	0	9707	111	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 5.

All (111) 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:554:SER:HB3	1:B:607:PHE:HB2	1.68	0.75
1:B:703:ARG:N	1:B:723:VAL:O	2.25	0.69
1:A:554:SER:HB3	1:A:607:PHE:HB2	1.78	0.66
1:B:439:LEU:HD13	1:B:456:ASP:HB3	1.78	0.65
1:A:535:LEU:HB3	1:A:587:VAL:HG13	1.80	0.64
1:A:579:PRO:HB2	1:A:580:LEU:HD12	1.80	0.63
1:A:569:LYS:NZ	1:A:571:GLU:OE2	2.32	0.62
1:B:268:ALA:HA	1:B:273:GLY:H	1.65	0.61
1:B:441:TYR:HH	2:H:9:NH2:N	1.98	0.61
1:B:244:ARG:NH2	1:B:272:GLU:OE1	2.33	0.60
1:B:52:LEU:HB2	1:B:54:LYS:HG3	1.83	0.59
1:A:217:VAL:HG22	1:A:338:TYR:HB3	1.85	0.58
1:A:663:VAL:HB	1:A:680:PHE:HB2	1.85	0.58
1:B:245:ALA:HB2	1:B:265:MET:HG3	1.87	0.57
1:B:385:LEU:HD22	1:B:424:PHE:HB3	1.87	0.56
1:B:223[B]:ARG:HH22	2:H:1:TRM:HZ21	1.70	0.56
1:A:136:MET:HB3	1:A:143:ARG:HB3	1.88	0.55
2:H:5:LEU:HD13	2:H:6:PRO:HD2	1.87	0.55
1:A:452:VAL:HG22	1:A:453:GLU:H	1.71	0.55
1:A:541:ASN:HB2	1:A:577:LEU:HD13	1.90	0.53
1:B:269:LYS:O	1:B:271:ASP:N	2.42	0.53
1:B:376:ASN:HB2	1:B:395:VAL:HG23	1.90	0.52
1:B:529:LEU:HD12	1:B:598:LEU:HD13	1.92	0.52
1:B:314:CYS:SG	1:B:315:TRP:N	2.83	0.52
1:B:541:ASN:HB2	1:B:577:LEU:HG	1.91	0.52
1:B:425:GLN:HB2	1:B:426:PHE:CD1	2.46	0.51
1:A:372:TYR:OH	2:G:1:TRM:NE1	2.32	0.51
1:B:611:ARG:NH1	1:B:613:ASN:OD1	2.44	0.50
1:A:268:ALA:HA	1:A:273:GLY:H	1.75	0.50
1:B:93:ASP:HB3	1:B:96:ARG:HG2	1.94	0.50
1:B:156:LYS:HD2	1:B:181:TYR:CZ	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:GLU:HA	1:A:194:TYR:CG	2.46	0.50
1:A:129:LYS:O	1:A:147:GLN:NE2	2.44	0.50
1:B:268:ALA:HA	1:B:273:GLY:N	2.27	0.50
1:A:41:LEU:HD13	1:A:170:LEU:HD21	1.93	0.49
1:B:229:GLN:HA	1:B:234:ILE:HG21	1.93	0.49
1:A:269:LYS:O	1:A:271:ASP:N	2.45	0.49
1:A:24:ASP:HB3	1:A:107:ARG:O	2.13	0.49
1:B:715:ARG:HG3	1:B:716:HIS:CD2	2.48	0.49
1:B:189:GLU:HA	1:B:194:TYR:CG	2.48	0.49
1:A:385:LEU:HD22	1:A:424:PHE:HB3	1.95	0.48
1:B:555:ALA:HB1	1:B:568:PHE:CZ	2.48	0.48
1:A:310:ARG:HA	1:A:311:TYR:HA	1.61	0.48
1:B:22:ALA:HB1	1:B:107:ARG:HB2	1.96	0.47
1:A:376:ASN:HB2	1:A:395:VAL:HG23	1.96	0.47
1:A:223:ARG:NH2	2:G:1:TRM:HH21	2.30	0.47
1:A:30:GLU:HB2	1:A:169:VAL:HG13	1.97	0.47
1:A:214:TYR:HB2	1:A:372:TYR:CZ	2.50	0.47
1:A:52:LEU:HB3	1:A:74:LEU:HD22	1.97	0.46
1:A:549:ILE:HG12	1:A:612:ILE:HD13	1.96	0.46
1:A:630:PRO:HB2	1:A:717:VAL:HG11	1.97	0.46
1:A:314:CYS:SG	1:A:315:TRP:N	2.88	0.46
1:A:51:HIS:HB2	1:A:85:GLN:HB3	1.98	0.46
1:A:591:ALA:HA	1:A:594:TYR:CE1	2.50	0.46
1:A:669:GLY:HA3	1:A:705:LEU:HD23	1.98	0.46
1:A:29:VAL:HG12	1:A:31:LEU:HG	1.97	0.46
1:A:388:GLY:O	1:A:564:PRO:HG3	2.16	0.46
1:A:314:CYS:HB3	2:G:2:1TX:C25	2.23	0.45
1:B:195:LEU:O	1:B:201:ARG:NH1	2.49	0.45
1:A:310:ARG:HB3	1:A:311:TYR:CG	2.52	0.45
1:B:223[B]:ARG:HH22	2:H:1:TRM:CZ2	2.29	0.45
1:B:400:GLN:OE1	2:H:2:1TX:H11	2.17	0.45
1:B:432:PHE:HZ	1:B:494:LEU:HA	1.82	0.45
1:A:156:LYS:HD2	1:A:181:TYR:CZ	2.51	0.45
1:A:552:TYR:CE1	1:A:609:THR:HB	2.52	0.45
1:A:90:ARG:NH2	1:A:97:ASP:OD1	2.41	0.44
1:A:367:ASP:O	2:G:7:TRP:NE1	2.48	0.44
1:A:27:PRO:HB2	1:A:30:GLU:HG3	1.99	0.44
1:B:310:ARG:HA	1:B:311:TYR:HA	1.57	0.44
1:A:314:CYS:H	2:G:2:1TX:H34	1.83	0.44
1:A:441:TYR:CD2	1:A:454:ASN:HB3	2.53	0.44
1:A:116:TYR:CE2	1:A:118:PRO:HG3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ALA:HB2	1:A:265:MET:HG3	1.99	0.43
1:B:436:ASN:HD21	1:B:490:GLU:HG2	1.83	0.43
1:A:184:PHE:HB3	1:A:193:VAL:HG21	2.01	0.43
1:B:496:THR:O	1:B:499:MET:HG2	2.18	0.43
1:A:154:VAL:HG13	1:A:183:LEU:HA	2.01	0.43
1:A:499:MET:HE3	1:A:499:MET:HB3	1.81	0.43
1:B:396:ASP:HB3	1:B:409:CYS:HB3	1.99	0.43
1:A:266:VAL:HB	1:A:397:SER:HB2	2.01	0.43
1:A:18:ASN:HB3	1:A:248:ASP:HA	2.01	0.43
1:A:229:GLN:HA	1:A:234:ILE:HG21	2.01	0.43
1:A:237:THR:HG21	1:A:299:LEU:HB3	2.01	0.42
1:B:439:LEU:HD11	1:B:459:HIS:HB3	2.00	0.42
1:B:29:VAL:HG12	1:B:31:LEU:HG	2.01	0.42
1:A:432:PHE:HZ	1:A:494:LEU:HA	1.83	0.42
1:B:44:PHE:CE1	1:B:166:PRO:HD2	2.53	0.42
1:B:197:ASN:HB3	1:B:200:GLU:HB2	2.00	0.42
1:A:67:ASP:OD1	1:A:67:ASP:N	2.52	0.42
1:B:214:TYR:CE1	1:B:223[A]:ARG:HB2	2.55	0.42
1:B:245:ALA:HB2	1:B:265:MET:CG	2.48	0.42
1:A:425:GLN:HA	1:A:426:PHE:HA	1.78	0.42
1:B:552:TYR:CE1	1:B:609:THR:HB	2.55	0.41
1:A:22:ALA:HB1	1:A:107:ARG:HB2	2.02	0.41
1:B:128:GLY:HA2	1:B:150:PRO:HD3	2.02	0.41
1:B:237:THR:O	1:B:241:VAL:HG23	2.20	0.41
1:B:441:TYR:CD2	1:B:454:ASN:HB3	2.55	0.41
1:B:27:PRO:HB2	1:B:30:GLU:HG3	2.02	0.41
1:B:237:THR:HG21	1:B:299:LEU:HB3	2.00	0.41
1:B:590:GLN:N	1:B:593:GLU:OE1	2.49	0.41
1:B:67:ASP:OD1	1:B:67:ASP:N	2.52	0.41
1:B:254:ASN:OD1	1:B:256:ILE:HG23	2.21	0.41
1:B:432:PHE:CZ	1:B:494:LEU:HA	2.55	0.41
1:B:314:CYS:HB3	2:H:2:1TX:C25	2.26	0.41
1:B:709:MET:HE2	1:B:709:MET:HB2	1.96	0.41
1:B:214:TYR:HB2	1:B:372:TYR:CZ	2.56	0.41
1:B:634:ILE:O	1:B:721:LEU:HD22	2.21	0.41
1:A:245:ALA:HB2	1:A:265:MET:CG	2.51	0.40
1:B:652:PHE:CE2	1:B:709:MET:HE3	2.56	0.40
1:A:632:ILE:HB	1:A:719:GLY:HA3	2.03	0.40
1:B:277:GLY:HA2	1:B:312:GLY:O	2.22	0.40

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	668/738 (90%)	638 (96%)	27 (4%)	3 (0%)	30	58
1	B	665/738 (90%)	637 (96%)	26 (4%)	2 (0%)	36	64
2	G	5/9 (56%)	5 (100%)	0	0	100	100
2	H	6/9 (67%)	5 (83%)	1 (17%)	0	100	100
All	All	1344/1494 (90%)	1285 (96%)	54 (4%)	5 (0%)	30	58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	270	ASP
1	B	270	ASP
1	A	453	GLU
1	B	669	GLY
1	A	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	518/651 (80%)	490 (95%)	28 (5%)	20	49
1	B	523/651 (80%)	501 (96%)	22 (4%)	26	59
2	G	3/6 (50%)	1 (33%)	2 (67%)	0	0
2	H	4/6 (67%)	3 (75%)	1 (25%)	0	2
All	All	1048/1314 (80%)	995 (95%)	53 (5%)	22	51

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	VAL
1	A	59	THR
1	A	96	ARG
1	A	124	GLU
1	A	137	ARG
1	A	169	VAL
1	A	246	GLN
1	A	301	GLU
1	A	303	ARG
1	A	360	VAL
1	A	408	ARG
1	A	469	ILE
1	A	499	MET
1	A	535	LEU
1	A	553	LEU
1	A	572	THR
1	A	578	GLU
1	A	587	VAL
1	A	590	GLN
1	A	599	LEU
1	A	603	SER
1	A	619	LEU
1	A	659	THR
1	A	679	MET
1	A	689	VAL
1	A	692	GLU
1	A	710	SER
1	A	720	GLU
1	B	18	ASN
1	B	59	THR
1	B	147	GLN
1	B	222	THR
1	B	223[A]	ARG
1	B	223[B]	ARG
1	B	256	ILE
1	B	301	GLU
1	B	387	VAL
1	B	408	ARG
1	B	458	THR
1	B	528	VAL
1	B	529	LEU
1	B	535	LEU

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Mol	Chain	Res	Type
1	B	553	LEU
1	B	571	GLU
1	B	599	LEU
1	B	619	LEU
1	B	628	THR
1	B	651	GLU
1	B	673	THR
1	B	714	LEU
2	G	5	LEU
2	G	7	TRP
2	H	5	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	HIS
1	A	544	HIS
1	A	597	GLN
1	A	666	HIS
1	B	46	ASN
1	B	147	GLN
1	B	342	HIS
1	B	454	ASN
1	B	468	GLN
1	B	597	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	G	2	1,2	10,11,12	0.56	0	7,12,14	0.32	0
2	1TX	H	2	1,2	10,11,12	0.48	0	7,12,14	0.30	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	G	2	1,2	-	3/10/11/13	-
2	1TX	H	2	1,2	-	2/10/11/13	-

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
2	G	2	1TX	O-C-CA-C21
2	G	2	1TX	C22-C23-C24-C25
2	H	2	1TX	C22-C23-C24-C25
2	G	2	1TX	C21-C22-C23-C24
2	H	2	1TX	C21-C22-C23-C24

There are no ring outliers.

2 monomers are involved in 4 short contacts:

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	B	805	-	4,4,4	0.23	0	6,6,6	0.07	0
4	SO4	B	804	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	A	804	-	4,4,4	0.24	0	6,6,6	0.07	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	678/738 (91%)	-0.13	3 (0%) 88 85	26, 45, 73, 95	0
1	B	676/738 (91%)	-0.02	4 (0%) 85 81	23, 46, 74, 93	1 (0%)
2	G	6/9 (66%)	0.29	0 100 100	53, 53, 53, 53	0
2	H	6/9 (66%)	0.81	0 100 100	65, 65, 65, 65	0
All	All	1366/1494 (91%)	-0.07	7 (0%) 87 83	23, 46, 73, 95	1 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	436	ASN	2.7
1	B	532	ASP	2.5
1	B	639	THR	2.4
1	A	637	ARG	2.4
1	A	271	ASP	2.3
1	A	725	ILE	2.2
1	B	698	TRP	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	H	2	12/13	0.86	0.14	65,65,65,65	0
2	1TX	G	2	12/13	0.90	0.12	53,53,53,53	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
3	CA	B	803	1/1	0.85	0.07	53,53,53,53	0
4	SO4	B	804	5/5	0.90	0.09	50,56,65,71	0
4	SO4	A	804	5/5	0.93	0.08	48,51,59,68	0
3	CA	A	802	1/1	0.94	0.05	56,56,56,56	0
3	CA	A	803	1/1	0.97	0.04	49,49,49,49	0
3	CA	A	801	1/1	0.97	0.13	45,45,45,45	0
4	SO4	B	805	5/5	0.97	0.10	31,37,40,45	5
3	CA	B	801	1/1	0.98	0.05	35,35,35,35	0
3	CA	B	802	1/1	0.98	0.05	71,71,71,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.