



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:12 PM UTC

PDB ID : 7TFF / pdb_00007tff
Title : Crystal structure of human platelet phosphofructokinase-1 mutant- D564N
Authors : Hansen, H.; Webb, B.A.; Robart, A.R.; Narayanasami, S.
Deposited on : 2022-01-06
Resolution : 3.60 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)	:	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

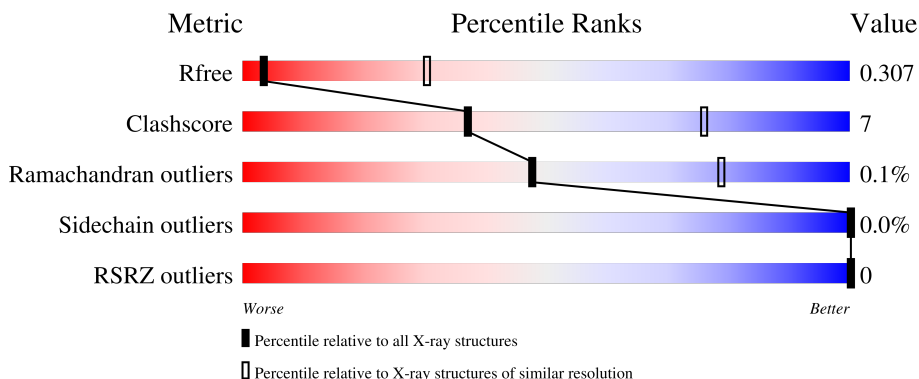
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

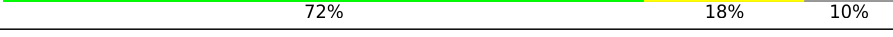
The reported resolution of this entry is 3.60 Å.

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	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	812	 75% 16% 9%
1	B	812	 77% 13% 9%
1	C	812	 74% 16% 10%
1	D	812	 72% 18% 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	804	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 22572 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 ATP-dependent 6-phosphofructokinase, platelet type.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	738	Total	C	N	O	S	0	0	0
			5633	3534	1000	1060	39			
1	B	735	Total	C	N	O	S	0	0	0
			5613	3522	996	1056	39			
1	C	731	Total	C	N	O	S	0	0	0
			5583	3507	988	1049	39			
1	D	730	Total	C	N	O	S	0	0	0
			5574	3501	988	1047	38			

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	expression tag	UNP Q01813
A	-26	SER	-	expression tag	UNP Q01813
A	-25	TYR	-	expression tag	UNP Q01813
A	-24	TYR	-	expression tag	UNP Q01813
A	-23	HIS	-	expression tag	UNP Q01813
A	-22	HIS	-	expression tag	UNP Q01813
A	-21	HIS	-	expression tag	UNP Q01813
A	-20	HIS	-	expression tag	UNP Q01813
A	-19	HIS	-	expression tag	UNP Q01813
A	-18	HIS	-	expression tag	UNP Q01813
A	-17	ASP	-	expression tag	UNP Q01813
A	-16	TYR	-	expression tag	UNP Q01813
A	-15	ASP	-	expression tag	UNP Q01813
A	-14	ILE	-	expression tag	UNP Q01813
A	-13	PRO	-	expression tag	UNP Q01813
A	-12	THR	-	expression tag	UNP Q01813
A	-11	THR	-	expression tag	UNP Q01813
A	-10	GLU	-	expression tag	UNP Q01813
A	-9	ASN	-	expression tag	UNP Q01813
A	-8	LEU	-	expression tag	UNP Q01813
A	-7	TYR	-	expression tag	UNP Q01813

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	PHE	-	expression tag	UNP Q01813
A	-5	GLN	-	expression tag	UNP Q01813
A	-4	GLY	-	expression tag	UNP Q01813
A	-3	ALA	-	expression tag	UNP Q01813
A	-2	MET	-	expression tag	UNP Q01813
A	-1	ASP	-	expression tag	UNP Q01813
A	0	PRO	-	expression tag	UNP Q01813
A	564	ASN	ASP	engineered mutation	UNP Q01813
B	-27	MET	-	expression tag	UNP Q01813
B	-26	SER	-	expression tag	UNP Q01813
B	-25	TYR	-	expression tag	UNP Q01813
B	-24	TYR	-	expression tag	UNP Q01813
B	-23	HIS	-	expression tag	UNP Q01813
B	-22	HIS	-	expression tag	UNP Q01813
B	-21	HIS	-	expression tag	UNP Q01813
B	-20	HIS	-	expression tag	UNP Q01813
B	-19	HIS	-	expression tag	UNP Q01813
B	-18	HIS	-	expression tag	UNP Q01813
B	-17	ASP	-	expression tag	UNP Q01813
B	-16	TYR	-	expression tag	UNP Q01813
B	-15	ASP	-	expression tag	UNP Q01813
B	-14	ILE	-	expression tag	UNP Q01813
B	-13	PRO	-	expression tag	UNP Q01813
B	-12	THR	-	expression tag	UNP Q01813
B	-11	THR	-	expression tag	UNP Q01813
B	-10	GLU	-	expression tag	UNP Q01813
B	-9	ASN	-	expression tag	UNP Q01813
B	-8	LEU	-	expression tag	UNP Q01813
B	-7	TYR	-	expression tag	UNP Q01813
B	-6	PHE	-	expression tag	UNP Q01813
B	-5	GLN	-	expression tag	UNP Q01813
B	-4	GLY	-	expression tag	UNP Q01813
B	-3	ALA	-	expression tag	UNP Q01813
B	-2	MET	-	expression tag	UNP Q01813
B	-1	ASP	-	expression tag	UNP Q01813
B	0	PRO	-	expression tag	UNP Q01813
B	564	ASN	ASP	engineered mutation	UNP Q01813
C	-27	MET	-	expression tag	UNP Q01813
C	-26	SER	-	expression tag	UNP Q01813
C	-25	TYR	-	expression tag	UNP Q01813
C	-24	TYR	-	expression tag	UNP Q01813
C	-23	HIS	-	expression tag	UNP Q01813

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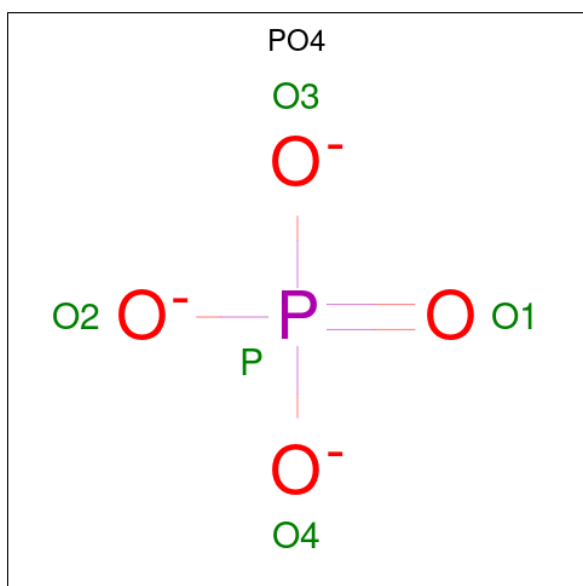
Chain	Residue	Modelled	Actual	Comment	Reference
C	-22	HIS	-	expression tag	UNP Q01813
C	-21	HIS	-	expression tag	UNP Q01813
C	-20	HIS	-	expression tag	UNP Q01813
C	-19	HIS	-	expression tag	UNP Q01813
C	-18	HIS	-	expression tag	UNP Q01813
C	-17	ASP	-	expression tag	UNP Q01813
C	-16	TYR	-	expression tag	UNP Q01813
C	-15	ASP	-	expression tag	UNP Q01813
C	-14	ILE	-	expression tag	UNP Q01813
C	-13	PRO	-	expression tag	UNP Q01813
C	-12	THR	-	expression tag	UNP Q01813
C	-11	THR	-	expression tag	UNP Q01813
C	-10	GLU	-	expression tag	UNP Q01813
C	-9	ASN	-	expression tag	UNP Q01813
C	-8	LEU	-	expression tag	UNP Q01813
C	-7	TYR	-	expression tag	UNP Q01813
C	-6	PHE	-	expression tag	UNP Q01813
C	-5	GLN	-	expression tag	UNP Q01813
C	-4	GLY	-	expression tag	UNP Q01813
C	-3	ALA	-	expression tag	UNP Q01813
C	-2	MET	-	expression tag	UNP Q01813
C	-1	ASP	-	expression tag	UNP Q01813
C	0	PRO	-	expression tag	UNP Q01813
C	564	ASN	ASP	engineered mutation	UNP Q01813
D	-27	MET	-	expression tag	UNP Q01813
D	-26	SER	-	expression tag	UNP Q01813
D	-25	TYR	-	expression tag	UNP Q01813
D	-24	TYR	-	expression tag	UNP Q01813
D	-23	HIS	-	expression tag	UNP Q01813
D	-22	HIS	-	expression tag	UNP Q01813
D	-21	HIS	-	expression tag	UNP Q01813
D	-20	HIS	-	expression tag	UNP Q01813
D	-19	HIS	-	expression tag	UNP Q01813
D	-18	HIS	-	expression tag	UNP Q01813
D	-17	ASP	-	expression tag	UNP Q01813
D	-16	TYR	-	expression tag	UNP Q01813
D	-15	ASP	-	expression tag	UNP Q01813
D	-14	ILE	-	expression tag	UNP Q01813
D	-13	PRO	-	expression tag	UNP Q01813
D	-12	THR	-	expression tag	UNP Q01813
D	-11	THR	-	expression tag	UNP Q01813
D	-10	GLU	-	expression tag	UNP Q01813

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-9	ASN	-	expression tag	UNP Q01813
D	-8	LEU	-	expression tag	UNP Q01813
D	-7	TYR	-	expression tag	UNP Q01813
D	-6	PHE	-	expression tag	UNP Q01813
D	-5	GLN	-	expression tag	UNP Q01813
D	-4	GLY	-	expression tag	UNP Q01813
D	-3	ALA	-	expression tag	UNP Q01813
D	-2	MET	-	expression tag	UNP Q01813
D	-1	ASP	-	expression tag	UNP Q01813
D	0	PRO	-	expression tag	UNP Q01813
D	564	ASN	ASP	engineered mutation	UNP Q01813

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



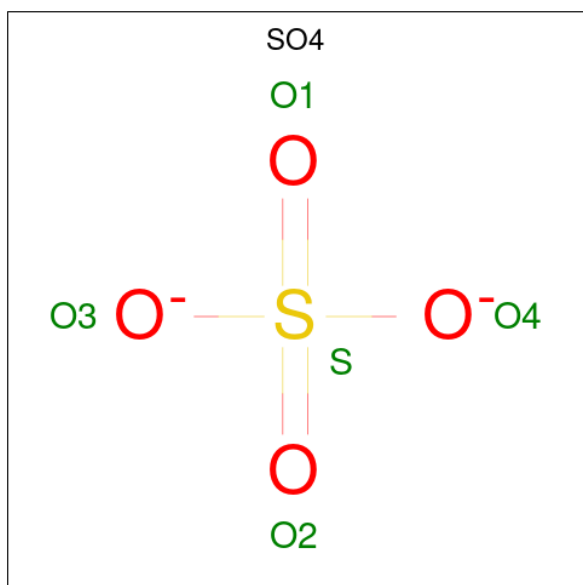
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

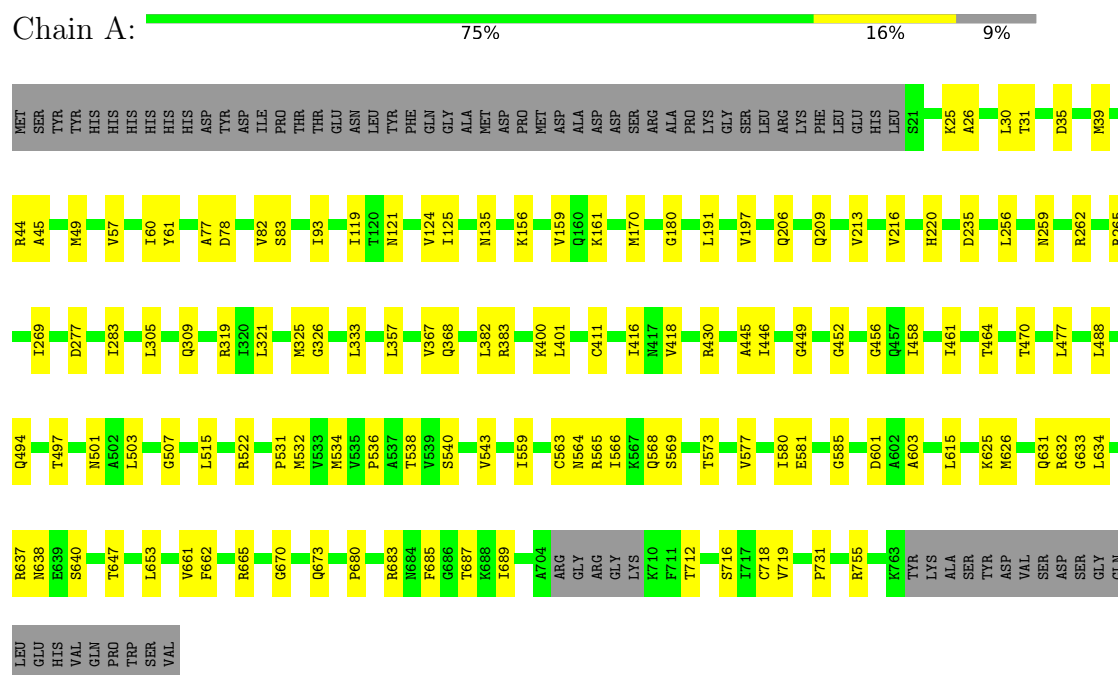
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	33	Total	O	0	0
			33	33		
4	B	10	Total	O	0	0
			10	10		
4	C	11	Total	O	0	0
			11	11		
4	D	10	Total	O	0	0
			10	10		

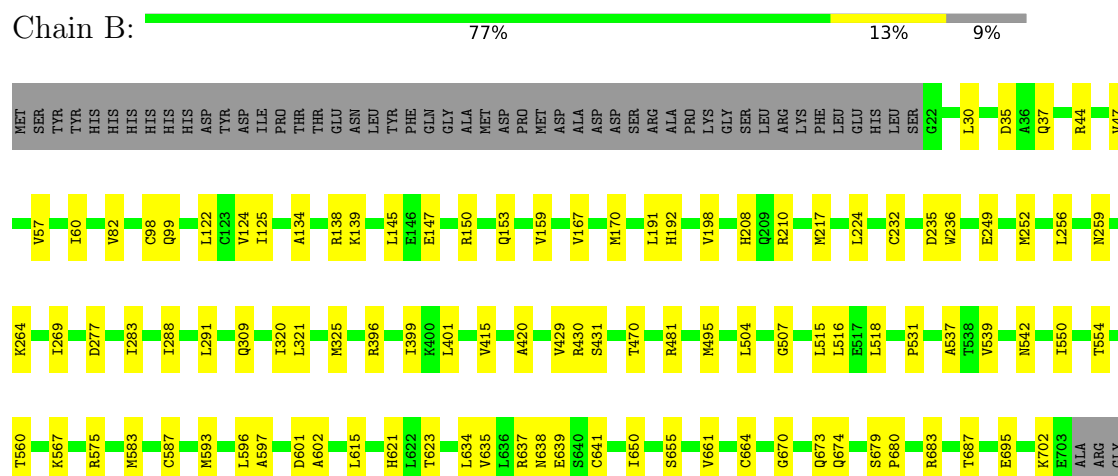
3 Residue-property plots

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: ATP-dependent 6-phosphofructokinase, platelet type



- Molecule 1: ATP-dependent 6-phosphofructokinase, platelet type



ARG
GLY
LYS
LYS
F711
T712
T713
D714
S716
K736
M758
A762
K763
TYR
LYS
ALA
SER
TYR
ASP
GLN
VAL
SER
ASP
SER
GLY
GLN
LEU
GLU
HIS
VAL
GLN
PRO
TRP
SER
VAL

- Molecule 1: ATP-dependent 6-phosphofructokinase, platelet type

Chain C: 

TYR	ASP	VAL	SER	ASP	SER	GLY	GLN	LEU	GLU	HIS	VAL	GLN	PRO	TRP	SER	VAL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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- Molecule 1: ATP-dependent 6-phosphofructokinase, platelet type

Chain D: 

K710	R565	D403	Q206	R44	MET
F711	I566	D404	S207	V47	SER
T712	I580	Q405	H208		TYR
D714	G585	L406	Q209	V57	HIS
D715		P407	R210		HIS
S716		K408		I60	HIS
T717	L596	V415	V216	Y61	HIS
C718	F606	L416	N217		HIS
V719	E607	N417	G218	N73	ASP
P731	E608	A420	A225	D78	TYR
V732	V619	M425	S228	E79	ASP
A733	T623	M426	C232	E80	ILE
E734				S81	PRO
T739	M626	V429	D235	S83	THR
P746	T630	R430	L256	S84	GLU
R755	Q631	S431		I85	ASN
P756	R637	K432	N259	V88	LEU
L757	N638	V433	R265	G89	PHE
M758		M443	I269	I93	GLN
K759	C641	G452	A272		GLY
K763	S655	K455	D277	A96	ALA
TYR	E556	V463	I283	ARG	MET
LYS	E657			CYS	ASP
ALA	V661	T470	V293	GLN	ASP
SER	F662	Q473	THR	L108	ALA
ASP	D663		GLN	I119	ASP
VAL	C664	R481	LEU	T120	SER
SER	R665	L488	GLY	N121	ARG
GLY	K666		V298	V124	ALA
GLN	N667	M495	H307	I125	PRO
LEU	M672		V308	D128	GLY
LEU		I500	Q309		SER
HIS	G676	R522	R310	E147	LEU
VAL	A677	E523	G311	L148	ARG
GLN	P678	K524	G312	A149	LYS
PRO	S679			R150	PHE
TRP	P680	C529	L321		LEU
SER	R683			Q153	GLU
VAL		M532	M326	I154	H19
	T687	V533		D155	K25
	L701	M534	A370	K156	A26
	LYS	A537	M371	V159	L30
	GLU		D372		T31
	ALA	N541	R375	L191	D35
	ARG	F548	F376	H192	A36
	GLY	S549	K400	R193	Q37
	ARG	L550	L401	V198	N40
	GLY		P402		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.89Å 159.66Å 131.25Å 90.00° 104.01° 90.00°	Depositor
Resolution (Å)	66.57 – 3.60 66.57 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (66.57-3.60) 99.5 (66.57-3.60)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 3.58Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158, PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.250 , 0.307 0.249 , 0.307	Depositor DCC
R_{free} test set	2002 reflections (5.54%)	wwPDB-VP
Wilson B-factor (Å ²)	127.2	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 83.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	22572	wwPDB-VP
Average B, all atoms (Å ²)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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: SO4, PO4

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	0.06	0/5723	0.19	0/7727
1	B	0.06	0/5703	0.17	0/7701
1	C	0.06	0/5673	0.20	0/7661
1	D	0.06	0/5663	0.19	0/7645
All	All	0.06	0/22762	0.19	0/30734

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	5633	0	5667	78	0
1	B	5613	0	5644	67	0
1	C	5583	0	5614	83	0
1	D	5574	0	5604	96	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
2	C	10	0	0	1	0
2	D	10	0	0	0	0
3	A	20	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	0	0	0
3	C	20	0	0	0	0
3	D	15	0	0	0	0
4	A	33	0	0	1	0
4	B	10	0	0	0	0
4	C	11	0	0	2	0
4	D	10	0	0	1	0
All	All	22572	0	22529	319	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 319 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:A:191:LEU:HD22	1:A:680:PRO:HB3	1.46	0.98
1:D:757:LEU:HD23	1:D:758:MET:H	1.46	0.80
1:A:445:ALA:HB1	1:A:477:LEU:HD21	1.66	0.76
1:D:406:ILE:HG13	1:D:408:LYS:HE2	1.69	0.74
1:B:145:LEU:HB3	1:B:159:VAL:HG23	1.73	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	734/812 (90%)	679 (92%)	55 (8%)	0	100	100
1	B	731/812 (90%)	682 (93%)	49 (7%)	0	100	100
1	C	725/812 (89%)	657 (91%)	66 (9%)	2 (0%)	36	65
1	D	722/812 (89%)	657 (91%)	63 (9%)	2 (0%)	36	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2912/3248 (90%)	2675 (92%)	233 (8%)	4 (0%)	48 79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	83	SER
1	C	22	GLY
1	C	133	GLY
1	D	407	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	593/658 (90%)	593 (100%)	0	100 100
1	B	591/658 (90%)	591 (100%)	0	100 100
1	C	589/658 (90%)	589 (100%)	0	100 100
1	D	587/658 (89%)	586 (100%)	1 (0%)	87 85
All	All	2360/2632 (90%)	2359 (100%)	1 (0%)	100 100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	108	LEU

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	176	ASN
1	D	644	ASN
1	C	501	ASN
1	D	749	GLN
1	D	498	HIS

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](#)

21 ligands 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	$\# Z > 2$
3	SO4	A	806	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	C	805	-	4,4,4	0.23	0	6,6,6	0.08	0
2	PO4	D	801	-	4,4,4	0.97	0	6,6,6	0.46	0
3	SO4	A	805	-	4,4,4	0.23	0	6,6,6	0.07	0
2	PO4	A	802	-	4,4,4	0.96	0	6,6,6	0.46	0
3	SO4	A	803	-	4,4,4	0.23	0	6,6,6	0.07	0
2	PO4	C	802	-	4,4,4	0.96	0	6,6,6	0.46	0
2	PO4	B	802	-	4,4,4	0.96	0	6,6,6	0.47	0
3	SO4	A	804	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	C	804	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	804	-	4,4,4	0.23	0	6,6,6	0.08	0
2	PO4	C	801	-	4,4,4	0.96	0	6,6,6	0.46	0
3	SO4	C	806	-	4,4,4	0.23	0	6,6,6	0.09	0
2	PO4	A	801	-	4,4,4	0.96	0	6,6,6	0.46	0
3	SO4	C	803	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	803	-	4,4,4	0.23	0	6,6,6	0.07	0
2	PO4	B	801	-	4,4,4	0.96	0	6,6,6	0.46	0
2	PO4	D	802	-	4,4,4	0.96	0	6,6,6	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	D	804	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	D	805	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	D	803	-	4,4,4	0.24	0	6,6,6	0.08	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.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	805	SO4	1	0
3	A	803	SO4	1	0
3	A	804	SO4	2	0
2	C	801	PO4	1	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 [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	738/812 (90%)	-0.46	0 100 100	65, 104, 146, 183	0
1	B	735/812 (90%)	-0.48	0 100 100	69, 110, 156, 175	0
1	C	731/812 (90%)	-0.51	0 100 100	74, 119, 159, 193	0
1	D	730/812 (89%)	-0.45	0 100 100	78, 122, 167, 203	0
All	All	2934/3248 (90%)	-0.48	0 100 100	65, 114, 159, 203	0

There are no RSRZ outliers to report.

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(Å ²)	Q<0.9
3	SO4	C	806	5/5	0.57	0.11	165,169,175,177	0
3	SO4	B	804	5/5	0.61	0.10	130,135,144,149	0
3	SO4	A	806	5/5	0.61	0.12	127,133,148,159	0
3	SO4	C	805	5/5	0.65	0.09	148,162,176,180	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PO4	C	801	5/5	0.76	0.09	112,115,119,121	0
3	SO4	D	803	5/5	0.76	0.10	101,122,128,128	0
3	SO4	C	804	5/5	0.77	0.06	115,116,126,127	0
2	PO4	B	802	5/5	0.80	0.08	110,113,124,127	0
3	SO4	D	804	5/5	0.81	0.05	122,124,133,142	0
3	SO4	A	805	5/5	0.82	0.06	119,135,146,149	0
2	PO4	D	801	5/5	0.83	0.09	90,101,105,106	0
2	PO4	D	802	5/5	0.83	0.09	102,116,121,125	0
2	PO4	B	801	5/5	0.84	0.08	76,95,107,108	0
3	SO4	C	803	5/5	0.86	0.08	113,117,118,130	0
3	SO4	A	804	5/5	0.86	0.07	103,105,123,125	0
3	SO4	D	805	5/5	0.86	0.08	125,128,143,147	0
2	PO4	C	802	5/5	0.87	0.06	112,115,121,132	0
2	PO4	A	801	5/5	0.88	0.05	95,102,108,110	0
3	SO4	B	803	5/5	0.89	0.04	108,125,126,127	0
3	SO4	A	803	5/5	0.90	0.08	98,107,116,118	0
2	PO4	A	802	5/5	0.92	0.05	87,89,98,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.